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(54) Title: NOVEL METHODS OF DIAGNOSING COLORECTAL CANCER, COMPOSITIONS, AND METHODS OF SCREENING FOR COLORECTAL CANCER MODULATORS (54) Titre: METHODES PERMETTANT DE DIAGNOSTIQUER DU CANCER COLO-RECTAL, COMPOSITIONS, ET METHODES PERMETTANT DE DETECTER DES MODULATEURS DU CANCER COLO-RECTAL (57) Abstract <p>Described herein are methods that can be used for diagnosis and prognosis of colorectal cancer. Also described herein are methods that can be used to screen candidate bioactive agents for the ability to modulate colorectal cancer. Additionally, methods and molecular targets (genes and their products) for therapeutic intervention in colorectal and other cancers are described.</p> (57) Abrégé <p>L'invention concerne des méthodes utiles pour le diagnostic et le pronostic du cancer colo-rectal. L'invention concerne également des méthodes permettant de détecter la capacité que possèdent des agents bioactifs candidats pour moduler un cancer colo-rectal. L'invention concerne en outre des méthodes et des cibles moléculaires (gènes et leurs produits) permettant d'effectuer une intervention thérapeutique pour lutter contre le cancer colo-rectal et d'autres types cancers.</p>		

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Described herein are methods that can be used for diagnosis and prognosis of colorectal cancer. Also described herein are methods that can be used to screen candidate bioactive agents for the ability to modulate colorectal cancer. Additionally, methods and molecular targets (genes and their products) for therapeutic intervention in colorectal and other cancers are described.

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Description

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**NOVEL METHODS OF DIAGNOSING COLORECTAL CANCER, COMPOSITIONS, AND
METHODS OF SCREENING FOR COLORECTAL CANCER MODULATORS**

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FIELD OF THE INVENTION

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The invention relates to the identification of expression profiles and the nucleic acids involved in colorectal cancer, and to the use of such expression profiles and nucleic acids in diagnosis and prognosis of colorectal cancer. The invention further relates to methods for identifying and using candidate agents and/or targets which modulate colorectal cancer.

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BACKGROUND OF THE INVENTION

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Colorectal cancer is a significant cancer in Western populations. It develops as the result of a pathologic transformation of normal colon epithelium to an invasive cancer. There have been a number of recently characterized genetic alterations that have been implicated in colorectal cancer, including mutations in two classes of genes, tumor-suppressor genes and proto-oncogenes, with recent work suggesting that mutations in DNA repair genes may also be involved in tumorigenesis. For example, inactivating mutations of both alleles of the adenomatous polyposis coli (APC) gene, a tumor suppressor gene, appears to be one of the earliest events in colorectal cancer, and may even be the initiating event. Other genes implicated in colorectal cancer include the MCC gene, the p53 gene, the DCC (deleted in colorectal carcinoma) gene and other chromosome 18q genes, and genes in the TGF- β signaling pathway. For a review, see Molecular Biology of Colorectal Cancer, pp238-299, in Curr. Probl. Cancer, Sept/Oct 1997.

Imaging of colorectal cancer for diagnosis has been problematic and limited. In addition, dissemination of tumor cells (metastases) to locoregional lymph nodes is an important prognostic factor; five year survival rates drop from 80 percent in patients with no lymph node metastases to 45 to 50 percent in those patients who do have lymph node metastases. A recent report showed that micrometastases can be detected from lymph nodes using reverse transcriptase-PCR methods based on the presence of mRNA for carcinoembryonic antigen, which has previously been shown to be present in the vast

majority of colorectal cancers but not in normal tissues. Liefers et al., New England J. of Med. 339(4):223 (1998).

Thus, methods that can be used for diagnosis and prognosis of colorectal cancer would be desirable. Accordingly, provided herein are methods that can be used in diagnosis and prognosis of colorectal cancer. Further provided are methods that can be used to screen candidate bioactive agents for the ability to modulate colorectal cancer. Additionally, provided herein are molecular targets for therapeutic intervention in colorectal and other cancers.

SUMMARY OF THE INVENTION

The present invention provides methods for screening for compositions which modulate colorectal cancer. Also provided herein are methods of inhibiting proliferation of cell, preferably a colorectal cancer cell. Methods of treatment of cancer, as well as compositions, are also provided herein.

In one aspect, a method of screening drug candidates comprises providing a cell that expresses an expression profile gene or fragments thereof. Preferred embodiments of the expression profile gene are genes which are differentially expressed in cancer cells, preferably colorectal cancer cells, compared to other cells. Preferred embodiments of expression profile genes used in the methods herein include but are not limited to the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7, CQA2, CGA8, CAA7 and CAA9; fragments of the proteins of this group are also preferred. It is understood that molecules for use in the present invention may be from any figure or any subset of listed molecules. Therefore, for example, any one or more of the genes listed above can be used in the methods herein. In another embodiment, a nucleic acid is selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14. Preferred nucleic acids are in Figure 12, more preferably Figure 13, and most preferably in Figure 14. The method further includes adding a drug candidate to the cell and determining the effect of the drug candidate on the expression of the expression profile gene.

In one embodiment, the method of screening drug candidates includes comparing the level of expression in the absence of the drug candidate to the level of expression in the presence of the drug candidate, wherein the concentration of the drug candidate can vary when present, and wherein the comparison can occur after addition or removal of the drug candidate. In a preferred embodiment, the cell expresses at least two expression profile genes. The profile genes may show an increase or decrease.

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Also provided herein is a method of screening for a bioactive agent capable of binding to a colorectal cancer modulator protein (CCMP), the method comprising combining the CCMP and a candidate bioactive agent, and determining the binding of the candidate agent to the CCMP. Preferably the CCMP is a protein or fragment thereof selected from the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7, CQA2, CGA8, CAA7 and CAA9. In another embodiment, the protein is encoded by a nucleic acid selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14. Preferred nucleic acids are in Figure 12, more preferably Figure 13, and most preferably in Figure 14.

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Further provided herein is a method for screening for a bioactive agent capable of modulating the activity of a CCMP. In one embodiment, the method comprises combining the CCMP and a candidate bioactive agent, and determining the effect of the candidate agent on the bioactivity of the CCMP. Preferably the CCMP is a protein or fragment thereof selected from the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7, CQA2, CGA8, CAA7 and CAA9. In another embodiment, the protein is encoded by a nucleic acid selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14. Preferred nucleic acids are in Figure 12, more preferably Figure 13, and most preferably in Figure 14.

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Also provided is a method of evaluating the effect of a candidate colorectal cancer drug comprising administering the drug to a transgenic animal expressing or over-expressing the CCMP, or an animal lacking the CCMP, for example as a result of a gene knockout.

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Additionally, provided herein is a method of evaluating the effect of a candidate colorectal cancer drug comprising administering the drug to a patient and removing a cell sample from the patient. The expression profile of the cell is then determined. This method may further comprise comparing the expression profile to an expression profile of a healthy individual.

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Moreover, provided herein is a biochip comprising a nucleic acid segment which encodes a colorectal cancer protein, preferably selected from the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7, CQA2, CGA8, CAA7 and CAA9, or a fragment thereof, wherein the biochip comprises fewer than 1000 nucleic acid probes. Preferably at least two nucleic acid segments are included. In another embodiment, the nucleic acid selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14. Preferred nucleic acids are in Figure 12, more preferably Figure 13, and most preferably in Figure 14.

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Furthermore, a method of diagnosing a disorder associated with colorectal cancer is provided. The method comprises determining the expression of a gene which encodes a colorectal cancer protein preferably selected from the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7, CQA2, CGA8, CAA7 and CAA9 or a fragment thereof in a first tissue type of a first individual, and comparing the distribution to the expression of the gene from a second normal tissue type from the first individual or a second unaffected individual. In another embodiment, the protein is encoded by a nucleic acid selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14. Preferred nucleic acids are in Figure 12, more preferably Figure 13, and most preferably in Figure 14. A difference in the expression indicates that the first individual has a disorder associated with colorectal cancer.

In another aspect, the present invention provides an antibody which specifically binds to a colorectal cancer protein, preferably selected from the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7, CQA2, CGA8, CAA7 and CAA9, or a fragment thereof. In another embodiment, the protein is encoded by a nucleic acid selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14. Preferred nucleic acids are in Figure 12, more preferably Figure 13, and most preferably in Figure 14. In a preferred embodiment, the fragment of CAA9 is selected from CAA9p1, CAA9p2, CAA9p3, CAA9p4, CAA9p4MAPS, CAA9p5 and CAA9p5MAPS. Other preferred fragments for the breast cancer proteins are shown in the figures. Preferably the antibody is a monoclonal antibody. The antibody can be a fragment of an antibody such as a single stranded antibody as further described herein, or can be conjugated to another molecule. In one embodiment, the antibody is a humanized antibody.

In one embodiment a method for screening for a bioactive agent capable of interfering with the binding of a colorectal cancer protein (CCMP) or a fragment thereof and an antibody which binds to said CCMP or fragment thereof. In a preferred embodiment, the method comprises combining a CCMP or fragment thereof, a candidate bioactive agent and an antibody which binds to said CCMP or fragment thereof. The method further includes determining the binding of said CCMP or fragment thereof and said antibody. Wherein there is a change in binding, an agent is identified as an interfering agent. The interfering agent can be an agonist or an antagonist. Preferably, the antibody as well as the agent inhibits colorectal cancer.

In a further aspect, a method for inhibiting colorectal cancer is provided. In one embodiment, the method comprises administering to a cell a composition comprising an antibody to a colorectal modulating protein, preferably selected from the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7, CQA2, CGA8, CAA7 and CAA9, or a fragment

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thereof. In another embodiment, the protein is encoded by a nucleic acid selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14. Preferred nucleic acids are in Figure 12, more preferably Figure 13, and most preferably in Figure 14. The method can be performed in vitro or in vivo, preferably in vivo to an individual. In a preferred embodiment the method of inhibiting colorectal cancer is provided to an individual with cancer. As described herein, methods of inhibiting colorectal cancer can be performed by administering an inhibitor of colorectal cancer protein activity, including antisense molecules, and preferably small molecules.

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Also provided herein are methods eliciting an immune response in an individual. In one embodiment a method provided herein comprises administering to an individual a composition comprising a colorectal modulating protein, preferably selected from the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7, CQA2, CGA8, CAA7 and CAA9, or a fragment thereof. In another embodiment, the protein is encoded by a nucleic acid selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14. Preferred nucleic acids are in Figure 12, more preferably Figure 13, and most preferably in Figure 14. In another aspect, said composition comprises a nucleic acid comprising a sequence encoding a colorectal cancer modulating protein, preferably selected from the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7, CQA2, CGA8, CAA7 and CAA9, or a fragment thereof. In another embodiment, the nucleic acid is selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14. Preferred nucleic acids are in Figure 12, more preferably Figure 13, and most preferably in Figure 14.

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Further provided herein are compositions capable of eliciting an immune response in an individual. In one embodiment, a composition provided herein comprises a colorectal cancer modulating protein, preferably selected from the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7, CQA2, CGA8, CAA7 and CAA9, or a fragment thereof, and a pharmaceutically acceptable carrier. In another embodiment, the protein is encoded by a nucleic acid selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14. Preferred nucleic acids are in Figure 12, more preferably Figure 13, and most preferably in Figure 14. In another embodiment, said composition comprises a nucleic acid comprising a sequence encoding a colorectal cancer modulating protein, preferably selected from the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7, CQA2, CGA8, CAA7 and CAA9, or a fragment thereof, and a pharmaceutically acceptable carrier. In another embodiment, the nucleic acid is selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14. Preferred nucleic acids are in Figure 12, more preferably Figure 13, and most preferably in Figure 14.

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DETAILED DESCRIPTION OF THE FIGURES

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A method of neutralizing the effect of a colorectal cancer protein, preferably selected from the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7, CQA2, CGA8, CAA7 and CAA9, or a fragment thereof, comprising contacting an agent specific for said protein with said protein in an amount sufficient to effect neutralization. In another embodiment, the protein is encoded by a nucleic acid selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14. Preferred nucleic acids are in Figure 12, more preferably Figure 13, and most preferably in Figure 14.

In another aspect of the invention, a method of treating an individual for colorectal cancer is provided. In one embodiment, the method comprises administering to said individual an inhibitor of CJA8. In another embodiment, the method comprises administering to a patient having colorectal cancer an antibody to CJA8 conjugated to a therapeutic moiety. Such a therapeutic moiety can be a cytotoxic agent or a radiolotope.

Also provided herein is a method for determining the prognosis of an individual with colorectal cancer comprising determining the level of CJA8 in a sample, wherein a high level of CJA8 indicates a poor prognosis.

Novel sequences are also provided herein. Other aspects of the invention will become apparent to the skilled artisan by the following description of the invention.

Figure 1 provides the Accession numbers for genes, including expression sequence tags, (incorporated in their entirety here and throughout the application where Accession numbers are provided), upregulated in tumor tissue compared to normal colon tissue.

Figure 2 provides the Accession numbers for genes, including expression sequence tags, upregulated in tumor tissue compared to normal colon tissue.

Figure 3 provides the Accession numbers for genes, including expression sequence tags, upregulated in tumor tissue compared to normal colon tissue.

Figure 4 provides the Accession numbers for genes, including expression sequence tags, upregulated in tumor tissue compared to normal colon tissue.

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Figure 5 provides the Accession numbers for genes, including expression sequence tags, downregulated in tumor tissue compared to normal colon tissue.

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Figure 6 provides the Accession numbers for genes, including expression sequence tags, downregulated in tumor tissue compared to normal colon tissue.

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Figure 8 provides the Accession numbers for genes, including expression sequence tags, upregulated in tumor tissue compared to normal colon tissue. Open reading frames in the sequences have been characterized as having a signal sequence (SS), a transmembrane domain (TM) or other.

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Figure 9 provides the Accession numbers for genes, including expression sequence tags, upregulated in tumor tissue compared to normal colon tissue. Open reading frames in the sequences have been characterized as having a signal sequence (SS), a transmembrane domain (TM) or other.

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Figure 10 provides the Accession numbers for genes, including expression sequence tags, upregulated in tumor tissue compared to normal colon tissue. Open reading frames have been characterized as having a signal sequence (SS), a transmembrane domain (TM) or other.

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Figure 11 provides the Accession numbers for genes, including expression sequence tags, upregulated in tumor tissue compared to normal colon tissue. Open reading frames have been characterized as having a signal sequence (SS), a transmembrane domain (TM) or other.

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Figure 12 provides the Accession numbers for genes, including expression sequence tags, upregulated in tumor tissue compared to normal colon tissue. Open reading frames have been characterized as having a signal sequence (SS), a transmembrane domain (TM) or other.

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Figure 13 provides the Accession numbers for genes or fragments thereof, including descriptions of the gene or encoded protein, upregulated in tumor tissue compared to normal colon tissue.

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Figure 14 provides a list of proteins, including Accession numbers for nucleic acid sequences associated with the encoding genes thereof, upregulated in tumor tissue compared to normal colon tissue.

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Figure 15 shows an embodiment of a nucleic acid which includes a sequence which encodes a colorectal protein provided herein, CAA2. The start and stop codon are shaded. The sequence within the two cross marks indicates a preferred novel fragment of CAA2 provided herein, referred to herein as the "CAA2 5' end". Preferred embodiments of CAA2 include at least a portion of the CAA2 5'. The sequence in bold and indicated with a bar at the bottom right beginning with "GGC" and ending with "AAA" can be found in Accession no. AA505133.

Figure 16 shows an embodiment of a nucleic acid encoding CAA2, wherein the start and stop codons are shaded.

Figure 17 shows an embodiment of an amino acid sequence of CAA2. Preferred fragments include at least about 10 amino acids in the N-terminal end. The N-terminus as defined herein includes an embodiment beginning at the first amino acid until about any one of the three amino acids marked with a dot above them. In another embodiment, the N-terminus of CAA2 is defined as the amino acid sequence encoded by the CAA2 5' end.

Figure 18 shows the amino acid sequence of CAA2p1, a preferred CAA2 fragment provided herein.

Figure 19 shows the amino acid sequence of CAA2p2, a preferred CAA2 fragment provided herein.

Figure 20 shows an alignment of the human and mouse CAA2 polypeptides provided herein. The mouse polypeptide contains at least some of the sequence of each of the following Accession numbers: AA386837; A1508773; AA505293; and AA636546.

Figure 21 shows the relative amount of expression of CAA2 in various samples of colon cancer tissue (dark bars) and many normal tissue types (light bars).

Figure 22 shows an embodiment of a colorectal cancer nucleic acid, CAA9 mRNA. The start and stop codons are underlined.

Figure 23 shows the open reading frame of the CAA9 gene wherein the start and stop codons are underlined.

Figure 24 shows an embodiment of the amino acid sequence of a colorectal cancer protein, CAA9, wherein putative transmembrane sequences are underlined. In one embodiment, CAA9 or fragments

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of CAA9 are soluble, therefore, the transmembrane domains are deleted, inactivated, and/or the peptide is truncated (with or without re-ligation) to form soluble CAA9.

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Figure 25 shows embodiments of colorectal cancer proteins (also termed colorectal cancer modulator proteins). Specifically, Figure 25 shows CAA9p1, CAA9p2, CAA9p3, CAA9p4, CAA9p4MAPS, CAA9p5 and CAA9p5MAPS and their respective solubilities.

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Figure 26 shows the relative amount of CAA9 expression in several different samples of colon cancer tissue (dark bars) and normal tissues (light bars).

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Figure 27 shows the nucleic acid sequence for the gene encoding CGA7. Start (ATG) and stop (TAG) codons are indicated by shaded boxes. In bold is the sequence of Accession No. AA331393. Underlined is the consensus sequence derived from the compilation and alignment of published est sequences.

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Figures 28A and 28B show the alignment summary and descriptions, respectively, of the various est's (by accession number) compiled to generate the consensus sequence of figure 1.

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Figure 29 shows the amino acid sequence of CGA7.

Figures 30A and 30B show the relative expression of CGA7 in normal tissue and colon cancer tissue, respectively.

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Figure 31 shows the nucleic acid sequence for the mRNA encoding CGA8. Start (ATG) and stop (TAG) codons are indicated by shaded boxes. In bold is the sequence of Accession No. AA2786503. Underlined is the consensus sequence derived from the compilation and alignment of published est sequences.

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Figures 32A and 32B show the alignment summary and descriptions, respectively, of the various est's (by accession number) compiled to generate the consensus sequence of figure 1.

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Figure 33 shows the amino acid sequence of CGA8.

Figure 34 shows the relative expression of CGA8 in breast cancer tissue, colon cancer tissue, normal tissue and fetal tissue.

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Figure 35 shows the sequence for the mRNA encoding CJA8. Start (ATG) and stop (TAA) codons are indicated by shaded boxes.

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Figure 36 shows the amino acid sequence for CJA8. A putative transmembrane region is designated by shading. A mouse homolog of this human protein is found at Accession Number AAF21308.1.

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5 Figure 37 shows the relative amount of expression of CJA8 in several different samples of colon tissues (dark bars) and normal tissues (light bars).

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Figure 38 shows the relative amount of expression of BCN7 in several different samples of colon tissues (dark bars) and normal tissues (light bars), as determined using the sequence of Accession Number N22107 as a probe.

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Figure 39 shows an embodiment of a nucleic acid which includes a sequence which encodes a colorectal cancer protein provided herein, BCN7.

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Figure 40 shows the sequence for the mRNA encoding CZA8. Start (ATG) and stop (TGA) codons are indicated by underlining.

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Figure 41 shows the sequence for the mRNA encoding BCX2. Start (ATG) and stop (TGA) codons are indicated by underlining.

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Figure 42 shows the sequence for the mRNA encoding CBC2. Start (ATG) and stop (TAA) codons are indicated by underlining.

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Figure 44 shows the sequence for the mRNA encoding CBC3. Start (ATG) and stop (TGA) codons are indicated by underlining.

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Figure 45 shows the sequence for the mRNA encoding BCN5. Start (ATG) and stop (TAA) codons are indicated by underlining.

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Figure 46 shows an embodiment of a nucleic acid which includes a sequence which encodes a colorectal cancer protein provided herein, CJA9.

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Figure 47 shows an embodiment of a nucleic acid which includes a sequence which encodes a colorectal cancer protein provided herein, CQA1.

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Figure 48 shows an embodiment of a nucleic acid which includes a sequence which encodes a colorectal cancer protein provided herein, CQA2.

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DETAILED DESCRIPTION OF THE INVENTION

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The present invention provides novel methods for diagnosis and prognosis evaluation for colorectal cancer (CRC), as well as methods for screening for compositions which modulate CRC. In one aspect, the expression levels of genes are determined in different patient samples for which either diagnosis or prognosis information is desired, to provide expression profiles. An expression profile of a particular sample is essentially a "fingerprint" of the state of the sample; while two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is unique to the state of the cell. That is, normal tissue may be distinguished from CRC tissue, and within CRC tissue, different prognosis states (good or poor long term survival prospects, for example) may be determined. By comparing expression profiles of colon tissue in known different states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. The identification of sequences that are differentially expressed in CRC versus normal colon tissue, as well as differential expression resulting in different prognostic outcomes, allows the use of this information in a number of ways. For example, the evaluation of a particular treatment regime may be evaluated: does a chemotherapeutic drug act to improve the long-term prognosis in a particular patient. Similarly, diagnosis may be done or confirmed by comparing patient samples with the known expression profiles. Furthermore, these gene expression profiles (or individual genes) allow screening of drug candidates with an eye to mimicking or altering a particular expression profile; for example, screening can be done for drugs that suppress the CRC expression profile or convert a poor prognosis profile to a better prognosis profile. This may be done by making biochips comprising sets of the important CRC genes, which can then be used in these screens. These methods can also be done on the protein basis; that is, protein expression levels of the CRC proteins can be evaluated for diagnostic and prognostic purposes or to screen candidate agents. In addition, the CRC nucleic acid sequences can be administered for gene therapy purposes, including the administration of antisense nucleic acids, or the CRC proteins (including antibodies and other modulators thereof) administered as therapeutic drugs.

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Thus the present invention provides nucleic acid and protein sequences that are differentially expressed in colorectal cancer, CRC, herein termed "CRC sequences". As outlined below, CRC sequences include those that are up-regulated (i.e. expressed at a higher level) in CRC, as well as those that are down-regulated (i.e. expressed at a lower level) in CRC. In a preferred embodiment, the CRC sequences are from humans; however, as will be appreciated by those in the art, CRC sequences from other organisms may be useful in animal models of disease and drug evaluation; thus, other CRC sequences are provided, from vertebrates, including mammals, including rodents (rats, mice, hamsters, guinea pigs, etc.), primates, farm animals (including sheep, goats, pigs, cows, horses, etc). CRC sequences from other organisms may be obtained using the techniques outlined below.

CRC sequences can include both nucleic acid and amino acid sequences. In a preferred embodiment, the CRC sequences are recombinant nucleic acids. By the term "recombinant nucleic acid" herein is meant nucleic acid, originally formed in vitro, in general, by the manipulation of nucleic acid by polymerases and endonucleases, in a form not normally found in nature. Thus an isolated nucleic acid, in a linear form, or an expression vector formed in vitro by ligating DNA molecules that are not normally joined, are both considered recombinant for the purposes of this invention. It is understood that once a recombinant nucleic acid is made and reintroduced into a host cell or organism, it will replicate non-recombinantly, i.e. using the in vivo cellular machinery of the host cell rather than in vitro manipulations; however, such nucleic acids, once produced recombinantly, although subsequently replicated non-recombinantly, are still considered recombinant for the purposes of the invention.

Similarly, a "recombinant protein" is a protein made using recombinant techniques, i.e. through the expression of a recombinant nucleic acid as depicted above. A recombinant protein is distinguished from naturally occurring protein by at least one or more characteristics. For example, the protein may be isolated or purified away from some or all of the proteins and compounds with which it is normally associated in its wild type host, and thus may be substantially pure. For example, an isolated protein is unaccompanied by at least some of the material with which it is normally associated in its natural state, preferably constituting at least about 0.5%, more preferably at least about 5% by weight of the total protein in a given sample. A substantially pure protein comprises at least about 75% by weight of the total protein, with at least about 80% being preferred, and at least about 90% being particularly preferred. The definition includes the production of a CRC protein from one organism in a different organism or host cell. Alternatively, the protein may be made at a significantly higher concentration than is normally seen, through the use of an inducible promoter or high expression promoter, such that the protein is made at increased concentration levels. Alternatively, the protein may be in a form

not normally found in nature, as in the addition of an epitope tag or amino acid substitutions, insertions and deletions, as discussed below.

In a preferred embodiment, the CRC sequences are nucleic acids. As will be appreciated by those in the art and is more fully outlined below, CRC sequences are useful in a variety of applications, including diagnostic applications, which will detect naturally occurring nucleic acids, as well as screening applications; for example, biochips comprising nucleic acid probes to the CRC sequences can be generated. In the broadest sense, then, by "nucleic acid" or "oligonucleotide" or grammatical equivalents herein means at least two nucleotides covalently linked together. A nucleic acid of the present invention will generally contain phosphodiester bonds, although in some cases, as outlined below, nucleic acid analogs are included that may have alternate backbones, comprising, for example, phosphoramidate (Beaucage et al., *Tetrahedron* 49(10):1925 (1993) and references therein; Letsinger, *J. Org. Chem.* 35:3800 (1970); Sprinzi et al., *Eur. J. Biochem.* 81:579 (1977); Letsinger et al., *Nucl. Acids Res.* 14:3487 (1986); Sawai et al, *Chem. Lett.* 805 (1984), Letsinger et al., *J. Am. Chem. Soc.* 110:4470 (1988); and Pauwels et al., *Chemica Scripta* 26:141 (1986)), phosphorothioate (Mag et al., *Nucleic Acids Res.* 19:1437 (1991); and U.S. Patent No. 5,644,048), phosphorodithioate (Briu et al., *J. Am. Chem. Soc.* 111:2321 (1989), O-methylphosphoramidite linkages (see Eckstein, *Oligonucleotides and Analogues: A Practical Approach*, Oxford University Press), and peptide nucleic acid backbones and linkages (see Egholm, *J. Am. Chem. Soc.* 114:1895 (1992); Meier et al., *Chem. Int. Ed. Engl.* 31:1008 (1992); Nielsen, *Nature*, 365:566 (1993); Carlsson et al., *Nature* 380:207 (1996), all of which are incorporated by reference). Other analog nucleic acids include those with positive backbones (Denpcy et al., *Proc. Natl. Acad. Sci. USA* 92:6097 (1995); non-ionic backbones (U.S. Patent Nos. 5,386,023, 5,637,684, 5,602,240, 5,216,141 and 4,469,863; Kiedrowski et al., *Angew. Chem. Intl. Ed. English* 30:423 (1991); Letsinger et al., *J. Am. Chem. Soc.* 110:4470 (1988); Letsinger et al., *Nucleoside & Nucleotide* 13:1597 (1994); Chapters 2 and 3, *ASC Symposium Series* 580, "Carbohydrate Modifications in Antisense Research", Ed. Y.S. Sanghui and P. Dan Cook; Mesmaeker et al., *Bioorganic & Medicinal Chem. Lett.* 4:395 (1994); Jeffs et al., *J. Biomolecular NMR* 34:17 (1994); *Tetrahedron Lett.* 37:743 (1996)) and non-ribose backbones, including those described in U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7, *ASC Symposium Series* 580, "Carbohydrate Modifications in Antisense Research", Ed. Y.S. Sanghui and P. Dan Cook. Nucleic acids containing one or more carbocyclic sugars are also included within one definition of nucleic acids (see Jenkins et al., *Chem. Soc. Rev.* (1995) pp169-176). Several nucleic acid analogs are described in Rawls, *C & E News* June 2, 1997 page 35. All of these references are hereby expressly incorporated by reference. These modifications of the ribose-phosphate backbone may be done for a variety of reasons, for example to increase the stability and half-life of such molecules in physiological environments or as probes on a biochip.

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As will be appreciated by those in the art, all of these nucleic acid analogs may find use in the present invention. In addition, mixtures of naturally occurring nucleic acids and analogs can be made; alternatively, mixtures of different nucleic acid analogs, and mixtures of naturally occurring nucleic acids and analogs may be made.

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5 Particularly preferred are peptide nucleic acids (PNA) which includes peptide nucleic acid analogs. These backbones are substantially non-ionic under neutral conditions, in contrast to the highly charged phosphodiester backbone of naturally occurring nucleic acids. This results in two advantages. First, the PNA backbone exhibits improved hybridization kinetics. PNAs have larger changes in the melting temperature (T_m) for mismatched versus perfectly matched basepairs. DNA and RNA typically exhibit a 2-4°C drop in T_m for an internal mismatch. With the non-ionic PNA backbone, the drop is closer to 7-9°C. Similarly, due to their non-ionic nature, hybridization of the bases attached to these backbones is relatively insensitive to salt concentration. In addition, PNAs are not degraded by cellular enzymes, and thus can be more stable.

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15 The nucleic acids may be single stranded or double stranded, as specified, or contain portions of both double stranded or single stranded sequence. As will be appreciated by those in the art, the depiction of a single strand ("Watson") also defines the sequence of the other strand ("Crick"); thus the sequences described herein also includes the complement of the sequence. The nucleic acid may be DNA, both genomic and cDNA, RNA or a hybrid, where the nucleic acid contains any combination of deoxyribo- and ribo-nucleotides, and any combination of bases, including uracil, adenine, thymine, cytosine, guanine, inosine, xanthine hypoxanthine, isocytosine, isoguanine, etc. As used herein, the term "nucleoside" includes nucleotides and nucleoside and nucleotide analogs, and modified nucleosides such as amino modified nucleosides. In addition, "nucleoside" includes non-naturally occurring analog structures. Thus for example the individual units of a peptide nucleic acid, each containing a base, are referred to herein as a nucleoside.

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25 A CRC sequence can be initially identified by substantial nucleic acid and/or amino acid sequence homology to the CRC sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions.

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30 The CRC sequences of the invention can be identified as follows. Samples of normal and tumor tissue are applied to biochips comprising nucleic acid probes. The samples are first microdissected, if applicable, and treated as is known in the art for the preparation of mRNA. Suitable biochips are

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commercially available, for example from Affymetrix. Gene expression profiles as described herein are generated, and the data analyzed.

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In a preferred embodiment, the genes showing changes in expression as between normal and disease states are compared to genes expressed in other normal tissues, including, but not limited to lung, heart, brain, liver, breast, kidney, muscle, prostate, small intestine, large intestine, spleen, bone, and placenta. In a preferred embodiment, those genes identified during the CRC screen that are expressed in any significant amount in other tissues are removed from the profile, although in some embodiments, this is not necessary. That is, when screening for drugs, it is preferable that the target be disease specific, to minimize possible side effects.

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10 In a preferred embodiment, CRC sequences are those that are up-regulated in CRC; that is, the expression of these genes is higher in colorectal carcinoma as compared to normal colon tissue. "Up-regulation" as used herein means at least about a two-fold change, preferably at least about a three fold change, with at least about five-fold or higher being preferred. All accession numbers herein are for the GenBank sequence database and the sequences of the accession numbers are hereby expressly incorporated by reference. GenBank is known in the art, see, e.g., Benson, DA, et al., Nucleic Acids Research 26:1-7 (1998) and <http://www.ncbi.nlm.nih.gov/>. In addition, these genes were found to be expressed in a limited amount or not at all in heart, brain, lung, liver, breast, kidney, prostate, small intestine and spleen.

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20 In a preferred embodiment, CRC sequences are those that are down-regulated in CRC; that is, the expression of these genes is lower in colorectal carcinoma as compared to normal colon tissue. "Down-regulation" as used herein means at least about a two-fold change, preferably at least about a three fold change, with at least about five-fold or higher being preferred.

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CRC proteins of the present invention may be classified as secreted proteins, transmembrane proteins or intracellular proteins. In a preferred embodiment the CRC protein is an intracellular protein. Intracellular proteins may be found in the cytoplasm and/or in the nucleus. Intracellular proteins are involved in all aspects of cellular function and replication (including, for example, signaling pathways); aberrant expression of such proteins results in unregulated or disregulated cellular processes. For example, many intracellular proteins have enzymatic activity such as protein kinase activity, protein phosphatase activity, protease activity, nucleotide cyclase activity, polymerase activity and the like. Intracellular proteins also serve as docking proteins that are involved in organizing complexes of proteins, or targeting proteins to various subcellular localizations, and are involved in maintaining the structural integrity of organelles.

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An increasingly appreciated concept in characterizing intracellular proteins is the presence in the proteins of one or more motifs for which defined functions have been attributed. In addition to the highly conserved sequences found in the enzymatic domain of proteins, highly conserved sequences have been identified in proteins that are involved in protein-protein interaction. For example, Src-homology-2 (SH2) domains bind tyrosine-phosphorylated targets in a sequence dependent manner. PTB domains, which are distinct from SH2 domains, also bind tyrosine phosphorylated targets. SH3 domains bind to proline-rich targets. In addition, PH domains, tetratricopeptide repeats and WD domains to name only a few, have been shown to mediate protein-protein interactions. Some of these may also be involved in binding to phospholipids or other second messengers. As will be appreciated by one of ordinary skill in the art, these motifs can be identified on the basis of primary sequence; thus, an analysis of the sequence of proteins may provide insight into both the enzymatic potential of the molecule and/or molecules with which the protein may associate.

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In a preferred embodiment, the CRC sequences are transmembrane proteins. Transmembrane proteins are molecules that span the phospholipid bilayer of a cell. They may have an intracellular domain, an extracellular domain, or both. The intracellular domains of such proteins may have a number of functions including those already described for intracellular proteins. For example, the intracellular domain may have enzymatic activity and/or may serve as a binding site for additional proteins. Frequently the intracellular domain of transmembrane proteins serves both roles. For example certain receptor tyrosine kinases have both protein kinase activity and SH2 domains. In addition, autophosphorylation of tyrosines on the receptor molecule itself, creates binding sites for additional SH2 domain containing proteins.

Transmembrane proteins may contain from one to many transmembrane domains. For example, receptor tyrosine kinases, certain cytokine receptors, receptor guanylyl cyclases and receptor serine/threonine protein kinases contain a single transmembrane domain. However, various other proteins including channels and adenylyl cyclases contain numerous transmembrane domains. Many important cell surface receptors are classified as "seven transmembrane domain" proteins, as they contain 7 membrane spanning regions. Important transmembrane protein receptors include, but are not limited to insulin receptor, insulin-like growth factor receptor, human growth hormone receptor, glucose transporters, transferrin receptor, epidermal growth factor receptor, low density lipoprotein receptor, epidermal growth factor receptor, leptin receptor, interleukin receptors, e.g. IL-1 receptor, IL-2 receptor, etc.

Characteristics of transmembrane domains include approximately 20 consecutive hydrophobic amino acids that may be followed by charged amino acids. Therefore, upon analysis of the amino acid

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sequence of a particular protein, the localization and number of transmembrane domains within the protein may be predicted.

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The extracellular domains of transmembrane proteins are diverse; however, conserved motifs are found repeatedly among various extracellular domains. Conserved structure and/or functions have been ascribed to different extracellular motifs. For example, cytokine receptors are characterized by a cluster of cysteines and a WSXWS (W= tryptophan, S= serine, X=any amino acid) motif. Immunoglobulin-like domains are highly conserved. Mucin-like domains may be involved in cell adhesion and leucine-rich repeats participate in protein-protein interactions.

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Many extracellular domains are involved in binding to other molecules. In one aspect, extracellular domains are receptors. Factors that bind the receptor domain include circulating ligands, which may be peptides, proteins, or small molecules such as adenosine and the like. For example, growth factors such as EGF, FGF and PDGF are circulating growth factors that bind to their cognate receptors to initiate a variety of cellular responses. Other factors include cytokines, mitogenic factors, neurotrophic factors and the like. Extracellular domains also bind to cell-associated molecules. In this respect, they mediate cell-cell interactions. Cell-associated ligands can be tethered to the cell for example via a glycosylphosphatidylinositol (GPI) anchor, or may themselves be transmembrane proteins. Extracellular domains also associate with the extracellular matrix and contribute to the maintenance of the cell structure.

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CRC proteins that are transmembrane are particularly preferred in the present invention as they are good targets for immunotherapeutics, as are described herein. In addition, as outlined below, transmembrane proteins can be also useful in imaging modalities.

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It will also be appreciated by those in the art that a transmembrane protein can be made soluble by removing transmembrane sequences, for example through recombinant methods. Furthermore, transmembrane proteins that have been made soluble can be made to be secreted through recombinant means by adding an appropriate signal sequence.

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In a preferred embodiment, the CRC proteins are secreted proteins; the secretion of which can be either constitutive or regulated. These proteins have a signal peptide or signal sequence that targets the molecule to the secretory pathway. Secreted proteins are involved in numerous physiological events; by virtue of their circulating nature, they serve to transmit signals to various other cell types. The secreted protein may function in an autocrine manner (acting on the cell that secreted the factor), a paracrine manner (acting on cells in close proximity to the cell that secreted the factor) or an

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endocrine manner (acting on cells at a distance). Thus secreted molecules find use in modulating or altering numerous aspects of physiology. CRC proteins that are secreted proteins are particularly preferred in the present invention as they serve as good targets for diagnostic markers, for example for blood tests.

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5 A CRC sequence is initially identified by substantial nucleic acid and/or amino acid sequence homology to the CRC sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions.

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As used herein, a nucleic acid is a "CRC nucleic acid" if the overall homology of the nucleic acid sequence to the nucleic acid sequences encoding the amino acid sequences of the figures is preferably greater than about 75%, more preferably greater than about 80%, even more preferably greater than about 85% and most preferably greater than 90%. In some embodiments the homology will be as high as about 93 to 95 or 98%. Homology in this context means sequence similarity or identity, with identity being preferred. A preferred comparison for homology purposes is to compare the sequence containing sequencing errors to the correct sequence. This homology will be determined using standard techniques known in the art, including, but not limited to, the local homology algorithm of Smith & Waterman, Adv. Appl. Math. 2:482 (1981), by the homology alignment algorithm of Needleman & Wunsch, J. Mol. Biol. 48:443 (1970), by the search for similarity method of Pearson & Lipman, PNAS USA 85:2444 (1988), by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Drive, Madison, WI), the Best Fit sequence program described by Devereux et al., Nucl. Acid Res. 12:387-395 (1984), preferably using the default settings, or by inspection.

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In a preferred embodiment, the sequences which are used to determine sequence identity or similarity are selected from the sequences set forth in the figures, preferably those represented in Figure 12, more preferably those represented in Figures 13A and 13B, still more preferably those of Figures 14-20, 22-25, 27-29, 31-33, 35-37 and 39-48, and fragments thereof. In one embodiment the sequences utilized herein are those set forth in the figures. In another embodiment, the sequences are naturally occurring allelic variants of the sequences set forth in the figures. In another embodiment, the sequences are sequence variants as further described herein.

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One example of a useful algorithm is PILEUP. PILEUP creates a multiple sequence alignment from a group of related sequences using progressive, pairwise alignments. It can also plot a tree showing the

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clustering relationships used to create the alignment. PILEUP uses a simplification of the progressive alignment method of Feng & Doolittle, J. Mol. Evol. 35:351-360 (1987); the method is similar to that described by Higgins & Sharp CABIOS 5:151-153 (1989). Useful PILEUP parameters including a default gap weight of 3.00, a default gap length weight of 0.10, and weighted end gaps.

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5 Another example of a useful algorithm is the BLAST algorithm, described in Altschul et al., J. Mol. Biol. 215, 403-410, (1990) and Karlin et al., PNAS USA 90:5873-5787 (1993). A particularly useful BLAST
15 program is the WU-BLAST-2 program which was obtained from Altschul et al., Methods in Enzymology, 266: 460-480 (1996); [http://blast.wustl.edu/blast/ REACRCE.html](http://blast.wustl.edu/blast/REACRCE.html)]. WU-BLAST-2 uses several search parameters, most of which are set to the default values. The adjustable parameters
20 are set with the following values: overlap span = 1, overlap fraction = 0.125, word threshold (T) = 11. The HSP S and HSP S2 parameters are dynamic values and are established by the program itself depending upon the composition of the particular sequence and composition of the particular
25 database against which the sequence of interest is being searched; however, the values may be adjusted to increase sensitivity. A % amino acid sequence identity value is determined by the number of matching identical residues divided by the total number of residues of the "longer" sequence in the
30 aligned region. The "longer" sequence is the one having the most actual residues in the aligned region (gaps introduced by WU-Blast-2 to maximize the alignment score are ignored).

Thus, "percent (%) nucleic acid sequence identity" is defined as the percentage of nucleotide residues
35 in a candidate sequence that are identical with the nucleotide residues of the sequences of the figures. A preferred method utilizes the BLASTN module of WU-BLAST-2 set to the default parameters, with
40 overlap span and overlap fraction set to 1 and 0.125, respectively.

The alignment may include the introduction of gaps in the sequences to be aligned. In addition, for
45 sequences which contain either more or fewer nucleosides than those of the figures, it is understood that the percentage of homology will be determined based on the number of homologous nucleosides
50 in relation to the total number of nucleosides. Thus, for example, homology of sequences shorter than those of the sequences identified herein and as discussed below, will be determined using the number
55 of nucleosides in the shorter sequence.

In one embodiment, the nucleic acid homology is determined through hybridization studies. Thus, for
55 example, nucleic acids which hybridize under high stringency to the nucleic acid sequences which encode the peptides identified in the figures, or their complements, are considered a CRC sequence. High stringency conditions are known in the art; see for example Maniatis et al., Molecular Cloning: A Laboratory Manual, 2d Edition, 1989, and Short Protocols in Molecular Biology, ed. Ausubel, et al.,

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both of which are hereby incorporated by reference. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. An extensive guide to the hybridization of nucleic acids is found in Tijssen, *Techniques in Biochemistry and Molecular Biology--Hybridization with Nucleic Acid Probes*, "Overview of principles of hybridization and the strategy of nucleic acid assays" (1993). Generally, stringent conditions are selected to be about 5-10°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength pH. The T_m is the temperature (under defined ionic strength, pH and nucleic acid concentration) at which 50% of the probes complementary to the target hybridize to the target sequence at equilibrium (as the target sequences are present in excess, at T_m, 50% of the probes are occupied at equilibrium). Stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30°C for short probes (e.g. 10 to 50 nucleotides) and at least about 60°C for long probes (e.g. greater than 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide.

15 In another embodiment, less stringent hybridization conditions are used; for example, moderate or low stringency conditions may be used, as are known in the art; see Maniatis and Ausubel, *supra*, and Tijssen, *supra*.

20 In addition, the CRC nucleic acid sequences of the invention are fragments of larger genes, i.e. they are nucleic acid segments. "Genes" in this context includes coding regions, non-coding regions, and mixtures of coding and non-coding regions. Accordingly, as will be appreciated by those in the art, using the sequences provided herein, additional sequences of the CRC genes can be obtained, using techniques well known in the art for cloning either longer sequences or the full length sequences; see Maniatis et al., and Ausubel, et al., *supra*, hereby expressly incorporated by reference.

25 Once the CRC nucleic acid is identified, it can be cloned and, if necessary, its constituent parts recombined to form the entire CRC nucleic acid. Once isolated from its natural source, e.g., contained within a plasmid or other vector or excised therefrom as a linear nucleic acid segment, the recombinant CRC nucleic acid can be further-used as a probe to identify and isolate other CRC nucleic acids, for example additional coding regions. It can also be used as a "precursor" nucleic acid to make modified or variant CRC nucleic acids and proteins.

30 The CRC nucleic acids of the present invention are used in several ways. In a first embodiment, nucleic acid probes to the CRC nucleic acids are made and attached to biochips to be used in screening and diagnostic methods, as outlined below, or for administration, for example for gene

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therapy and/or antisense applications. Alternatively, the CRC nucleic acids that include coding regions of CRC proteins can be put into expression vectors for the expression of CRC proteins, again either for screening purposes or for administration to a patient.

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5 In a preferred embodiment, nucleic acid probes to CRC nucleic acids (both the nucleic acid sequences encoding peptides outlined in the figures and/or the complements thereof) are made. The
15 nucleic acid probes attached to the biochip are designed to be substantially complementary to the CRC nucleic acids, i.e. the target sequence (either the target sequence of the sample or to other probe sequences, for example in sandwich assays), such that hybridization of the target sequence and the probes of the present invention occurs. As outlined below, this complementarity need not be
20 perfect; there may be any number of base pair mismatches which will interfere with hybridization between the target sequence and the single stranded nucleic acids of the present invention. However, if the number of mutations is so great that no hybridization can occur under even the least stringent of hybridization conditions, the sequence is not a complementary target sequence. Thus, by
25 "substantially complementary" herein is meant that the probes are sufficiently complementary to the target sequences to hybridize under normal reaction conditions, particularly high stringency conditions, as outlined herein.

A nucleic acid probe is generally single stranded but can be partially single and partially double
30 stranded. The strandedness of the probe is dictated by the structure, composition, and properties of the target sequence. In general, the nucleic acid probes range from about 8 to about 100 bases long, with from about 10 to about 80 bases being preferred, and from about 30 to about 50 bases being
35 particularly preferred. That is, generally whole genes are not used. In some embodiments, much longer nucleic acids can be used, up to hundreds of bases.

In a preferred embodiment, more than one probe per sequence is used, with either overlapping
40 probes or probes to different sections of the target being used. That is, two, three, four or more probes, with three being preferred, are used to build in a redundancy for a particular target. The probes can be overlapping (i.e. have some sequence in common), or separate.

As will be appreciated by those in the art, nucleic acids can be attached or immobilized to a solid
45 support in a wide variety of ways. By "immobilized" and grammatical equivalents herein is meant the association or binding between the nucleic acid probe and the solid support is sufficient to be stable under the conditions of binding, washing, analysis, and removal as outlined below. The binding can be
50 covalent or non-covalent. By "non-covalent binding" and grammatical equivalents herein is meant one or more of either electrostatic, hydrophilic, and hydrophobic interactions. Included in non-covalent

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binding is the covalent attachment of a molecule, such as, streptavidin to the support and the non-covalent binding of the biotinylated probe to the streptavidin. By "covalent binding" and grammatical equivalents herein is meant that the two moieties, the solid support and the probe, are attached by at least one bond, including sigma bonds, pi bonds and coordination bonds. Covalent bonds can be formed directly between the probe and the solid support or can be formed by a cross linker or by inclusion of a specific reactive group on either the solid support or the probe or both molecules. Immobilization may also involve a combination of covalent and non-covalent interactions.

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In general, the probes are attached to the biochip in a wide variety of ways, as will be appreciated by those in the art. As described herein, the nucleic acids can either be synthesized first, with subsequent attachment to the biochip, or can be directly synthesized on the biochip.

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The biochip comprises a suitable solid substrate. By "substrate" or "solid support" or other grammatical equivalents herein is meant any material that can be modified to contain discrete individual sites appropriate for the attachment or association of the nucleic acid probes and is amenable to at least one detection method. As will be appreciated by those in the art, the number of possible substrates are very large, and include, but are not limited to, glass and modified or functionalized glass, plastics (including acrylics, polystyrene and copolymers of styrene and other materials, polypropylene, polyethylene, polybutylene, polyurethanes, TeflonJ, etc.), polysaccharides, nylon or nitrocellulose, resins, silica or silica-based materials including silicon and modified silicon, carbon, metals, inorganic glasses, plastics, etc. In general, the substrates allow optical detection and do not appreciably fluoresce. A preferred substrate is described in copending application entitled Reusable Low Fluorescent Plastic Biochip, U.S. Application Serial No. 09/270,214, filed March 15, 1999, herein incorporated by reference in its entirety.

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Generally the substrate is planar, although as will be appreciated by those in the art, other configurations of substrates may be used as well. For example, the probes may be placed on the inside surface of a tube, for flow-through sample analysis to minimize sample volume. Similarly, the substrate may be flexible, such as a flexible foam, including closed cell foams made of particular plastics.

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In a preferred embodiment, the surface of the biochip and the probe may be derivatized with chemical functional groups for subsequent attachment of the two. Thus, for example, the biochip is derivatized with a chemical functional group including, but not limited to, amino groups, carboxy groups, oxo groups and thiol groups, with amino groups being particularly preferred. Using these functional groups, the probes can be attached using functional groups on the probes. For example, nucleic

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acids containing amino groups can be attached to surfaces comprising amino groups, for example using linkers as are known in the art; for example, homo- or hetero-bifunctional linkers as are well known (see 1994 Pierce Chemical Company catalog, technical section on cross-linkers, pages 155-200, incorporated herein by reference). In addition, in some cases, additional linkers, such as alkyl groups (including substituted and heteroalkyl groups) may be used.

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In this embodiment, the oligonucleotides are synthesized as is known in the art, and then attached to the surface of the solid support. As will be appreciated by those skilled in the art, either the 5' or 3' terminus may be attached to the solid support, or attachment may be via an internal nucleoside.

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In an additional embodiment, the immobilization to the solid support may be very strong, yet non-covalent. For example, biotinylated oligonucleotides can be made, which bind to surfaces covalently coated with streptavidin, resulting in attachment.

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Alternatively, the oligonucleotides may be synthesized on the surface, as is known in the art. For example, photoactivation techniques utilizing photopolymerization compounds and techniques are used. In a preferred embodiment, the nucleic acids can be synthesized in situ, using well known photolithographic techniques, such as those described in WO 95/25116; WO 95/35505; U.S. Patent Nos. 5,700,637 and 5,445,934; and references cited within, all of which are expressly incorporated by reference; these methods of attachment form the basis of the Affimetrix GeneChip™ technology.

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In a preferred embodiment, CRC nucleic acids encoding CRC proteins are used to make a variety of expression vectors to express CRC proteins which can then be used in screening assays, as described below. The expression vectors may be either self-replicating extrachromosomal vectors or vectors which integrate into a host genome. Generally, these expression vectors include transcriptional and translational regulatory nucleic acid operably linked to the nucleic acid encoding the CRC protein. The term "control sequences" refers to DNA sequences necessary for the expression of an operably linked coding sequence in a particular host organism. The control sequences that are suitable for prokaryotes, for example, include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

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Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the

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sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is accomplished by ligation at convenient restriction sites. If such sites do not exist, the synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice. The transcriptional and translational regulatory nucleic acid will generally be appropriate to the host cell used to express the CRC protein; for example, transcriptional and translational regulatory nucleic acid sequences from *Bacillus* are preferably used to express the CRC protein in *Bacillus*. Numerous types of appropriate expression vectors, and suitable regulatory sequences are known in the art for a variety of host cells.

In general, the transcriptional and translational regulatory sequences may include, but are not limited to, promoter sequences, ribosomal binding sites, transcriptional start and stop sequences, translational start and stop sequences, and enhancer or activator sequences. In a preferred embodiment, the regulatory sequences include a promoter and transcriptional start and stop sequences.

Promoter sequences encode either constitutive or inducible promoters. The promoters may be either naturally occurring promoters or hybrid promoters. Hybrid promoters, which combine elements of more than one promoter, are also known in the art, and are useful in the present invention.

In addition, the expression vector may comprise additional elements. For example, the expression vector may have two replication systems, thus allowing it to be maintained in two organisms, for example in mammalian or insect cells for expression and in a procaryotic host for cloning and amplification. Furthermore, for integrating expression vectors, the expression vector contains at least one sequence homologous to the host cell genome, and preferably two homologous sequences which flank the expression construct. The integrating vector may be directed to a specific locus in the host cell by selecting the appropriate homologous sequence for inclusion in the vector. Constructs for integrating vectors are well known in the art.

In addition, in a preferred embodiment, the expression vector contains a selectable marker gene to allow the selection of transformed host cells. Selection genes are well known in the art and will vary with the host cell used.

The CRC proteins of the present invention are produced by culturing a host cell transformed with an expression vector containing nucleic acid encoding a CRC protein, under the appropriate conditions to

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induce or cause expression of the CRC protein. The conditions appropriate for CRC protein expression will vary with the choice of the expression vector and the host cell, and will be easily ascertained by one skilled in the art through routine experimentation. For example, the use of constitutive promoters in the expression vector will require optimizing the growth and proliferation of the host cell, while the use of an inducible promoter requires the appropriate growth conditions for induction. In addition, in some embodiments, the timing of the harvest is important. For example, the baculoviral systems used in insect cell expression are lytic viruses, and thus harvest time selection can be crucial for product yield.

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Appropriate host cells include yeast, bacteria, archaeobacteria, fungi, and insect and animal cells, including mammalian cells. Of particular interest are *Drosophila melanogaster* cells, *Saccharomyces cerevisiae* and other yeasts, *E. coli*, *Bacillus subtilis*, Sf9 cells, C129 cells, 293 cells, *Neurospora*, BHK, CHO, COS, HeLa cells, THP1 cell line (a macrophage cell line) and human cells and cell lines.

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In a preferred embodiment, the CRC proteins are expressed in mammalian cells. Mammalian expression systems are also known in the art, and include retroviral systems. A preferred expression vector system is a retroviral vector system such as is generally described in PCT/US97/01019 and PCT/US97/01048, both of which are hereby expressly incorporated by reference. Of particular use as mammalian promoters are the promoters from mammalian viral genes, since the viral genes are often highly expressed and have a broad host range. Examples include the SV40 early promoter, mouse mammary tumor virus LTR promoter, adenovirus major late promoter, herpes simplex virus promoter, and the CMV promoter. Typically, transcription termination and polyadenylation sequences recognized by mammalian cells are regulatory regions located 3' to the translation stop codon and thus, together with the promoter elements, flank the coding sequence. Examples of transcription terminator and polyadenylation signals include those derived from SV40.

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The methods of introducing exogenous nucleic acid into mammalian hosts, as well as other hosts, is well known in the art, and will vary with the host cell used. Techniques include dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, viral infection, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei.

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In a preferred embodiment, CRC proteins are expressed in bacterial systems. Bacterial expression systems are well known in the art. Promoters from bacteriophage may also be used and are known in the art. In addition, synthetic promoters and hybrid promoters are also useful; for example, the tac promoter is a hybrid of the trp and lac promoter sequences. Furthermore, a bacterial promoter can

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include naturally occurring promoters of non-bacterial origin that have the ability to bind bacterial RNA polymerase and initiate transcription. In addition to a functioning promoter sequence, an efficient ribosome binding site is desirable. The expression vector may also include a signal peptide sequence that provides for secretion of the CRC protein in bacteria. The protein is either secreted into the growth media (gram-positive bacteria) or into the periplasmic space, located between the inner and outer membrane of the cell (gram-negative bacteria). The bacterial expression vector may also include a selectable marker gene to allow for the selection of bacterial strains that have been transformed. Suitable selection genes include genes which render the bacteria resistant to drugs such as ampicillin, chloramphenicol, erythromycin, kanamycin, neomycin and tetracycline. Selectable markers also include biosynthetic genes, such as those in the histidine, tryptophan and leucine biosynthetic pathways. These components are assembled into expression vectors. Expression vectors for bacteria are well known in the art, and include vectors for *Bacillus subtilis*, *E. coli*, *Streptococcus cremoris*, and *Streptococcus lividans*, among others. The bacterial expression vectors are transformed into bacterial host cells using techniques well known in the art, such as calcium chloride treatment, electroporation, and others.

In one embodiment, CRC proteins are produced in insect cells. Expression vectors for the transformation of insect cells, and in particular, baculovirus-based expression vectors, are well known in the art.

In a preferred embodiment, CRC protein is produced in yeast cells. Yeast expression systems are well known in the art, and include expression vectors for *Saccharomyces cerevisiae*, *Candida albicans* and *C. maltosa*, *Hansenula polymorpha*, *Kluyveromyces fragilis* and *K. lactis*, *Pichia guilliermondii* and *P. pastoris*, *Schizosaccharomyces pombe*, and *Yarrowia lipolytica*.

The CRC protein may also be made as a fusion protein, using techniques well known in the art. Thus, for example, for the creation of monoclonal antibodies, if the desired epitope is small, the CRC protein may be fused to a carrier protein to form an immunogen. Alternatively, the CRC protein may be made as a fusion protein to increase expression, or for other reasons. For example, when the CRC protein is a CRC peptide, the nucleic acid encoding the peptide may be linked to other nucleic acid for expression purposes.

In one embodiment, the CRC nucleic acids, proteins and antibodies of the invention are labeled. By "labeled" herein is meant that a compound has at least one element, isotope or chemical compound attached to enable the detection of the compound. In general, labels fall into three classes: a) isotopic labels, which may be radioactive or heavy isotopes; b) immune labels, which may be antibodies or

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antigens; and c) colored or fluorescent dyes. The labels may be incorporated into the CRC nucleic acids, proteins and antibodies at any position. For example, the label should be capable of producing, either directly or indirectly, a detectable signal. The detectable moiety may be a radioisotope, such as ^3H , ^{14}C , ^{32}P , ^{35}S , or ^{125}I , a fluorescent or chemiluminescent compound, such as fluorescein isothiocyanate, rhodamine, or luciferin, or an enzyme, such as alkaline phosphatase, beta-galactosidase or horseradish peroxidase. Any method known in the art for conjugating the antibody to the label may be employed, including those methods described by Hunter et al., *Nature*, **144**:945 (1962); David et al., *Biochemistry*, **13**:1014 (1974); Pain et al., *J. Immunol. Meth.*, **40**:219 (1981); and Nygren, *J. Histochem. and Cytochem.*, **30**:407 (1982).

10 Accordingly, the present invention also provides CRC protein sequences. A CRC protein of the present invention may be identified in several ways. "Protein" in this sense includes proteins, polypeptides, and peptides. As will be appreciated by those in the art, the nucleic acid sequences of the invention can be used to generate protein sequences. There are a variety of ways to do this, including cloning the entire gene and verifying its frame and amino acid sequence, or by comparing it to known sequences to search for homology to provide a frame, assuming the CRC protein has homology to some protein in the database being used. Generally, the nucleic acid sequences are input into a program that will search all three frames for homology. This is done in a preferred embodiment using the following NCBI Advanced BLAST parameters. The program is blastx or blastn. The database is nr. The input data is as "Sequence in FASTA format". The organism list is "none". The "expect" is 10; the filter is default. The "descriptions" is 500, the "alignments" is 500, and the "alignment view" is pairwise. The "Query Genetic Codes" is standard (1). The matrix is BLOSUM62; gap existence cost is 11, per residue gap cost is 1; and the lambda ratio is .85 default. This results in the generation of a putative protein sequence.

25 Also included within one embodiment of CRC proteins are amino acid variants of the naturally occurring sequences, as determined herein. Preferably, the variants are preferably greater than about 75% homologous to the wild-type sequence, more preferably greater than about 80%, even more preferably greater than about 85% and most preferably greater than 90%. In some embodiments the homology will be as high as about 93 to 95 or 98%. As for nucleic acids, homology in this context means sequence similarity or identity, with identity being preferred. This homology will be determined using standard techniques known in the art as are outlined above for the nucleic acid homologies.

CRC proteins of the present invention may be shorter or longer than the wild type amino acid sequences. Thus, in a preferred embodiment, included within the definition of CRC proteins are portions or fragments of the wild type sequences. herein. In addition, as outlined above, the CRC

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nucleic acids of the invention may be used to obtain additional coding regions, and thus additional protein sequence, using techniques known in the art.

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In a preferred embodiment, the CRC proteins are derivative or variant CRC proteins as compared to the wild-type sequence. That is, as outlined more fully below, the derivative CRC peptide will contain at least one amino acid substitution, deletion or insertion, with amino acid substitutions being particularly preferred. The amino acid substitution, insertion or deletion may occur at any residue within the CRC peptide.

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Also included in an embodiment of CRC proteins of the present invention are amino acid sequence variants. These variants fall into one or more of three classes: substitutional, insertional or deletional variants. These variants ordinarily are prepared by site specific mutagenesis of nucleotides in the DNA encoding the CRC protein, using cassette or PCR mutagenesis or other techniques well known in the art, to produce DNA encoding the variant, and thereafter expressing the DNA in recombinant cell culture as outlined above. However, variant CRC protein fragments having up to about 100-150 residues may be prepared by in vitro synthesis using established techniques. Amino acid sequence variants are characterized by the predetermined nature of the variation, a feature that sets them apart from naturally occurring allelic or interspecies variation of the CRC protein amino acid sequence. The variants typically exhibit the same qualitative biological activity as the naturally occurring analogue, although variants can also be selected which have modified characteristics as will be more fully outlined below.

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While the site or region for introducing an amino acid sequence variation is predetermined, the mutation per se need not be predetermined. For example, in order to optimize the performance of a mutation at a given site, random mutagenesis may be conducted at the target codon or region and the expressed CRC variants screened for the optimal combination of desired activity. Techniques for making substitution mutations at predetermined sites in DNA having a known sequence are well known, for example, M13 primer mutagenesis and PCR mutagenesis. Screening of the mutants is done using assays of CRC protein activities.

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Amino acid substitutions are typically of single residues; insertions usually will be on the order of from about 1 to 20 amino acids, although considerably larger insertions may be tolerated. Deletions range from about 1 to about 20 residues, although in some cases deletions may be much larger.

Substitutions, deletions, insertions or any combination thereof may be used to arrive at a final derivative. Generally these changes are done on a few amino acids to minimize the alteration of the

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molecule. However, larger changes may be tolerated in certain circumstances. When small alterations in the characteristics of the CRC protein are desired, substitutions are generally made in accordance with the following chart:

		Chart I	
		Original Residue	Exemplary Substitutions
15	10	Ala	Ser
		Arg	Lys
		Asn	Gln, His
20	15	Asp	Glu
		Cys	Ser
		Gln	Asn
25	20	Glu	Asp
		Gly	Pro
		His	Asn, Gln
30	25	Ile	Leu, Val
		Leu	Ile, Val
		Lys	Arg, Gln, Glu
35	30	Met	Leu, Ile
		Phe	Met, Leu, Tyr
		Ser	Thr
40	35	Thr	Ser
		Trp	Tyr
		Tyr	Trp, Phe
45	40	Val	Ile, Leu

Substantial changes in function or immunological identity are made by selecting substitutions that are less conservative than those shown in Chart I. For example, substitutions may be made which more significantly affect: the structure of the polypeptide backbone in the area of the alteration, for example the alpha-helical or beta-sheet structure; the charge or hydrophobicity of the molecule at the target site; or the bulk of the side chain. The substitutions which in general are expected to produce the greatest changes in the polypeptide's properties are those in which (a) a hydrophilic residue, e.g. seryl or threonyl is substituted for (or by) a hydrophobic residue, e.g. leucyl, isoleucyl, phenylalanyl, valyl or alanyl; (b) a cysteine or proline is substituted for (or by) any other residue; (c) a residue having an electropositive side chain, e.g. lysyl, arginyl, or histidyl, is substituted for (or by) an electronegative residue, e.g. glutamyl or aspartyl; or (d) a residue having a bulky side chain, e.g. phenylalanine, is substituted for (or by) one not having a side chain, e.g. glycine.

The variants typically exhibit the same qualitative biological activity and will elicit the same immune response as the naturally-occurring analogue, although variants also are selected to modify the characteristics of the CRC proteins as needed. Alternatively, the variant may be designed such that the biological activity of the CRC protein is altered. For example, glycosylation sites may be altered or removed.

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Covalent modifications of CRC polypeptides are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of a CRC polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N- or C-terminal residues of a CRC polypeptide. Derivatization with bifunctional agents is useful, for instance, for crosslinking CRC to a water-insoluble support matrix or surface for use in the method for purifying anti-CRC antibodies or screening assays, as is more fully described below. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxy-succinimide esters, for example, esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-[(p-azidophenyl)dithio]propionimide.

Other modifications include deamidation of glutaminyl and asparaginyl residues to the corresponding glutamyl and aspartyl residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of seryl, threonyl or tyrosyl residues, methylation of the α -amino groups of lysine, arginine, and histidine side chains [T.E. Creighton, *Proteins: Structure and Molecular Properties*, W.H. Freeman & Co., San Francisco, pp. 79-86 (1983)], acetylation of the N-terminal amine, and amidation of any C-terminal carboxyl group.

Another type of covalent modification of the CRC polypeptide included within the scope of this invention comprises altering the native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended for purposes herein to mean deleting one or more carbohydrate moieties found in native sequence CRC polypeptide, and/or adding one or more glycosylation sites that are not present in the native sequence CRC polypeptide.

Addition of glycosylation sites to CRC polypeptides may be accomplished by altering the amino acid sequence thereof. The alteration may be made, for example, by the addition of, or substitution by, one or more serine or threonine residues to the native sequence CRC polypeptide (for O-linked glycosylation sites). The CRC amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding the CRC polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the CRC polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide. Such methods are described in the art, e.g., in WO 87/05330 published 11 September 1987, and in Aplin and Wriston, *CRC Crit. Rev. Biochem.*, pp. 259-306 (1981).

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Removal of carbohydrate moieties present on the CRC polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding for amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are known in the art and described, for instance, by Hakimuddin, et al., Arch. Biochem. Biophys., 259:52 (1987) and by Edge et al., Anal. Biochem., 118:131 (1981). Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo-and exo-glycosidases as described by Thotakura et al., Math. Enzymol., 138:350 (1987).

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Another type of covalent modification of CRC comprises linking the CRC polypeptide to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol, polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192 or 4,179,337.

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CRC polypeptides of the present invention may also be modified in a way to form chimeric molecules comprising a CRC polypeptide fused to another, heterologous polypeptide or amino acid sequence. In one embodiment, such a chimeric molecule comprises a fusion of a CRC polypeptide with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino-or carboxyl-terminus of the CRC polypeptide. The presence of such epitope-tagged forms of a CRC polypeptide can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the CRC polypeptide to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. In an alternative embodiment, the chimeric molecule may comprise a fusion of a CRC polypeptide with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule, such a fusion could be to the Fc region of an IgG molecule.

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Various tag polypeptides and their respective antibodies are well known in the art. Examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; the flu HA tag polypeptide and its antibody 12CA5 [Field et al., Mol. Cell. Biol., 8:2159-2165 (1988)]; the c-myc tag and the 8F9, 3C7, 6E10, G4, B7 and 9E10 antibodies thereto [Evan et al., Molecular and Cellular Biology, 5:3610-3616 (1985)]; and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody [Paborsky et al., Protein Engineering, 3(6):547-553 (1990)]. Other tag polypeptides include the Flag-peptide [Hopp et al., BioTechnology, 6:1204-1210 (1988)]; the KT3 epitope peptide [Martin et al., Science, 255:192-194 (1992)]; tubulin epitope peptide [Skinner et al., J. Biol. Chem., 266:15163-15166 (1991)]; and the T7 gene 10 protein peptide tag [Lutz-Freyermuth et al., Proc. Natl. Acad. Sci. USA, 87:6393-6397 (1990)].

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Also included with the definition of CRC protein in one embodiment are other CRC proteins of the CRC family, and CRC proteins from other organisms, which are cloned and expressed as outlined below. Thus, probe or degenerate polymerase chain reaction (PCR) primer sequences may be used to find other related CRC proteins from humans or other organisms. As will be appreciated by those in the art, particularly useful probe and/or PCR primer sequences include the unique areas of the CRC nucleic acid sequence. As is generally known in the art, preferred PCR primers are from about 15 to about 35 nucleotides in length, with from about 20 to about 30 being preferred, and may contain inosine as needed. The conditions for the PCR reaction are well known in the art.

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In addition, as is outlined herein, CRC proteins can be made that are longer than those depicted in the figures, for example, by the elucidation of additional sequences, the addition of epitope or purification tags, the addition of other fusion sequences, etc.

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CRC proteins may also be identified as being encoded by CRC nucleic acids. Thus, CRC proteins are encoded by nucleic acids that will hybridize to the sequences of the sequence listings, or their complements, as outlined herein.

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In a preferred embodiment, when the CRC protein is to be used to generate antibodies, for example for immunotherapy, the CRC protein should share at least one epitope or determinant with the full length protein. By "epitope" or "determinant" herein is meant a portion of a protein which will generate and/or bind an antibody or T-cell receptor in the context of MHC. Thus, in most instances, antibodies made to a smaller CRC protein will be able to bind to the full length protein. In a preferred embodiment, the epitope is unique; that is, antibodies generated to a unique epitope show little or no cross-reactivity. In a preferred embodiment, the epitope is selected from CAA2p1 and CAA2p2. In another preferred embodiment, the epitope is selected from CAA9p1, CAA9p2, CAA9p3, CAA9p4, CAA9p4MAPS, CAA89p5 and CAA9p5MAPS.

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In one embodiment, the term "antibody" includes antibody fragments, as are known in the art, including Fab, Fab₂, single chain antibodies (Fv for example), chimeric antibodies, etc., either produced by the modification of whole antibodies or those synthesized de novo using recombinant DNA technologies.

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Methods of preparing polyclonal antibodies are known to the skilled artisan. Polyclonal antibodies can be raised in a mammal, for example, by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include the CAA2 or

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fragment thereof or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Examples of adjuvants which may be employed include Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). The immunization protocol may be selected by one skilled in the art without undue experimentation.

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The antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler and Milstein, Nature, 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes may be immunized *in vitro*. The immunizing agent will typically include the CAA2 polypeptide or fragment thereof or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell [Goding, Monoclonal Antibodies: Principles and Practice, Academic Press, (1986) pp. 59-103]. Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

In one embodiment, the antibodies are bispecific antibodies. Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one of the binding specificities is for a CRC protein or a fragment thereof, the other one is for any other antigen, and preferably for a cell-surface protein or receptor or receptor subunit, preferably one that is tumor specific.

In a preferred embodiment, the antibodies to CRC are capable of reducing or eliminating the biological function of CRC, as is described below. That is, the addition of anti-CRC antibodies (either polyclonal or preferably monoclonal) to CRC (or cells containing CRC) may reduce or eliminate the CRC activity.

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Generally, at least a 25% decrease in activity is preferred, with at least about 50% being particularly preferred and about a 95-100% decrease being especially preferred.

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In a preferred embodiment the antibodies to the CRC proteins are humanized antibodies. Humanized forms of non-human (e.g., murine) antibodies are chimeric molecules of immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')₂ or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues form a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the FR regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin [Jones et al., *Nature*, 321:522-525 (1986); Riechmann et al., *Nature*, 332:323-329 (1988); and Presta, *Curr. Op. Struct. Biol.*, 2:593-596 (1992)].

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Methods for humanizing non-human antibodies are well known in the art. Generally, a humanized antibody has one or more amino acid residues introduced into it from a source which is non-human. These non-human amino acid residues are often referred to as import residues, which are typically taken from an import variable domain. Humanization can be essentially performed following the method of Winter and co-workers [Jones et al., *Nature*, 321:522-525 (1986); Riechmann et al., *Nature*, 332:323-327 (1988); Verhoeven et al., *Science*, 239:1534-1536 (1988)], by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. Accordingly, such humanized antibodies are chimeric antibodies (U.S. Patent No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by the corresponding sequence from a non-human species. In practice, humanized antibodies are typically human antibodies in which some CDR residues and possibly some FR residues are substituted by residues from analogous sites in rodent antibodies.

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Human antibodies can also be produced using various techniques known in the art, including phage display libraries [Hoogenboom and Winter, *J. Mol. Biol.*, 227:381 (1991); Marks et al., *J. Mol. Biol.*,

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222:581 (1991)]. The techniques of Cole et al. and Boerner et al. are also available for the preparation of human monoclonal antibodies (Cole et al., Monoclonal Antibodies and Cancer Therapy, Alan R. Liss, p. 77 (1985) and Boerner et al., J. Immunol., 147(1):86-95 (1991)]. Similarly, human antibodies can be made by introducing of human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, for example, in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in the following scientific publications: Marks et al., Bio/Technology 10, 779-783 (1992); Lonberg et al., Nature 368 856-859 (1994); Morrison, Nature 368, 812-13 (1994); Fishwild et al., Nature Biotechnology 14, 845-51 (1996); Neuberger, Nature Biotechnology 14, 826 (1996); Lonberg and Huszar, Intern. Rev. Immunol. 13 65-93 (1995).

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By immunotherapy is meant treatment of CRC with an antibody raised against CRC proteins. As used herein, immunotherapy can be passive or active. Passive immunotherapy as defined herein is the passive transfer of antibody to a recipient (patient). Active immunization is the induction of antibody and/or T-cell responses in a recipient (patient). Induction of an immune response is the result of providing the recipient with an antigen to which antibodies are raised. As appreciated by one of ordinary skill in the art, the antigen may be provided by injecting a polypeptide against which antibodies are desired to be raised into a recipient, or contacting the recipient with a nucleic acid capable of expressing the antigen and under conditions for expression of the antigen.

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In a preferred embodiment the CRC proteins against which antibodies are raised are secreted proteins as described above. Without being bound by theory, antibodies used for treatment, bind and prevent the secreted protein from binding to its receptor, thereby inactivating the secreted CRC protein.

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In another preferred embodiment, the CRC protein to which antibodies are raised is a transmembrane protein. Without being bound by theory, antibodies used for treatment, bind the extracellular domain of the CRC protein and prevent it from binding to other proteins, such as circulating ligands or cell-associated molecules. The antibody may cause down-regulation of the transmembrane CRC protein. As will be appreciated by one of ordinary skill in the art, the antibody may be a competitive, non-competitive or uncompetitive inhibitor of protein binding to the extracellular domain of the CRC protein. The antibody is also an antagonist of the CRC protein. Further, the antibody prevents activation of the transmembrane CRC protein. In one aspect, when the antibody prevents the binding of other molecules to the CRC protein, the antibody prevents growth of the cell. The antibody also sensitizes

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the cell to cytotoxic agents, including, but not limited to TNF- α , TNF- β , IL-1, INF- γ and IL-2, or chemotherapeutic agents including 5FU, vinblastine, actinomycin D, cisplatin, methotrexate, and the like. In some instances the antibody belongs to a sub-type that activates serum complement when complexed with the transmembrane protein thereby mediating cytotoxicity. Thus, CRC is treated by administering to a patient antibodies directed against the transmembrane CRC protein.

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In another preferred embodiment, the antibody is conjugated to a therapeutic moiety. In one aspect the therapeutic moiety is a small molecule that modulates the activity of the CRC protein. In another aspect the therapeutic moiety modulates the activity of molecules associated with or in close proximity to the CRC protein. The therapeutic moiety may inhibit enzymatic activity such as protease or protein kinase activity associated with CRC.

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In a preferred embodiment, the therapeutic moiety may also be a cytotoxic agent. In this method, targeting the cytotoxic agent to tumor tissue or cells, results in a reduction in the number of afflicted cells, thereby reducing symptoms associated with CRC. Cytotoxic agents are numerous and varied and include, but are not limited to, cytotoxic drugs or toxins or active fragments of such toxins.

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Suitable toxins and their corresponding fragments include diphtheria A chain, exotoxin A chain, ricin A chain, abrin A chain, curcin, crotin, phenomycin, enomycin and the like. Cytotoxic agents also include radiochemicals made by conjugating radioisotopes to antibodies raised against CRC proteins, or binding of a radionuclide to a chelating agent that has been covalently attached to the antibody. Targeting the therapeutic moiety to transmembrane CRC proteins not only serves to increase the local concentration of therapeutic moiety in the CRC afflicted area, but also serves to reduce deleterious side effects that may be associated with the therapeutic moiety.

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In another preferred embodiment, the CRC protein against which the antibodies are raised is an intracellular protein. In this case, the antibody may be conjugated to a protein which facilitates entry into the cell. In one case, the antibody enters the cell by endocytosis. In another embodiment, a nucleic acid encoding the antibody is administered to the individual or cell. Moreover, wherein the CRC protein can be targeted within a cell, i.e., the nucleus, an antibody thereto contains a signal for that target localization, i.e., a nuclear localization signal.

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The CRC antibodies of the invention specifically bind to CRC proteins. By "specifically bind" herein is meant that the antibodies bind to the protein with a binding constant in the range of at least 10^4 - 10^6 M^{-1} , with a preferred range being 10^7 - 10^9 M^{-1} .

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In a preferred embodiment, the CRC protein is purified or isolated after expression. CRC proteins may be isolated or purified in a variety of ways known to those skilled in the art depending on what other components are present in the sample. Standard purification methods include electrophoretic, molecular, immunological and chromatographic techniques, including ion exchange, hydrophobic, affinity, and reverse-phase HPLC chromatography, and chromatofocusing. For example, the CRC protein may be purified using a standard anti-CRC antibody column. Ultrafiltration and diafiltration techniques, in conjunction with protein concentration, are also useful. For general guidance in suitable purification techniques, see Scopes, R., Protein Purification, Springer-Verlag, NY (1982). The degree of purification necessary will vary depending on the use of the CRC protein. In some instances no purification will be necessary.

Once expressed and purified if necessary, the CRC proteins and nucleic acids are useful in a number of applications.

In one aspect, the expression levels of genes are determined for different cellular states in the CRC phenotype; that is, the expression levels of genes in normal colon tissue and in CRC tissue (and in some cases, for varying severities of CRC that relate to prognosis, as outlined below) are evaluated to provide expression profiles. An expression profile of a particular cell state or point of development is essentially a "fingerprint" of the state; while two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is unique to the state of the cell. By comparing expression profiles of cells in different states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. Then, diagnosis may be done or confirmed: does tissue from a particular patient have the gene expression profile of normal or CRC tissue.

"Differential expression," or grammatical equivalents as used herein, refers to both qualitative as well as quantitative differences in the genes' temporal and/or cellular expression patterns within and among the cells. Thus, a differentially expressed gene can qualitatively have its expression altered, including an activation or inactivation, in, for example, normal versus CRC tissue. That is, genes may be turned on or turned off in a particular state, relative to another state. As is apparent to the skilled artisan, any comparison of two or more states can be made. Such a qualitatively regulated gene will exhibit an expression pattern within a state or cell type which is detectable by standard techniques in one such state or cell type, but is not detectable in both. Alternatively, the determination is quantitative in that expression is increased or decreased; that is, the expression of the gene is either upregulated, resulting in an increased amount of transcript, or downregulated, resulting in a decreased amount of transcript. The degree to which expression differs need only be large enough to quantify via standard

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characterization techniques as outlined below, such as by use of Affymetrix GeneChip™ expression arrays, Lockhart, Nature Biotechnology, 14:1675-1680 (1996), hereby expressly incorporated by reference. Other techniques include, but are not limited to, quantitative reverse transcriptase PCR, Northern analysis and RNase protection. As outlined above, preferably the change in expression (i.e. upregulation or downregulation) is at least about 50%, more preferably at least about 100%, more preferably at least about 150%, more preferably, at least about 200%, with from 300 to at least 1000% being especially preferred.

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As will be appreciated by those in the art, this may be done by evaluation at either the gene transcript, or the protein level; that is, the amount of gene expression may be monitored using nucleic acid probes to the DNA or RNA equivalent of the gene transcript, and the quantification of gene expression levels, or, alternatively, the final gene product itself (protein) can be monitored, for example through the use of antibodies to the CRC protein and standard immunoassays (ELISAs, etc.) or other techniques, including mass spectroscopy assays, 2D gel electrophoresis assays, etc. Thus, the proteins corresponding to CRC genes, i.e. those identified as being important in a CRC phenotype, can be evaluated in a CRC diagnostic test.

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In a preferred embodiment, gene expression monitoring is done and a number of genes, i.e. an expression profile, is monitored simultaneously, although multiple protein expression monitoring can be done as well. Similarly, these assays may be done on an individual basis as well.

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In this embodiment, the CRC nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of CRC sequences in a particular cell. The assays are further described below in the example.

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In a preferred embodiment nucleic acids encoding the CRC protein are detected. Although DNA or RNA encoding the CRC protein may be detected, of particular interest are methods wherein the mRNA encoding a CRC protein is detected. The presence of mRNA in a sample is an indication that the CRC gene has been transcribed to form the mRNA, and suggests that the protein is expressed. Probes to detect the mRNA can be any nucleotide/deoxynucleotide probe that is complementary to and base pairs with the mRNA and includes but is not limited to oligonucleotides, cDNA or RNA. Probes also should contain a detectable label, as defined herein. In one method the mRNA is detected after immobilizing the nucleic acid to be examined on a solid support such as nylon membranes and hybridizing the probe with the sample. Following washing to remove the non-specifically bound probe, the label is detected. In another method detection of the mRNA is performed in situ. In this method permeabilized cells or tissue samples are contacted with a detectably labeled

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nucleic acid probe for sufficient time to allow the probe to hybridize with the target mRNA. Following washing to remove the non-specifically bound probe, the label is detected. For example a digoxigenin labeled riboprobe (RNA probe) that is complementary to the mRNA encoding a CRC protein is detected by binding the digoxigenin with an anti-digoxigenin secondary antibody and developed with nitro blue tetrazolium and 5-bromo-4-chloro-3-indoyl phosphate.

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In a preferred embodiment, any of the three classes of proteins as described herein (secreted, transmembrane or intracellular proteins) are used in diagnostic assays. The CRC proteins, antibodies, nucleic acids, modified proteins and cells containing CRC sequences are used in diagnostic assays. This can be done on an individual gene or corresponding polypeptide level. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes and/or corresponding polypeptides.

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As described and defined herein, CRC proteins, including intracellular, transmembrane or secreted proteins, find use as markers of CRC. Detection of these proteins in putative CRC tissue or patients allows for a determination or diagnosis of CRC. Numerous methods known to those of ordinary skill in the art find use in detecting CRC. In one embodiment, antibodies are used to detect CRC proteins. A preferred method separates proteins from a sample or patient by electrophoresis on a gel (typically a denaturing and reducing protein gel, but may be any other type of gel including isoelectric focusing gels and the like). Following separation of proteins, the CRC protein is detected by immunoblotting with antibodies raised against the CRC protein. Methods of immunoblotting are well known to those of ordinary skill in the art.

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In another preferred method, antibodies to the CRC protein find use in in situ imaging techniques. In this method cells are contacted with from one to many antibodies to the CRC protein(s). Following washing to remove non-specific antibody binding, the presence of the antibody or antibodies is detected. In one embodiment the antibody is detected by incubating with a secondary antibody that contains a detectable label. In another method the primary antibody to the CRC protein(s) contains a detectable label. In another preferred embodiment each one of multiple primary antibodies contains a distinct and detectable label. This method finds particular use in simultaneous screening for a plurality of CRC proteins. As will be appreciated by one of ordinary skill in the art, numerous other histological imaging techniques are useful in the invention.

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In a preferred embodiment the label is detected in a fluorometer which has the ability to detect and distinguish emissions of different wavelengths. In addition, a fluorescence activated cell sorter (FACS) can be used in the method.

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In another preferred embodiment, antibodies find use in diagnosing CRC from blood samples. As previously described, certain CRC proteins are secreted/circulating molecules. Blood samples, therefore, are useful as samples to be probed or tested for the presence of secreted CRC proteins. Antibodies can be used to detect the CRC by any of the previously described immunoassay techniques including ELISA, immunoblotting (Western blotting), immunoprecipitation, BIACORE technology and the like, as will be appreciated by one of ordinary skill in the art.

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1.0

In a preferred embodiment, in situ hybridization of labeled CRC nucleic acid probes to tissue arrays is done. For example, arrays of tissue samples, including CRC tissue and/or normal tissue, are made. In situ hybridization as is known in the art can then be done.

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It is understood that when comparing the fingerprints between an individual and a standard, the skilled artisan can make a diagnosis as well as a prognosis. It is further understood that the genes which indicate the diagnosis may differ from those which indicate the prognosis.

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2.0

In a preferred embodiment, the CRC proteins, antibodies, nucleic acids, modified proteins and cells containing CRC sequences are used in prognosis assays. As above, gene expression profiles can be generated that correlate to CRC severity, in terms of long term prognosis. Again, this may be done on either a protein or gene level, with the use of genes being preferred. As above, the CRC probes are attached to biochips for the detection and quantification of CRC sequences in a tissue or patient. The assays proceed as outlined for diagnosis.

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2.5

In a preferred embodiment, any of the three classes of proteins as described herein are used in drug screening assays. The CRC proteins, antibodies, nucleic acids, modified proteins and cells containing CRC sequences are used in drug screening assays or by evaluating the effect of drug candidates on a "gene expression profile" or expression profile of polypeptides. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent, Zlokarnik, et al., Science 279, 84-8 (1998), Heid, 1996 #69.

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In a preferred embodiment, the CRC proteins, antibodies, nucleic acids, modified proteins and cells containing the native or modified CRC proteins are used in screening assays. That is, the present

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invention provides novel methods for screening for compositions which modulate the CRC phenotype. As above, this can be done on an individual gene level or by evaluating the effect of drug candidates on a "gene expression profile". In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent, see Zlokarnik, supra.

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Having identified the differentially expressed genes herein, a variety of assays may be executed. In a preferred embodiment, assays may be run on an individual gene or protein level. That is, having identified a particular gene as up regulated in CRC, candidate bioactive agents may be screened to modulate this gene's response; preferably to down regulate the gene, although in some circumstances to up regulate the gene. "Modulation" thus includes both an increase and a decrease in gene expression. The preferred amount of modulation will depend on the original change of the gene expression in normal versus tumor tissue, with changes of at least 10%, preferably 50%, more preferably 100-300%, and in some embodiments 300-1000% or greater. Thus, if a gene exhibits a 4 fold increase in tumor compared to normal tissue, a decrease of about four fold is desired; a 10 fold decrease in tumor compared to normal tissue gives a 10 fold increase in expression for a candidate agent is desired.

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As will be appreciated by those in the art, this may be done by evaluation at either the gene or the protein level; that is, the amount of gene expression may be monitored using nucleic acid probes and the quantification of gene expression levels, or, alternatively, the gene product itself can be monitored, for example through the use of antibodies to the CRC protein and standard immunoassays.

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In a preferred embodiment, gene expression monitoring is done and a number of genes, i.e. an expression profile, is monitored simultaneously, although multiple protein expression monitoring can be done as well.

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In this embodiment, the CRC nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of CRC sequences in a particular cell. The assays are further described below.

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Generally, in a preferred embodiment, a candidate bioactive agent is added to the cells prior to analysis. Moreover, screens are provided to identify a candidate bioactive agent which modulates colorectal cancer, modulates CRC proteins, binds to a CRC protein, or interferes between the binding of a CRC protein and an antibody.

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The term "candidate bioactive agent" or "drug candidate" or grammatical equivalents as used herein describes any molecule, e.g., protein, oligopeptide, small organic molecule, polysaccharide, polynucleotide, etc., to be tested for bioactive agents that are capable of directly or indirectly altering either the CRC phenotype or the expression of a CRC sequence, including both nucleic acid sequences and protein sequences. In preferred embodiments, the bioactive agents modulate the expression profiles, or expression profile nucleic acids or proteins provided herein. In a particularly preferred embodiment, the candidate agent suppresses a CRC phenotype, for example to a normal colon tissue fingerprint. Similarly, the candidate agent preferably suppresses a severe CRC phenotype. Generally a plurality of assay mixtures are run in parallel with different agent concentrations to obtain a differential response to the various concentrations. Typically, one of these concentrations serves as a negative control, i.e., at zero concentration or below the level of detection.

In one aspect, a candidate agent will neutralize the effect of a CRC protein. By "neutralize" is meant that activity of a protein is either inhibited or counter acted against so as to have substantially no effect on a cell.

Candidate agents encompass numerous chemical classes, though typically they are organic molecules, preferably small organic compounds having a molecular weight of more than 100 and less than about 2,500 daltons. Preferred small molecules are less than 2000, or less than 1500 or less than 1000 or less than 500 D. Candidate agents comprise functional groups necessary for structural interaction with proteins, particularly hydrogen bonding, and typically include at least an amine, carbonyl, hydroxyl or carboxyl group, preferably at least two of the functional chemical groups. The candidate agents often comprise cyclical carbon or heterocyclic structures and/or aromatic or polyaromatic structures substituted with one or more of the above functional groups. Candidate agents are also found among biomolecules including peptides, saccharides, fatty acids, steroids, purines, pyrimidines, derivatives, structural analogs or combinations thereof. Particularly preferred are peptides.

Candidate agents are obtained from a wide variety of sources including libraries of synthetic or natural compounds. For example, numerous means are available for random and directed synthesis of a wide variety of organic compounds and biomolecules, including expression of randomized oligonucleotides. Alternatively, libraries of natural compounds in the form of bacterial, fungal, plant and animal extracts are available or readily produced. Additionally, natural or synthetically produced libraries and compounds are readily modified through conventional chemical, physical and biochemical means. Known pharmacological agents may be subjected to directed or random

chemical modifications, such as acylation, alkylation, esterification, amidification to produce structural analogs.

In a preferred embodiment, the candidate bioactive agents are proteins. By "protein" herein is meant at least two covalently attached amino acids, which includes proteins, polypeptides, oligopeptides and peptides. The protein may be made up of naturally occurring amino acids and peptide bonds, or synthetic peptidomimetic structures. Thus "amino acid", or "peptide residue", as used herein means both naturally occurring and synthetic amino acids. For example, homo-phenylalanine, citrulline and noreleucine are considered amino acids for the purposes of the invention. "Amino acid" also includes imino acid residues such as proline and hydroxyproline. The side chains may be in either the (R) or the (S) configuration. In the preferred embodiment, the amino acids are in the (S) or L-configuration. If non-naturally occurring side chains are used, non-amino acid substituents may be used, for example to prevent or retard in vivo degradations.

In a preferred embodiment, the candidate bioactive agents are naturally occurring proteins or fragments of naturally occurring proteins. Thus, for example, cellular extracts containing proteins, or random or directed digests of proteinaceous cellular extracts, may be used. In this way libraries of procaryotic and eucaryotic proteins may be made for screening in the methods of the invention. Particularly preferred in this embodiment are libraries of bacterial, fungal, viral, and mammalian proteins, with the latter being preferred, and human proteins being especially preferred.

In a preferred embodiment, the candidate bioactive agents are peptides of from about 5 to about 30 amino acids, with from about 5 to about 20 amino acids being preferred, and from about 7 to about 15 being particularly preferred. The peptides may be digests of naturally occurring proteins as is outlined above, random peptides, or "biased" random peptides. By "randomized" or grammatical equivalents herein is meant that each nucleic acid and peptide consists of essentially random nucleotides and amino acids, respectively. Since generally these random peptides (or nucleic acids, discussed below) are chemically synthesized, they may incorporate any nucleotide or amino acid at any position. The synthetic process can be designed to generate randomized proteins or nucleic acids, to allow the formation of all or most of the possible combinations over the length of the sequence, thus forming a library of randomized candidate bioactive proteinaceous agents.

In one embodiment, the library is fully randomized, with no sequence preferences or constants at any position. In a preferred embodiment, the library is biased. That is, some positions within the sequence are either held constant, or are selected from a limited number of possibilities. For example, in a preferred embodiment, the nucleotides or amino acid residues are randomized within a

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defined class, for example, of hydrophobic amino acids, hydrophilic residues, sterically biased (either small or large) residues, towards the creation of nucleic acid binding domains, the creation of cysteines, for cross-linking, prolines for SH-3 domains, serines, threonines, tyrosines or histidines for phosphorylation sites, etc., or to purines, etc.

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5 In a preferred embodiment, the candidate bioactive agents are nucleic acids, as defined above.

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As described above generally for proteins, nucleic acid candidate bioactive agents may be naturally occurring nucleic acids, random nucleic acids, or "biased" random nucleic acids. For example, digests of procaryotic or eucaryotic genomes may be used as is outlined above for proteins.

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In a preferred embodiment, the candidate bioactive agents are organic chemical moieties, a wide variety of which are available in the literature.

After the candidate agent has been added and the cells allowed to incubate for some period of time, the sample containing the target sequences to be analyzed is added to the biochip. If required, the target sequence is prepared using known techniques. For example, the sample may be treated to lyse the cells, using known lysis buffers, electroporation, etc., with purification and/or amplification such as PCR occurring as needed, as will be appreciated by those in the art. For example, an in vitro transcription with labels covalently attached to the nucleosides is done. Generally, the nucleic acids are labeled with biotin-FITC or PE, or with cy3 or cy5.

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In a preferred embodiment, the target sequence is labeled with, for example, a fluorescent, a chemiluminescent, a chemical, or a radioactive signal, to provide a means of detecting the target sequence's specific binding to a probe. The label also can be an enzyme, such as, alkaline phosphatase or horseradish peroxidase, which when provided with an appropriate substrate produces a product that can be detected. Alternatively, the label can be a labeled compound or small molecule, such as an enzyme inhibitor, that binds but is not catalyzed or altered by the enzyme. The label also can be a moiety or compound, such as, an epitope tag or biotin which specifically binds to streptavidin. For the example of biotin, the streptavidin is labeled as described above, thereby, providing a detectable signal for the bound target sequence. As known in the art, unbound labeled streptavidin is removed prior to analysis.

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As will be appreciated by those in the art, these assays can be direct hybridization assays or can comprise "sandwich assays", which include the use of multiple probes, as is generally outlined in U.S. Patent Nos. 5,681,702, 5,597,909, 5,545,730, 5,594,117, 5,591,584, 5,571,670, 5,580,731, 5,571,670,

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5,591,584, 5,624,802, 5,635,352, 5,594,118, 5,359,100, 5,124,246 and 5,681,697, all of which are hereby incorporated by reference. In this embodiment, in general, the target nucleic acid is prepared as outlined above, and then added to the biochip comprising a plurality of nucleic acid probes, under conditions that allow the formation of a hybridization complex.

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5 A variety of hybridization conditions may be used in the present invention, including high, moderate and low stringency conditions as outlined above. The assays are generally run under stringency conditions which allows formation of the label probe hybridization complex only in the presence of target. Stringency can be controlled by altering a step parameter that is a thermodynamic variable, including, but not limited to, temperature, formamide concentration, salt concentration, chaotropic salt concentration pH, organic solvent concentration, etc.

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These parameters may also be used to control non-specific binding, as is generally outlined in U.S. Patent No. 5,681,697. Thus it may be desirable to perform certain steps at higher stringency conditions to reduce non-specific binding.

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1.5 The reactions outlined herein may be accomplished in a variety of ways, as will be appreciated by those in the art. Components of the reaction may be added simultaneously, or sequentially, in any order, with preferred embodiments outlined below. In addition, the reaction may include a variety of other reagents may be included in the assays. These include reagents like salts, buffers, neutral proteins, e.g. albumin, detergents, etc which may be used to facilitate optimal hybridization and detection, and/or reduce non-specific or background interactions. Also reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may be used, depending on the sample preparation methods and purity of the target.

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Once the assay is run, the data is analyzed to determine the expression levels, and changes in expression levels as between states, of individual genes, forming a gene expression profile.

2.5 The screens are done to identify drugs or bioactive agents that modulate the CRC phenotype. Specifically, there are several types of screens that can be run. A preferred embodiment is in the screening of candidate agents that can induce or suppress a particular expression profile, thus preferably generating the associated phenotype. That is, candidate agents that can mimic or produce an expression profile in CRC similar to the expression profile of normal colon tissue is expected to result in a suppression of the CRC phenotype. Thus, in this embodiment, mimicking an expression profile, or changing one profile to another, is the goal.

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In a preferred embodiment, as for the diagnosis and prognosis applications, having identified the differentially expressed genes important in any one state, screens can be run to alter the expression of the genes individually. That is, screening for modulation of regulation of expression of a single gene can be done; that is, rather than try to mimic all or part of an expression profile, screening for regulation of individual genes can be done. Thus, for example, particularly in the case of target genes whose presence or absence is unique between two states, screening is done for modulators of the target gene expression.

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In a preferred embodiment, screening is done to alter the biological function of the expression product of the differentially expressed gene. Again, having identified the importance of a gene in a particular state, screening for agents that bind and/or modulate the biological activity of the gene product can be run as is more fully outlined below.

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Thus, screening of candidate agents that modulate the CRC phenotype either at the gene expression level or the protein level can be done.

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In addition screens can be done for novel genes that are induced in response to a candidate agent. After identifying a candidate agent based upon its ability to suppress a CRC expression pattern leading to a normal expression pattern, or modulate a single CRC gene expression profile so as to mimic the expression of the gene from normal tissue, a screen as described above can be performed to identify genes that are specifically modulated in response to the agent. Comparing expression profiles between normal tissue and agent treated CRC tissue reveals genes that are not expressed in normal tissue or CRC tissue, but are expressed in agent treated tissue. These agent specific sequences can be identified and used by any of the methods described herein for CRC genes or proteins. In particular these sequences and the proteins they encode find use in marking or identifying agent treated cells. In addition, antibodies can be raised against the agent induced proteins and used to target novel therapeutics to the treated CRC tissue sample.

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Thus, in one embodiment, a candidate agent is administered to a population of CRC cells, that thus has an associated CRC expression profile. By "administration" or "contacting" herein is meant that the candidate agent is added to the cells in such a manner as to allow the agent to act upon the cell, whether by uptake and intracellular action, or by action at the cell surface. In some embodiments, nucleic acid encoding a proteinaceous candidate agent (i.e. a peptide) may be put into a viral construct such as a retroviral construct and added to the cell, such that expression of the peptide agent is accomplished; see PCT US97/01019, hereby expressly incorporated by reference.

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Once the candidate agent has been administered to the cells, the cells can be washed if desired and are allowed to incubate under preferably physiological conditions for some period of time. The cells are then harvested and a new gene expression profile is generated, as outlined herein.

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Thus, for example, CRC tissue may be screened for agents that reduce or suppress the CRC phenotype. A change in at least one gene of the expression profile indicates that the agent has an effect on CRC activity. By defining such a signature for the CRC phenotype, screens for new drugs that alter the phenotype can be devised. With this approach, the drug target need not be known and need not be represented in the original expression screening platform, nor does the level of transcript for the target protein need to change.

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In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of either the expression of the gene or the gene product itself can be done. The gene products of differentially expressed genes are sometimes referred to herein as "CRC proteins" or a "CCMP". In preferred embodiments, the CCMP is as depicted in Figures 17-20, 24, 25, 29, 33 and 36, more preferably the protein having the sequence shown in Figures 29 or 36 or encoded by the sequences of Figures 27, 36 and 39-48. The CCMP may be a fragment, or alternatively, be the full length protein to a fragment shown herein. Preferably, the CCMP is a fragment of approximately 14 to 24 amino acids long. More preferably the fragment is a soluble fragment.

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In a preferred embodiment, the fragment is from CAA9. Preferably, the fragment includes a non-transmembrane region. In a preferred embodiment, the CAA9 fragment has an N-terminal Cys to aid in solubility. Preferably, the fragment is selected from CAA9p1, Caa9p2, CAA9p3, CAA9p4, CAA9p4MAPS, CAA9p5 and CAA9p5MAPS.

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In a preferred embodiment, the fragment is charged and from the c-terminus of CAA2. In one embodiment, the c-terminus of the fragment is kept as a free acid and the n-terminus is a free amine to aid in coupling, i.e., to cysteine. In another embodiment, the fragment is an internal peptide overlapping hydrophilic stretch of CAA2. In a preferred embodiment, the termini is blocked. Preferably, the fragment of CAA2 is selected from CAA2p1 or CAA2p2. In another preferred embodiment, the fragment is a novel fragment from the N-terminal. In one embodiment, the fragment excludes sequence outside of the N-terminal, in another embodiment, the fragment includes at least a portion of the N-terminal. "N-terminal" is used interchangeably herein with "N-terminus" which is further described above.

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In one embodiment the CRC proteins are conjugated to an immunogenic agent as discussed herein.
In one embodiment the CRC protein is conjugated to BSA.

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Thus, in a preferred embodiment, screening for modulators of expression of specific genes can be done. This will be done as outlined above, but in general the expression of only one or a few genes are evaluated.

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In a preferred embodiment, screens are designed to first find candidate agents that can bind to differentially expressed proteins, and then these agents may be used in assays that evaluate the ability of the candidate agent to modulate differentially expressed activity. Thus, as will be appreciated by those in the art, there are a number of different assays which may be run; binding assays and activity assays.

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In a preferred embodiment, binding assays are done. In general, purified or isolated gene product is used; that is, the gene products of one or more differentially expressed nucleic acids are made. In general, this is done as is known in the art. For example, antibodies are generated to the protein gene products, and standard immunoassays are run to determine the amount of protein present. Alternatively, cells comprising the CRC proteins can be used in the assays.

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Thus, in a preferred embodiment, the methods comprise combining a CRC protein and a candidate bioactive agent, and determining the binding of the candidate agent to the CRC protein. Preferred embodiments utilize the human CRC protein, although other mammalian proteins may also be used, for example for the development of animal models of human disease. In some embodiments, as outlined herein, variant or derivative CRC proteins may be used.

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Generally, in a preferred embodiment of the methods herein, the CRC protein or the candidate agent is non-diffusably bound to an insoluble support having isolated sample receiving areas (e.g. a microtiter plate, an array, etc.). The insoluble supports may be made of any composition to which the compositions can be bound, is readily separated from soluble material, and is otherwise compatible with the overall method of screening. The surface of such supports may be solid or porous and of any convenient shape. Examples of suitable insoluble supports include microtiter plates, arrays, membranes and beads. These are typically made of glass, plastic (e.g., polystyrene), polysaccharides, nylon or nitrocellulose, teflon™, etc. Microtiter plates and arrays are especially convenient because a large number of assays can be carried out simultaneously, using small amounts of reagents and samples. The particular manner of binding of the composition is not crucial so long as it is compatible with the reagents and overall methods of the invention, maintains the activity of the

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composition and is nondiffusable. Preferred methods of binding include the use of antibodies (which do not sterically block either the ligand binding site or activation sequence when the protein is bound to the support), direct binding to "sticky" or ionic supports, chemical crosslinking, the synthesis of the protein or agent on the surface, etc. Following binding of the protein or agent, excess unbound material is removed by washing. The sample receiving areas may then be blocked through incubation with bovine serum albumin (BSA), casein or other innocuous protein or other moiety.

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In a preferred embodiment, the CRC protein is bound to the support, and a candidate bioactive agent is added to the assay. Alternatively, the candidate agent is bound to the support and the CRC protein is added. Novel binding agents include specific antibodies, non-natural binding agents identified in screens of chemical libraries, peptide analogs, etc. Of particular interest are screening assays for agents that have a low toxicity for human cells. A wide variety of assays may be used for this purpose, including labeled in vitro protein-protein binding assays, electrophoretic mobility shift assays, immunoassays for protein binding, functional assays (phosphorylation assays, etc.) and the like.

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The determination of the binding of the candidate bioactive agent to the CRC protein may be done in a number of ways. In a preferred embodiment, the candidate bioactive agent is labeled, and binding determined directly. For example, this may be done by attaching all or a portion of the CRC protein to a solid support, adding a labeled candidate agent (for example a fluorescent label), washing off excess reagent, and determining whether the label is present on the solid support. Various blocking and washing steps may be utilized as is known in the art.

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By "labeled" herein is meant that the compound is either directly or indirectly labeled with a label which provides a detectable signal, e.g. radioisotope, fluorescers, enzyme, antibodies, particles such as magnetic particles, chemiluminescers, or specific binding molecules, etc. Specific binding molecules include pairs, such as biotin and streptavidin, digoxin and antidigoxin etc. For the specific binding members, the complementary member would normally be labeled with a molecule which provides for detection, in accordance with known procedures, as outlined above. The label can directly or indirectly provide a detectable signal.

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In some embodiments, only one of the components is labeled. For example, the proteins (or proteinaceous candidate agents) may be labeled at tyrosine positions using ^{125}I , or with fluorophores. Alternatively, more than one component may be labeled with different labels; using ^{125}I for the proteins, for example, and a fluorophor for the candidate agents.

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In a preferred embodiment, the binding of the candidate bioactive agent is determined through the use of competitive binding assays. In this embodiment, the competitor is a binding moiety known to bind to the target molecule (i.e. CRC), such as an antibody, peptide, binding partner, ligand, etc. Under certain circumstances, there may be competitive binding as between the bioactive agent and the binding moiety, with the binding moiety displacing the bioactive agent.

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In one embodiment, the candidate bioactive agent is labeled. Either the candidate bioactive agent, or the competitor, or both, is added first to the protein for a time sufficient to allow binding, if present. Incubations may be performed at any temperature which facilitates optimal activity, typically between 4 and 40°C. Incubation periods are selected for optimum activity, but may also be optimized to facilitate rapid high through put screening. Typically between 0.1 and 1 hour will be sufficient. Excess reagent is generally removed or washed away. The second component is then added, and the presence or absence of the labeled component is followed, to indicate binding.

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In a preferred embodiment, the competitor is added first, followed by the candidate bioactive agent. Displacement of the competitor is an indication that the candidate bioactive agent is binding to the CRC protein and thus is capable of binding to, and potentially modulating, the activity of the CRC protein. In this embodiment, either component can be labeled. Thus, for example, if the competitor is labeled, the presence of label in the wash solution indicates displacement by the agent. Alternatively, if the candidate bioactive agent is labeled, the presence of the label on the support indicates displacement.

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In an alternative embodiment, the candidate bioactive agent is added first, with incubation and washing, followed by the competitor. The absence of binding by the competitor may indicate that the bioactive agent is bound to the CRC protein with a higher affinity. Thus, if the candidate bioactive agent is labeled, the presence of the label on the support, coupled with a lack of competitor binding, may indicate that the candidate agent is capable of binding to the CRC protein.

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In a preferred embodiment, the methods comprise differential screening to identify bioactive agents that are capable of modulating the activity of the CRC proteins. In this embodiment, the methods comprise combining a CRC protein and a competitor in a first sample. A second sample comprises a candidate bioactive agent, a CRC protein and a competitor. The binding of the competitor is determined for both samples, and a change, or difference in binding between the two samples indicates the presence of an agent capable of binding to the CRC protein and potentially modulating its activity. That is, if the binding of the competitor is different in the second sample relative to the first sample, the agent is capable of binding to the CRC protein.

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Alternatively, a preferred embodiment utilizes differential screening to identify drug candidates that bind to the native CRC protein, but cannot bind to modified CRC proteins. The structure of the CRC protein may be modeled, and used in rational drug design to synthesize agents that interact with that site. Drug candidates that affect CRC bioactivity are also identified by screening drugs for the ability to either enhance or reduce the activity of the protein.

Positive controls and negative controls may be used in the assays. Preferably all control and test samples are performed in at least triplicate to obtain statistically significant results. Incubation of all samples is for a time sufficient for the binding of the agent to the protein. Following incubation, all samples are washed free of non-specifically bound material and the amount of bound, generally labeled agent determined. For example, where a radiolabel is employed, the samples may be counted in a scintillation counter to determine the amount of bound compound.

A variety of other reagents may be included in the screening assays. These include reagents like salts, neutral proteins, e.g. albumin, detergents, etc which may be used to facilitate optimal protein-protein binding and/or reduce non-specific or background interactions. Also reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may be used. The mixture of components may be added in any order that provides for the requisite binding.

Screening for agents that modulate the activity of CRC proteins may also be done. In a preferred embodiment, methods for screening for a bioactive agent capable of modulating the activity of CRC proteins comprise the steps of adding a candidate bioactive agent to a sample of CRC proteins, as above, and determining an alteration in the biological activity of CRC proteins. "Modulating the activity of CRC" includes an increase in activity, a decrease in activity, or a change in the type or kind of activity present. Thus, in this embodiment, the candidate agent should both bind to CRC proteins (although this may not be necessary), and alter its biological or biochemical activity as defined herein. The methods include both in vitro screening methods, as are generally outlined above, and in vivo screening of cells for alterations in the presence, distribution, activity or amount of CRC proteins.

Thus, in this embodiment, the methods comprise combining a CRC sample and a candidate bioactive agent, and evaluating the effect on CRC activity. By "CRC activity" or grammatical equivalents herein is meant one of the CRC's biological activities, including, but not limited to, cell division, preferably in colon tissue, cell proliferation, tumor growth, transformation of cells. In one embodiment, CRC activity includes activation of CZA8, BCX2, CBC2, CBC1, CBC3, CJA9, BCN5, CQA1, BCN7, CQA2, CJA8,

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CAA2, CAA9, CGA7 and/or CGA8*, preferably one of the CRC proteins listed in Figure 14. An inhibitor of CRC activity is the inhibition of any one or more CRC activities.

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In a preferred embodiment, the activity of the CRC protein is increased; in another preferred embodiment, the activity of the CRC protein is decreased. Thus, bioactive agents that are antagonists are preferred in some embodiments, and bioactive agents that are agonists may be preferred in other embodiments.

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In a preferred embodiment, the invention provides methods for screening for bioactive agents capable of modulating the activity of a CRC protein. The methods comprise adding a candidate bioactive agent, as defined above, to a cell comprising CRC proteins. Preferred cell types include almost any cell. The cells contain a recombinant nucleic acid that encodes a CRC protein. In a preferred embodiment, a library of candidate agents are tested on a plurality of cells.

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In one aspect, the assays are evaluated in the presence or absence of previous or subsequent exposure of physiological signals, for example hormones, antibodies, peptides, antigens, cytokines, growth factors, action potentials, pharmacological agents including chemotherapeutics, radiation, carcinogenics, or other cells (i.e. cell-cell contacts). In another example, the determinations are determined at different stages of the cell cycle process.

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In this way, bioactive agents are identified. Compounds with pharmacological activity are able to enhance or interfere with the activity of the CRC protein. In one embodiment, "colorectal cancer protein activity" as used herein includes at least one of the following: colorectal cancer activity, binding to CJA8, activation of CJA8 or activation of substrates of CJA8 by CJA8. In one embodiment, colorectal cancer activity is defined as the unregulated proliferation of colon tissue, or the growth of cancer in colon tissue. In one aspect, colorectal cancer activity as defined herein is related to the activity of CJA8 in the upregulation of CJA8 in colon cancer tissue.

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In another embodiment, colorectal cancer protein activity includes at least one of the following: colorectal cancer activity, binding to one of CAA2, CAA9, CGA7 and CGA8, activation of one of CAA2, CAA9, CGA7, and CGA8 or activation of substrates of CAA2, CAA9, CGA7 or CGA8 by CAA2, CAA9, CGA7 or CGA8, respectively. In one preferred embodiment, CAA2 comprises its N-terminal end. In one aspect, colorectal cancer activity as defined herein is related to the activity of CAA2, CAA9, CGA7 and/or CGA8 in the upregulation of CAA2, CAA9, CGA7 and/or CGA8, respectively, in colon cancer tissue.

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In one embodiment, a method of inhibiting colon cancer cell division is provided. The method comprises administration of a colorectal cancer inhibitor.

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In another embodiment, a method of inhibiting tumor growth is provided. The method comprises administration of a colorectal cancer inhibitor.

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5 In a further embodiment, methods of treating cells or individuals with cancer are provided. The method comprises administration of a colorectal cancer inhibitor.

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In one embodiment, a colorectal cancer inhibitor is an antibody as discussed above. In another embodiment, the colorectal cancer inhibitor is an antisense molecule. Antisense molecules as used herein include antisense or sense oligonucleotides comprising a single-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target mRNA (sense) or DNA (antisense) sequences for colorectal cancer molecules. A preferred antisense molecule is for CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, BCN5, CQA1, BCN7, CQA2, CAA2, CAA9, CGA7 or CGA8, more preferably for the CRC sequences referenced in Figure 14, or for a ligand or activator thereof. A most preferred antisense molecule is for CJA8 or for a ligand or activator thereof. Antisense or sense oligonucleotides, according to the present invention, comprise a fragment generally at least about 14 nucleotides, preferably from about 14 to 30 nucleotides. The ability to derive an antisense or a sense oligonucleotide, based upon a cDNA sequence encoding a given protein is described in, for example, Stein and Cohen (Cancer Res. 48:2659, 1988) and van der Krol et al. (BioTechniques 6:958, 1988).

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20 Antisense molecules may be introduced into a cell containing the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does not substantially interfere with the ability of the ligand binding molecule to bind to its corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell. Alternatively, a sense or an antisense oligonucleotide may be introduced into a cell containing the target nucleic acid sequence by formation of an oligonucleotide-lipid complex, as described in WO 90/10448. It is understood that the use of antisense molecules or knock out and knock in models may also be used in screening assays as discussed above, in addition to methods of treatment.

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30 The compounds having the desired pharmacological activity may be administered in a physiologically acceptable carrier to a host, as previously described. The agents may be administered in a variety of

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ways, orally, parenterally e.g., subcutaneously, intraperitoneally, intravascularly, etc. Depending upon the manner of introduction, the compounds may be formulated in a variety of ways. The concentration of therapeutically active compound in the formulation may vary from about 0.1-100 wt.%. The agents may be administered alone or in combination with other treatments, i.e., radiation.

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5 The pharmaceutical compositions can be prepared in various forms, such as granules, tablets, pills, suppositories, capsules, suspensions, salves, lotions and the like. Pharmaceutical grade organic or inorganic carriers and/or diluents suitable for oral and topical use can be used to make up compositions containing the therapeutically-active compounds. Diluents known to the art include aqueous media, vegetable and animal oils and fats. Stabilizing agents, wetting and emulsifying agents, salts for varying the osmotic pressure or buffers for securing an adequate pH value, and skin penetration enhancers can be used as auxiliary agents.

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Without being bound by theory, it appears that the various CRC sequences are important in CRC. Accordingly, disorders based on mutant or variant CRC genes may be determined. In one embodiment, the invention provides methods for identifying cells containing variant CRC genes comprising determining all or part of the sequence of at least one endogenous CRC genes in a cell. As will be appreciated by those in the art, this may be done using any number of sequencing techniques. In a preferred embodiment, the invention provides methods of identifying the CRC genotype of an individual comprising determining all or part of the sequence of at least one CRC gene of the individual. This is generally done in at least one tissue of the individual, and may include the evaluation of a number of tissues or different samples of the same tissue. The method may include comparing the sequence of the sequenced CRC gene to a known CRC gene, i.e. a wild-type gene.

The sequence of all or part of the CRC gene can then be compared to the sequence of a known CRC gene to determine if any differences exist. This can be done using any number of known homology programs, such as Bestfit, etc. In a preferred embodiment, the presence of a difference in the sequence between the CRC gene of the patient and the known CRC gene is indicative of a disease state or a propensity for a disease state, as outlined herein.

In a preferred embodiment, the CRC genes are used as probes to determine the number of copies of the CRC gene in the genome.

In another preferred embodiment CRC genes are used as probed to determine the chromosomal localization of the CRC genes. Information such as chromosomal localization finds use in providing a

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diagnosis or prognosis in particular when chromosomal abnormalities such as translocations, and the like are identified in CRC gene loci.

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Thus, in one embodiment, methods of modulating CRC in cells or organisms are provided. In one embodiment, the methods comprise administering to a cell an anti-CRC antibody that reduces or eliminates the biological activity of an endogeneous CRC protein. Alternatively, the methods comprise administering to a cell or organism a recombinant nucleic acid encoding a CRC protein. As will be appreciated by those in the art, this may be accomplished in any number of ways. In a preferred embodiment, for example when the CRC sequence is down-regulated in CRC, the activity of the CRC gene is increased by increasing the amount of CRC in the cell, for example by overexpressing the endogeneous CRC or by administering a gene encoding the CRC sequence, using known gene-therapy techniques, for example. In a preferred embodiment, the gene therapy techniques include the incorporation of the endogeneous gene using enhanced homologous recombination (EHR), for example as described in PCT/US93/03868, hereby incorporated by reference in its entirety. Alternatively, for example when the CRC sequence is up-regulated in CRC, the activity of the endogeneous CRC gene is decreased, for example by the administration of a CRC antisense nucleic acid.

In one embodiment, the CRC proteins of the present invention may be used to generate polyclonal and monoclonal antibodies to CRC proteins, which are useful as described herein. Similarly, the CRC proteins can be coupled, using standard technology, to affinity chromatography columns. These columns may then be used to purify CRC antibodies. In a preferred embodiment, the antibodies are generated to epitopes unique to a CRC protein; that is, the antibodies show little or no cross-reactivity to other proteins. These antibodies find use in a number of applications. For example, the CRC antibodies may be coupled to standard affinity chromatography columns and used to purify CRC proteins. The antibodies may also be used as blocking polypeptides, as outlined above, since they will specifically bind to the CRC protein.

In one embodiment, a therapeutically effective dose of a CRC or modulator thereof is administered to a patient. By "therapeutically effective dose" herein is meant a dose that produces the effects for which it is administered. The exact dose will depend on the purpose of the treatment, and will be ascertainable by one skilled in the art using known techniques. As is known in the art, adjustments for CRC degradation, systemic versus localized delivery, and rate of new protease synthesis, as well as the age, body weight, general health, sex, diet, time of administration, drug interaction and the severity of the condition may be necessary, and will be ascertainable with routine experimentation by those skilled in the art.

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A "patient" for the purposes of the present invention includes both humans and other animals, particularly mammals, and organisms. Thus the methods are applicable to both human therapy and veterinary applications. In the preferred embodiment the patient is a mammal, and in the most preferred embodiment the patient is human.

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5 The administration of the CRC proteins and modulators of the present invention can be done in a variety of ways as discussed above, including, but not limited to, orally, subcutaneously, intravenously, intranasally, transdermally, intraperitoneally, intramuscularly, intrapulmonary, vaginally, rectally, or intraocularly. In some instances, for example, in the treatment of wounds and inflammation, the CRC proteins and modulators may be directly applied as a solution or spray.

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10 The pharmaceutical compositions of the present invention comprise a CRC protein in a form suitable for administration to a patient. In the preferred embodiment, the pharmaceutical compositions are in a water soluble form, such as being present as pharmaceutically acceptable salts, which is meant to include both acid and base addition salts. "Pharmaceutically acceptable acid addition salt" refers to those salts that retain the biological effectiveness of the free bases and that are not biologically or otherwise undesirable, formed with inorganic acids such as hydrochloric acid, hydrobromic acid, sulfuric acid, nitric acid, phosphoric acid and the like, and organic acids such as acetic acid, propionic acid, glycolic acid, pyruvic acid, oxalic acid, maleic acid, malonic acid, succinic acid, fumaric acid, tartaric acid, citric acid, benzoic acid, cinnamic acid, mandelic acid, methanesulfonic acid, ethanesulfonic acid, p-toluenesulfonic acid, salicylic acid and the like. "Pharmaceutically acceptable base addition salts" include those derived from inorganic bases such as sodium, potassium, lithium, ammonium, calcium, magnesium, iron, zinc, copper, manganese, aluminum salts and the like. Particularly preferred are the ammonium, potassium, sodium, calcium, and magnesium salts. Salts derived from pharmaceutically acceptable organic non-toxic bases include salts of primary, secondary, and tertiary amines, substituted amines including naturally occurring substituted amines, cyclic amines and basic ion exchange resins, such as isopropylamine, trimethylamine, diethylamine, triethylamine, tripropylamine, and ethanolamine.

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The pharmaceutical compositions may also include one or more of the following: carrier proteins such as serum albumin; buffers; fillers such as microcrystalline cellulose, lactose, corn and other starches; binding agents; sweeteners and other flavoring agents; coloring agents; and polyethylene glycol. Additives are well known in the art, and are used in a variety of formulations.

In a preferred embodiment, CRC proteins and modulators are administered as therapeutic agents, and can be formulated as outlined above. Similarly, CRC genes (including both the full-length

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sequence, partial sequences, or regulatory sequences of the CRC coding regions) can be administered in gene therapy applications, as is known in the art. These CRC genes can include antisense applications, either as gene therapy (i.e. for incorporation into the genome) or as antisense compositions, as will be appreciated by those in the art.

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5 In a preferred embodiment, CRC genes are administered as DNA vaccines, either single genes or combinations of CRC genes. Naked DNA vaccines are generally known in the art. Brower, Nature Biotechnology, 16:1304-1305 (1998).

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In one embodiment, CRC genes of the present invention are used as DNA vaccines. Methods for the use of genes as DNA vaccines are well known to one of ordinary skill in the art, and include placing a CRC gene or portion of a CRC gene under the control of a promoter for expression in a CRC patient. The CRC gene used for DNA vaccines can encode full-length CRC proteins, but more preferably encodes portions of the CRC proteins including peptides derived from the CRC protein. In a preferred embodiment a patient is immunized with a DNA vaccine comprising a plurality of nucleotide sequences derived from a CRC gene. Similarly, it is possible to immunize a patient with a plurality of CRC genes or portions thereof as defined herein. Without being bound by theory, expression of the polypeptide encoded by the DNA vaccine, cytotoxic T-cells, helper T-cells and antibodies are induced which recognize and destroy or eliminate cells expressing CRC proteins.

In a preferred embodiment, the DNA vaccines include a gene encoding an adjuvant molecule with the DNA vaccine. Such adjuvant molecules include cytokines that increase the immunogenic response to the CRC polypeptide encoded by the DNA vaccine. Additional or alternative adjuvants are known to those of ordinary skill in the art and find use in the invention.

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In another preferred embodiment CRC genes find use in generating animal models of CRC. As is appreciated by one of ordinary skill in the art, when the CRC gene identified is repressed or diminished in CRC tissue, gene therapy technology wherein antisense RNA directed to the CRC gene will also diminish or repress expression of the gene. An animal generated as such serves as an animal model of CRC that finds use in screening bioactive drug candidates. Similarly, gene knockout technology, for example as a result of homologous recombination with an appropriate gene targeting vector, will result in the absence of the CRC protein. When desired, tissue-specific expression or knockout of the CRC protein may be necessary.

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It is also possible that the CRC protein is overexpressed in CRC. As such, transgenic animals can be generated that overexpress the CRC protein. Depending on the desired expression level, promoters

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of various strengths can be employed to express the transgene. Also, the number of copies of the integrated transgene can be determined and compared for a determination of the expression level of the transgene. Animals generated by such methods find use as animal models of CRC and are additionally useful in screening for bioactive molecules to treat CRC.

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5 It is understood that the examples described herein in no way serve to limit the true scope of this invention, but rather are presented for illustrative purposes. All references and sequences of accession numbers cited herein are incorporated by reference in their entirety.

EXAMPLES

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Example 1

10 Tissue Preparation, Labeling Chips, and Fingerprints

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Purify total RNA from tissue using TRIzol Reagent

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Estimate tissue weight. Homogenize tissue samples in 1ml of TRIzol per 50mg of tissue using a Polytron 3100 homogenizer. The generator/probe used depends upon the tissue size. A generator that is too large for the amount of tissue to be homogenized will cause a loss of sample and lower RNA yield. Use the 20mm generator for tissue weighing more than 0.6g. If the working volume is greater than 2ml, then homogenize tissue in a 15ml polypropylene tube (Falcon 2059). Fill tube no greater than 10ml.

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HOMOGENIZATION

Before using generator, it should have been cleaned after last usage by running it through soapy H₂O and rinsing thoroughly. Run through with EtOH to sterilize. Keep tissue frozen until ready. Add TRIzol directly to frozen tissue then homogenize.

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Following homogenization, remove insoluble material from the homogenate by centrifugation at 7500 x g for 15 min. in a Sorvall superspeed or 12,000 x g for 10 min. in an Eppendorf centrifuge at 4°C. Transfer the cleared homogenate to a new tube(s). The samples may be frozen now at -60 to -70°C (and kept for at least one month) or you may continue with the purification.

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PHASE SEPARATION

Incubate the homogenized samples for 5 minutes at room temperature.

Add 0.2ml of chloroform per 1ml of TRIzol reagent used in the original homogenization.

Cap tubes securely and shake tubes vigorously by hand (do not vortex) for 15 seconds.

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Incubate samples at room temp. for 2-3 minutes. Centrifuge samples at 6500rpm in a Sorvall superspeed for 30 min. at 4°C. (You may spin at up to 12,000 x g for 10 min. but you risk breaking your tubes in the centrifuge.)

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RNA PRECIPITATION

5 Transfer the aqueous phase to a fresh tube. Save the organic phase if isolation of DNA or protein is desired. Add 0.5ml of isopropyl alcohol per 1ml of TRIzol reagent used in the original homogenization. Cap tubes securely and invert to mix. Incubate samples at room temp. for 10 minutes. Centrifuge samples at 6500rpm in Sorvall for 20min. at 4°C.

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RNA WASH

20 10 Pour off the supernate. Wash pellet with cold 75% ethanol. Use 1ml of 75% ethanol per 1ml of TRIzol reagent used in the initial homogenization. Cap tubes securely and invert several times to loosen pellet. (Do not vortex). Centrifuge at <8000rpm (<7500 x g) for 5 minutes at 4°C. Pour off the wash. Carefully transfer pellet to an eppendorf tube (let it slide down the tube into the new tube and use a pipet tip to help guide it in if necessary). Depending on the volumes you are working with, you can decide what size tube(s) you want to precipitate the RNA in. When I tried leaving the RNA in the large 15ml tube, it took so long to dry (i.e. it did not dry) that I eventually had to transfer it to a smaller tube. Let pellet dry in hood. Resuspend RNA in an appropriate volume of DEPC H₂O. Try for 2-5ug/ul. Take absorbance readings.

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Purify poly A⁺ mRNA from total RNA or clean up total RNA with Qiagen's

20 RNeasy kit

35 Purification of poly A⁺ mRNA from total RNA. Heat oligotex suspension to 37°C and mix immediately before adding to RNA. Incubate Elution Buffer at 70°C. Warm up 2 x Binding Buffer at 65°C if there is precipitate in the buffer. Mix total RNA with DEPC-treated water, 2 x Binding Buffer, and Oligotex according to Table 2 on page 16 of the Oligotex Handbook. Incubate for 3 minutes at 65°C. Incubate for 10 minutes at room temperature.

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Centrifuge for 2 minutes at 14,000 to 18,000 g. If centrifuge has a "soft setting," then use it. Remove supernatant without disturbing Oligotex pellet. A little bit of solution can be left behind to reduce the loss of Oligotex. Save sup until certain that satisfactory binding and elution of poly A⁺ mRNA has occurred.

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30 Gently resuspend in Wash Buffer OW2 and pipet onto spin column. Centrifuge the spin column at full speed (soft setting if possible) for 1 minute.

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Transfer spin column to a new collection tube and gently resuspend in Wash Buffer OW2 and centrifuge as describe herein.

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Transfer spin column to a new tube and elute with 20 to 100 ul of preheated (70°C) Elution Buffer. Gently resuspend Oligotex resin by pipetting up and down. Centrifuge as above. Repeat elution with fresh elution buffer or use first eluate to keep the elution volume low.

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Read absorbance, using diluted Elution Buffer as the blank.

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Before proceeding with cDNA synthesis, the mRNA must be precipitated. Some component leftover or in the Elution Buffer from the Oligotex purification procedure will inhibit downstream enzymatic reactions of the mRNA.

10 Ethanol Precipitation

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Add 0.4 vol. of 7.5 M NH_4OAc + 2.5 vol. of cold 100% ethanol. Precipitate at -20°C 1 hour to overnight (or 20-30 min. at -70°C). Centrifuge at 14,000-16,000 x g for 30 minutes at 4°C. Wash pellet with 0.5ml of 80% ethanol (-20°C) then centrifuge at 14,000-16,000 x g for 5 minutes at room temperature. Repeat 80% ethanol wash. Dry the last bit of ethanol from the pellet in the hood. (Do not speed vacuum). Suspend pellet in DEPC H_2O at 1ug/ul concentration.

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Clean up total RNA using Qiagen's RNeasy kit

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Add no more than 100ug to an RNeasy column. Adjust sample to a volume of 100ul with RNase-free water. Add 350ul Buffer RLT then 250ul ethanol (100%) to the sample. Mix by pipetting (do not centrifuge) then apply sample to an RNeasy mini spin column. Centrifuge for 15 sec at >10,000rpm. If concerned about yield, re-apply flowthrough to column and centrifuge again. Transfer column to a new 2-ml collection tube. Add 500ul Buffer RPE and centrifuge for 15 sec at >10,000rpm. Discard flowthrough. Add 500ul Buffer RPE and centrifuge for 15 sec at >10,000rpm. Discard flowthrough then centrifuge for 2 min at maximum speed to dry column membrane. Transfer column to a new 1.5-ml collection tube and apply 30-50ul of RNase-free water directly onto column membrane. Centrifuge 1 min at >10,000rpm. Repeat elution. Take absorbance reading. If necessary, ethanol precipitate with ammonium acetate and 2.5X volume 100% ethanol.

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Make cDNA using Gibco's "SuperScript Choice System for cDNA Synthesis" kit First Strand cDNA Synthesis

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Use 5ug of total RNA or 1ug of polyA+ mRNA as starting material. For total RNA, use 2ul of SuperScript RT. For polyA+ mRNA, use 1ul of SuperScript RT. Final volume of first strand synthesis mix is 20ul. RNA must be in a volume no greater than 10ul. Incubate RNA with 1ul of 100pmol T7-T24 oligo for 10 min at 70C. On ice, add 7 ul of: 4ul 5X 1st Strand Buffer, 2ul of 0.1M DTT, and 1 ul of 10mM dNTP mix. Incubate at 37C for 2 min then add SuperScript RT. Incubate at 37C for 1 hour.

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Second Strand Synthesis

Place 1st strand reactions on ice.

Add: 91ul DEPC H2O

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30ul 5X 2nd Strand Buffer

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3ul 10mM dNTP mix

1ul 10U/ul *E.coli* DNA Ligase

4ul 10U/ul *E.coli* DNA Polymerase

1ul 2U/ul RNase H

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Make the above into a mix if there are more than 2 samples. Mix and incubate 2 hours at 16C. Add 2ul T4 DNA Polymerase. Incubate 5 min at 16C. Add 10ul of 0.5M EDTA

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Clean up cDNA

Phenol:Chloroform:Isoamyl Alcohol (25:24:1) purification using Phase-Lock gel tubes:

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Centrifuge PLG tubes for 30 sec at maximum speed. Transfer cDNA mix to PLG tube. Add equal volume of phenol:chloroform:isamyl alcohol and shake vigorously (do not vortex). Centrifuge 5 minutes at maximum speed. Transfer top aqueous solution to a new tube. Ethanol precipitate:

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add 7.5X 5M NH4OAc and 2.5X volume of 100% ethanol. Centrifuge immediately at room temp. for 20 min, maximum speed. Remove sup then wash pellet 2X with cold 80% ethanol. Remove

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as much ethanol wash as possible then let pellet air dry. Resuspend pellet in 3ul RNase-free water.

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In vitro Transcription (IVT) and labeling with biotin

Pipet 1.5ul of cDNA into a thin-wall PCR tube.

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Make NTP labeling mix:

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Combine at room temperature: 2ul T7 10xATP (75mM) (Ambion)

2ul T7 10xGTP (75mM) (Ambion)

1.5ul T7 10xCTP (75mM) (Ambion)

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Enzo)

1.5ul T7 10xUTP (75mM) (Ambion)
 3.75ul 10mM Bio-11-UTP (Boehringer-Mannheim/Roche or
 3.75ul 10mM Bio-16-CTP (Enzo)
 2ul 10x T7 transcription buffer (Ambion)
 2ul 10x T7 enzyme mix (Ambion)

Final volume of total reaction is 20ul. Incubate 6 hours at 37C in a PCR machine.

RNeasy clean-up of IVT product

Follow previous instructions for RNeasy columns or refer to Qiagen's RNeasy protocol handbook.

cRNA will most likely need to be ethanol precipitated. Resuspend in a volume compatible with the fragmentation step.

Fragmentation

15 ug of labeled RNA is usually fragmented. Try to minimize the fragmentation reaction volume; a 10 ul volume is recommended but 20 ul is all right. Do not go higher than 20 ul because the magnesium in the fragmentation buffer contributes to precipitation in the hybridization buffer. Fragment RNA by incubation at 94 C for 35 minutes in 1 x Fragmentation buffer.

5 x Fragmentation buffer:

200 mM Tris-acetate, pH 8.1
 500 mM KOAc
 150 mM MgOAc

The labeled RNA transcript can be analyzed before and after fragmentation. Samples can be heated to 65C for 15 minutes and electrophoresed on 1% agarose/TBE gels to get an approximate idea of the transcript size range

Hybridization

200 ul (10ug cRNA) of a hybridization mix is put on the chip. If multiple hybridizations are to be done (such as cycling through a 5 chip set), then it is recommended that an initial hybridization mix of 300 ul or more be made.

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Hybridization Mix: fragment labeled RNA (50ng/ul final conc.)

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50 pM 948-b control oligo

1.5 pM BioB

5 pM BioC

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25 pM BioD

100 pM CRE

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0.1mg/ml herring sperm DNA

0.5mg/ml acetylated BSA

to 300 ul with 1xMES hyb. buffer

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10 The instruction manuals for the products used herein are incorporated herein in their entirety.

Labeling Protocol Provided Herein

Hybridization reaction:

Start with non-biotinylated IVT (purified by RNeasy columns)

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(see example 1 for steps from tissue to IVT)

15 IVT antisense RNA; 4 µg: µl

Random Hexamers (1 µg/µl): 4 µl

H₂O: µl

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14 µl

20 - Incubate 70°C, 10 min. Put on ice.

35

Reverse transcription:

5X First Strand (BRL) buffer: 6 µl

0.1 M DTT: 3 µl

50X dNTP mix: 0.6 µl

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25 H₂O: 2.4 µl

Cy3 or Cy5 dUTP (1mM): 3 µl

SS RT II (BRL): 1 µl

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16 µl

30 - Add to hybridization reaction.

- Incubate 30 min., 42°C.

- Add 1 µl SSII and let go for another hour.

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Put on ice.

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- 50X dNTP mix (25mM of cold dATP, dCTP, and dGTP, 10mM of dTTP: 25 µl each of 100mM dATP, dCTP, and dGTP; 10 µl of 100mM dTTP to 15 µl H₂O. dNTPs from Pharmacia)

RNA degradation:

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86 µl H₂O

15

- Add 1.5 µl 1M NaOH/ 2mM EDTA, incubate at 65°C, 10 min. 10 µl 10N NaOH

4 µl 50mM EDTA

U-Con 30

500 µl TE/sample spin at 7000g for 10 min, save flow through for purification

20

10

Qiagen purification:

-suspend u-con recovered material in 500µl buffer PB

-proceed w/ normal Qiagen protocol

DNAse digest:

25

- Add 1 µl of 1/100 dil of DNAse/30µl Rx and incubate at 37°C for 15 min.

15

-5 min 95°C to denature enzyme

Sample preparation:

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- Add:

Cot-1 DNA: 10 µl

50X dNTPs: 1 µl

20

20X SSC: 2.3 µl

Na pyro phosphate: 7.5 µl

35

10mg/ml Herring sperm DNA 1ul of 1/10 dilution

21.8 final vol.

- Dry down in speed vac.

25

- Resuspend in 15 µl H₂O.

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- Add 0.38 µl 10% SDS.

- Heat 95°C, 2 min.

- Slow cool at room temp. for 20 min.

Put on slide and hybridize overnight at 64°C.

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Washing after the hybridization:

3X SSC/0.03% SDS: 2 min. 37.5 mls 20X SSC+0.75mls 10% SDS in 250mls H₂O

1X SSC: 5 min. 12.5 mls 20X SSC in 250mls H₂O

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0.2X SSC: 5 min. 2.5 mls 20X SSC in 250mls H₂O

Dry slides in centrifuge, 1000 RPM, 1min.

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Scan at appropriate PMT's and channels.

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5 The results are shown in Figures 1 through 11. The lists of genes come from colorectal tumors
from a variety of stages of the disease. The genes that are up regulated in the tumors (overall)
10 were also found to be expressed at a limited amount or not at all in the body map. The body map
for the colorectal project consists of ten tissues: Heart, Brain, Lung, Liver, Breast, Kidney,
Prostate, Small Intestine, Spleen, and Colon. The down regulated genes in tumors (overall)
versus normal colon were not selected for their expression or lack of expression in the body map.
15 As indicated, some of the Accession numbers include expression sequence tags (ESTs). Thus, in
one embodiment herein, genes within an expression profile, also termed expression profile genes,
include ESTs and are not necessarily full length. Figure 1 shows 51 upregulated genes; Figure 2
shows 194 upregulated genes; Figure 3 shows 1144 upregulated genes and Figure 4 shows 1815
upregulated genes. The genes shown in Figures 1 and 5 are particularly preferred. Figure 5
20 shows 54 downregulated genes; Figure 6 shows 558 downregulated genes; and Figure 7 shows
1923 downregulated genes; and Figures 8, 9, 10 and 11 provide the Accession numbers for
genes, including expression sequence tags, upregulated in tumor tissue compared to normal
colon tissue.

Example 2

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20 Expression studies were performed herein.

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As indicated in Figure 21, CAA2 is upregulated in colon cancer tissue. CAA2 is found in
chromosome 15, cytoband 15q15-22, interval D15S146-D15S117. CAA2 has N-myristoylation
sites and a C-terminal microbody targeting signal. The preferred fragments shown in Figures 18
and 19 have a solubility of 1 mg/ 1 ml H₂O.

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25 As indicated in Figure 26, CAA9 is upregulated in colon cancer tissue. CAA9 is found in
chromosome 5, cytoband 5q23.3, interval D5S471-D5S393.

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As indicated in Figures 30A and 30B, CGA7 is upregulated in colon cancer tissue. CGA7 is found
in chromosome 2.

As indicated in Figure 34, CGA8 is upregulated in colon cancer tissue.

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As indicated in Figure 37, CJA8 is upregulated in colon cancer tissue. CJA8 is found in chromosome 11.

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As indicated in Figure 38, BCN7 is upregulated in colon cancer tissue. BCN7 is found in chromosome 5, cytoband 5q22, interval D5S471-D5S393.

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Claims

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CLAIMS

We claim:

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1. A method of screening drug candidates comprising:
- a) providing a cell that expresses an expression profile gene which encodes a protein selected from the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7 and CQA2 or a fragment thereof;
- b) adding a drug candidate to said cell; and
- c) determining the effect of said drug candidate on the expression of said expression profile gene.

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2. A method according to claim 1 wherein said determining comprises comparing the level of expression in the absence of said drug candidate to the level of expression in the presence of said drug candidate, wherein the concentration of said drug candidate can vary when present, and wherein said comparison can occur after addition or removal of the drug candidate.

25

3. A method according to claim 1 wherein the expression of said profile gene is decreased as a result of the introduction of the drug candidate.

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4. A method of screening for a bioactive agent capable of binding to a colorectal cancer modulator protein (CCMP), wherein said CCMP is CJA8 or a fragment thereof, said method comprising combining said CCMP and a candidate bioactive agent, and determining the binding of said candidate agent to said CCMP.

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5. A method for screening for a bioactive agent capable of modulating the activity of a colorectal cancer modulator protein (CCMP), wherein said CCMP is CJA8 or a fragment thereof, said method comprising combining said CCMP and a candidate bioactive agent, and determining the effect of said candidate agent on the bioactivity of said CCMP.

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6. A method of evaluating the effect of a candidate colorectal cancer drug comprising:
- a) administering said drug to a patient;
- b) removing a cell sample from said patient; and
- c) determining the expression profile of said cell.

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7. A method according to claim 6 further comprising comparing said expression profile to an expression profile of a healthy individual.

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8. A biochip comprising a nucleic acid segment encoding CJA81 or a fragment thereof, wherein said biochip comprises fewer than 1000 nucleic acid probes.

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9. A method of diagnosing colorectal cancer comprising:

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a) determining the expression of a gene encoding CJA8 or a fragment thereof in a first tissue type of a first individual; and

15

b) comparing said expression of said gene from a second normal tissue type from said first individual or a second unaffected individual;

wherein a difference in said expression indicates that the first individual has colorectal cancer.

20

10. An antibody which specifically binds to CJA8, or a fragment thereof.

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11. An antibody which specifically binds to CAA9, or a fragment thereof.

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12. The antibody of Claim 11 wherein said fragment is selected from the group CAA9p1, CAA9p2, CAA9p3, CAA9p4, CAA9p4MAPS, CAA9p5 and CAA9p5MAPS.

13. The antibody of Claim 10, wherein said antibody is a monoclonal antibody.

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14. The antibody of Claim 10, wherein said antibody is a humanized antibody.

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15. The antibody of Claim 10, wherein said antibody is an antibody fragment.

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16. A method for screening for a bioactive agent capable of interfering with the binding of a colorectal cancer modulator protein (CCMP) or a fragment thereof and an antibody which binds to said CCMP or fragment thereof, said method comprising:

20

a) combining a CCMP or fragment thereof, a candidate bioactive agent and an antibody

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which binds to said CCMP or fragment thereof; and

b) determining the binding of said CCMP or fragment thereof and said antibody.

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17. A method for inhibiting colorectal cancer, said method comprising administering to a cell a composition comprising an antibody to CAJ8 or a fragment thereof.

18. The method of Claim 17 wherein said cell is a cell of an individual.

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19. The method of Claim 18 wherein said individual has cancer.

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20. The method of Claim 17 wherein said antibody is a humanized antibody.

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21. The method of Claim 17 wherein said antibody is an antibody fragment.

22. A method for inhibiting colorectal cancer in a cell, wherein said method comprises administering to a cell a composition comprising antisense molecules to CJA8.

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5 23. A peptide consisting essentially of CAA9p1, CAA9p2, CAA9p3, CAA9p4, CAA9p4MAPS, CAA9p5 or CAA9p5MAPS.

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24. A composition comprising the peptide of Claim 23.

25. A method of eliciting an immune response in an individual, said method comprising administering to said individual a composition comprising CJA8 or a fragment thereof.

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10 26. A method of eliciting an immune response in an individual, said method comprising administering to said individual a composition comprising a nucleic acid comprising a sequence encoding CJA8 or a fragment thereof.

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27. A composition capable of eliciting an immune response in an individual, said composition comprising CJA8 or a fragment thereof and a pharmaceutically acceptable carrier.

15 28. A composition capable of eliciting an immune response in an individual, said composition comprising a nucleic acid comprising a sequence encoding CJA8 or a fragment thereof and a pharmaceutically acceptable carrier.

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29. A method of treating an individual for colorectal cancer comprising administering to said individual an inhibitor of CJA8.

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20 30. The method of Claim 29 wherein said inhibitor is an antibody.

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31. A method for determining the prognosis of an individual with colorectal cancer comprising determining the level of CJA8 in a sample, wherein a high level of CJA8 indicates a poor prognosis.

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32. A method of neutralizing the effect of a CJA8, or a fragment thereof, comprising contacting an agent specific for said protein with said protein in an amount sufficient to effect neutralization.

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33. A method for localizing a therapeutic moiety to colorectal cancer tissue comprising exposing said tissue to an antibody to CJA8 or fragment thereof conjugated to said therapeutic moiety.

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34. The method of Claim 33, wherein said therapeutic moiety is a cytotoxic agent.

35. The method of Claim 33, wherein said therapeutic moiety is a radioisotope.

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36. A method of treating colorectal cancer comprising administering to an individual having colorectal cancer an antibody to CJA8 or fragment thereof conjugated to a therapeutic moiety.

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37. The method of Claim 36, wherein said therapeutic moiety is a cytotoxic agent.

38. The method of Claim 36, wherein said therapeutic moiety is a radioisotope.

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FIGURE 1

Primary Key	fold upregulated in Tumor over normal colon	Accession	Unigene CLUSTER	Unigene Descriptor
37677	>10	AA460530	Hs 98384	Homo sapiens orphan G protein-coupled receptor HG38 mRNA complete cds
6449	>10	X89986	Hs 32935	H sapiens mRNA for NBK apoptotic inducer protein
4178	>10	U30246	Hs 110736	Human burninamide-sensitive Na-K-Cl cotransporter (NKCC1) mRNA complete cds
18330	>10	AA216722	Hs 54481	Human mRNA for apolipoprotein E receptor 2 complete cds
5692	>10	X17644	Hs 2707	G1 to S phase transition 1
16910	>10	AA053636	Hs 129849	PBK1
33109	>10	W59951	Hs 22564	Human mRNA for KIAA0389 gene complete cds
37246	>10	AA449311	Hs 98658	Homo sapiens mitotic checkpoint protein kinase (BUB1) mRNA complete cds
2857	>10	M58507	Hs 2173	Fucosyltransferase 4 (alpha (13) fucosyltransferase myeloid-specific)
14338	>10	AA598712	Hs 23723	ESTs Weakly similar to ORF YPL212c (S cerevisiae)
4676	9.6	U55206	Hs 78619	Homo sapiens human gamma-glutamyl hydrolase (hGlt) mRNA complete cds
2192	7.8	L48211	Hs 20954	Homo Sapiens angiotensin II receptor gene complete cds
5793	7.4	X54942	Hs 83758	CDC28 protein kinase 2
18231	6.3	AA198747	Hs 79025	Human mRNA for KIAA0096 gene partial cds
6061	6.1	X68314	Hs 2704	Glutathione peroxidase 2 gastrointestinal
27117	5.0	AA405098	Hs 38178	ESTs Weakly similar to MOESIN/ELAVIN/HOMOLOG (D melanogaster)
12659	5.0	AA417030	Hs 5101	Homo sapiens protein regulating cytokinesis 1 (PRC1) mRNA complete cds
1106	4.8	HG2981-HT3127		EST - HG2981-HT3127
2157	4.6	L41939	Hs 89403	Homo sapiens protein-tyrosine Kinase EPHB2v (EPIB2) mRNA complete cds
13193	4.4	AA442763	Hs 20483	ESTs Highly similar to C2MITOTIC-SPECIFIC CYCLIN B2 (Mesocricetus auratus)
5690	4.4	X17620	Hs 118638	NUCLEOSIDE DIPHOSPHATE KINASE A
28050	4.1	AA479139	Hs 75393	Acid phosphatase 1 soluble
4540	3.5	U48807	Hs 2359	Human MAP kinase phosphatase (MKP-2) mRNA complete cds
26105	3.1	AA243133	Hs 48915	Homo sapiens serine/threonine kinase (BTAK) mRNA complete cds
19177	3.1	H10984	Hs 12338	ESTs
5780	3.1	X54489	Hs 789	GRO1 oncogene (melanoma growth stimulating activity alpha)
33620	3.0	W93943	Hs 59509	ESTs
4536	2.9	U48705	Hs 75562	Receptor protein-tyrosine Kinase EDDR1
5928	2.9	X62048	Hs 75188	WEE1-LIKE PROTEIN KINASE
28258	2.8	AA505133	Hs 62273	ESTs
21266	2.7	R09195	Hs 151385	Homo sapiens mRNA for KIAA0564 protein partial cds

FIGURE 1 (CONT.)

27748	AA453159	Hs 41723	Human kinesin-like spindle protein HKSP (HKSP) mRNA complete cds
26310	AA048746	Hs 110457	ESTs
2640	M30448	EST - M30448	
3834	U12595	Hs 2204	Human tumor necrosis factor type 1 receptor associated protein (TRAP1) mRNA partial cds
4674	U54898	Hs 93121	Human LGN protein mRNA complete cds
5769	X53800	Hs 89690	GRO3 oncogene
25050	AA011134	Hs 25663	ESTs Weakly similar to renin [H sapiens]
41935	T29681	Hs 75761	Human serine kinase mRNA complete cds
26895	AA292765	Hs 42650	H sapiens mRNA for M-phase phosphoprotein mpp5
1782	L12711	Hs 89643	Transketolase (Wernicke-Korsakoff syndrome)
25593	AA113149	Hs 8130	Homo sapiens IPL (IPL) mRNA complete cds
1487	J03934	Hs 80705	NAD(P)H:menadiolone oxidoreductase
7656	AA203428	Hs 7758	ESTs Moderately similar to ANKYRIN BRAIN VARIANT 2 [Homo sapiens]
683	D79997	Hs 41697	Human mRNA for KIAA0175 gene complete cds
836	D87444	Hs 79305	Human mRNA for KIAA0255 gene complete cds
3098	M77836	Hs 78217	PYRROLINE-5-CARBOXYLATE REDUCTASE
5879	Z20066	Hs 80896	H sapiens nek2 mRNA for protein kinase
6880	Z29057	Hs 2236	H sapiens nek3 mRNA for protein kinase
2473	M21904	Hs 79748	Antigen identified by monoclonal antibodies 4F2 TRA1.10 TROP4 and T43
36508	AA428621	Hs 79093	Human 100 kDa coactivator mRNA complete cds

FIGURE 2

Primary Key	fold upregulated of Tumor	Accession	Unigene CLUSTER	Unigene Descriptor
33616	>10	W93726	Hs.55279	Protease inhibitor 5 (maspin)
34197	>10	AA232315	Hs.12540	Homo sapiens clone 23797 and 23917 mRNA partial cds
19387	>10	H20128	Hs.31656	ESTs
8125	>10	AA330771	Hs.82911	Human protein-tyrosine phosphatase (IU-PP-1) mRNA partial sequence
18362	>10	AA223912	Hs.12013	Ribonuclease L (2'-5'-oligoadenylate synthetase-dependent) inhibitor
39995	>10	H62474	Hs.108240	EST
18328	>10	H17808	Hs.22858	ESTs
39590	>10	AA598648	Hs.78202	Human mRNA for transcriptional activator RSNF2b complete cds
38456	>10	AA504343	Hs.101074	ESTs
17559	>10	AA128407	Hs.71190	ESTs
5519	>10	X14850	Hs.2711	HISTONE H2A.X
4029	>10	U21090	Hs.74598	Human DNA polymerase delta small subunit mRNA complete cds
15008	>10	U30246	Hs.110735	Human bumetanide-sensitive Na-K-Cl cotransporter (NKCC1) mRNA complete cds
3559	>10	U04313	Hs.55279	Protease inhibitor 5 (maspin)
26916	>10	AA331393	Hs.47378	ESTs
1346	>10	HG4716-HT5158	EST - HG4716-HT5158	
37491	10.0	AA455239	Hs.87630	ESTs Highly similar to CHROMOSOME CONDENSATION PROTEIN DPY-27 [Caenorhabditis elegans]
13110	9.8	AA435840	Hs.19114	Homo sapiens mRNA for high mobility group protein HMG2a
4676	9.8	U55206	Hs.78619	Homo sapiens human gamma-glutamyl hydrolase (NGH) mRNA complete cds
21655	8.7	R38239	Hs.34782	EST
14723	8.3	D59894	Hs.83758	CDC28 protein kinase 2
5793	7.4	X54942	Hs.124215	ESTs
29840	7.1	N22107	Hs.112013	ESTs
9347	7.0	H03686	Hs.48876	FARNESYL-DIPHOSPHATE FARNESYLTRANSFERASE
6078	7.0	X69141	Hs.89404	Msh (Drosophila) homeo box homolog 2
9326	6.8	D89377	Hs.54602	ESTs Highly similar to 60S RIBOSOMAL PROTEIN L22 [Rattus norvegicus]
1566	6.7	J05614	Hs.18457	ESTs
25875	6.7	AA129757	Hs.2704	Glutathione peroxidase 2 gastrointestinal
20126	6.4	N22015	Hs.19322	ESTs Weakly similar to XLU SUBFAMILY J1
6061	6.1	X68314	Hs.73625	ESTs Moderately similar to rabkinesin-3 [M. musculus]
10867	6.0	AA088458	Hs.83383	Human antioxidant enzyme AOE37.2 mRNA complete cds
18062	5.9	AA179845	Hs.86430	ESTs
4003	5.8	U25182	EST - U91327	Human chromosome segregation gene homolog CAS mRNA complete cds
18290	5.8	AA211001	Hs.90073	
5330	5.8	U91327		
4244	5.7	U33286		

FIGURE 2 (CONT.)

6928	5.7	246629	Hs.2316	SRY (sex-determining region Y)-box 9 (campomelic dysplasia autosomal sex-reversal)
6190	5.8	X74794	Hs.89599	CDG21 HOMOLOG
31487	5.4	N69507	Hs.120849	ESTs
9470	5.3	H46617	EST - H46617	
31458	5.0	W66835	Hs.14150	Homo sapiens mRNA for KIA0536 protein complete cds
12669	5.0	AA417030	Hs.5101	Homo sapiens protein regulating cytokinesis 1 (PRC1) mRNA complete cds
1106	4.8	HC2981-IT3127	EST - HC2981-IT3127	
34367	4.8	AA251758	Hs.40323	Homo sapiens spleen mitotic checkpoint BUB3 (BUB3) mRNA complete cds
11585	4.8	AA242819	Hs.32539	ESTs
17622	4.8	AA131584	Hs.71435	ESTs Weakly similar to SOF1 PROTEIN [Saccharomyces cerevisiae]
34754	4.7	AA287842	Hs.81848	Human mRNA for KIA0078 gene complete cds
25038	4.7	AA010085	Hs.83758	CDC28 protein kinase 2
5312	4.6	U90716	Hs.79187	Human cml surface protein HCAR mRNA complete cds
8095	4.6	AA314779	Hs.105484	ESTs Weakly similar to LITHOSTATHINE 1 BETA PRECURSOR [H.sapiens]
33556	4.6	W95477	Hs.50592	ESTs
8264	4.5	AA401334	Hs.106941	ESTs
34479	4.5	AA262080	Hs.110736	Human bumetanide-sensitive Na-K-Cl cotransporter (NKCC1) mRNA complete cds
7898	4.4	AA263032	Hs.61634	ESTs
10716	4.4	AA053319	Hs.5951	ESTs
5690	4.4	X17620	Hs.118638	NUCLEOSIDE DIPHOSPHATE KINASE A
20203	4.3	N26855	Hs.5858	ESTs Moderately similar to IIII ALU SUBFAMILY SQ WARNING ENTRY IIII [H.sapiens]
10923	4.2	AA116036	Hs.9329	ESTs
28050	4.1	AA479139	Hs.75393	Acid phosphatase 1 soluble
11670	4.1	AA126390	Hs.5285	ESTs
4149	4.1	U28386	Hs.2397	RAG (recombination activating gene) cohort 1
5767	4.1	X53763	Hs.118226	MULTIFUNCTIONAL PROTEIN ADE2
26596	4.0	AA279943	Hs.88671	ESTs
8861	3.9	AFFX-	AFFX-HUNTFRM11507_3	
38504	3.9	AA598803	Hs.111496	ESTs
30560	3.9	N49284	Hs.1334	MYB PROTO-ONCOGENE PROTEIN
8513	3.8	AA446890	Hs.103135	ESTs
14509	3.8	AA608843	Hs.32793	ESTs
25284	3.8	AA045074	Hs.10145	ESTs Weakly similar to 52 KD SS-A/Ro autoantigen [H.sapiens]
27354	3.8	AA425221	Hs.81688	ESTs
18385	3.8	AA227219	Hs.110828	Homo sapiens CAGf9 mRNA partial cds
25240	3.7	AA039713	Hs.110406	ESTs
16654	3.7	AA055552	Hs.71622	ESTs Weakly similar to KIA00319 [H.sapiens]
3709	3.7	U07550	Hs.1197	Heat shock 10 KD protein 1 (chaperonin 10)
13606	3.5	AA466437	Hs.20386	ESTs Weakly similar to CLEAVAGE STIMULATION FACTOR 64 KD SUBUNIT [H.sapiens]
8338	3.4	AA417152	Hs.5101	Homo sapiens protein regulating cytokinesis 1 (PRC1) mRNA complete cds

FIGURE 2 (CONT.)

387	D28589	EST - D28589	ESTs Highly similar to KINESIN-LIKE PROTEIN KIF4 [Mus musculus]
15643	W50247	Hs.27437	ESTs
13838	AA465342	Hs.34045	ESTs
251	D14520	Hs.84728	Basic transcription element binding protein 2
3778	U09848	Hs.363	Zinc finger protein 139 (clone pTZ-37)
5600	X16396	Hs.37791	NAD-DEPENDENT METHYLENETETRAHYDROFOLATE DEHYDROGENASE
17365	AA101551	Hs.68900	ESTs
33985	AA181580	Hs.81690	Homo sapiens importin beta subunit mRNA complete cds
19233	H12634	Hs.8104	ESTs
13767	AA463234	Hs.119387	ESTs
4738	U58766	Hs.75801	Human FX protein mRNA complete cds
17041	AA070364	EST - RC_AA070364	ESTs
15504	W28362	Hs.44131	ESTs
7401	AA094800	Hs.55582	Human translation initiation factor eIF3 p65 subunit mRNA complete cds
18683	F04258	Hs.36454	ESTs Highly similar to INORGANIC PYROPHOSPHATASE [Bos taurus]
23930	I96690	Hs.125123	ESTs Weakly similar to IIII ALU SUBFAMILY
11288	AA196512	Is.25916	ESTs
170	D00596	Hs.82962	Thymidylate synthase
11659	AA251809	Hs.38708	Homo sapiens MAD3-like protein kinase mRNA complete cds
14134	AA489080	Hs.3568	ESTs Highly similar to phosphorylation regulatory protein HP-10 [H.sapiens]
11140	AA158132	Hs.11817	ESTs Highly similar to YSA1 PROTEIN [Saccharomyces cerevisiae]
17925	AA164209	Hs.31730	Homo sapiens RRM RNA binding protein GRYBP (GRY-RBP) mRNA complete cds
28530	AA278650	Hs.73281	ESTs
7445	AA104023	Hs.110048	ESTs
18055	AA179387	Hs.73596	ESTs
15174	U82987	Hs.87246	Human Bcl-2 binding component 3 (bcl3) mRNA partial cds
33620	V93943	Hs.59509	ESTs
1932	I24804	Hs.75839	Human p23 mRNA complete cds
39556	F03738	Hs.3657	ESTs
1605	L00058	Hs.70070	V-myc avian myelocytomatosis viral oncogene homolog
4536	U48705	Hs.75562	Receptor protein-tyrosine kinase EDDR1
36200	AA421164	Hs.107213	ESTs
12313	AA387916	Hs.22595	ESTs
19867	H61476	Hs.15641	ESTs
6081	X59390	Hs.82685	CD47 antigen (Rb-related antigen integrin-associated signal transducer)
16708	AA043944	Hs.62663	ESTs
357	D28156	Hs.78202	Human mRNA for transcriptional activator hSNF2b complete cds
8059	AA310967	Hs.5080	ESTs Weakly similar to T04A6.11 [C.elegans]
38830	AA411448	Hs.139386	ESTs
20151	N22895	Hs.6831	Homo sapiens clone 1400 unknown protein mRNA partial cds

FIGURE 2 (CONT.)

28258	2.8	AA505133	Hs.62273	ESTs	
8616	2.8	AA460077	Hs.28555	ESTs	
6480	2.8	X91788	Hs.84874	H. sapiens mRNA for lcn protein	
14560	2.8	AA621122	Hs.51598	ESTs	
35955	2.7	AA400885	Hs.21766	ESTs	
17642	2.7	AA412528	Hs.20183	ESTs Weakly similar to ORF2 consensus sequence encoding endonuclease and reverse transcriptase minus RNaseH [R. norvegicus]	
6131	2.7	AA132983	Hs.44155	ESTs Moderately similar to C-1-TETRAHYDROFOLATE SYNTHASE CYTOPLASMIC [H. sapiens]	
6444	2.7	X72841	Hs.2758	Human retinoblastoma-binding protein (RbAp46) mRNA complete cds	
7701	2.7	X69750	Hs.90077	H. sapiens mRNA for TGIF protein	
42534	2.7	AA215333	Hs.97101	ESTs	
34796	2.7	W73189	Hs.89403	Homo sapiens protein-tyrosine kinase EPHB2v (EPHB2) mRNA complete cds	
1923	2.7	AA291259	Hs.97101	ESTs	
10951	2.7	L23808	Hs.1695	Matrix metalloproteinase 12 (macrophage elastase)	
11308	2.6	AA126719	Hs.25282	ESTs	
4086	2.6	AA207114	Hs.27842	ESTs	
5587	2.6	U24704	Hs.111709	Human anilase secretory factor-1 mRNA complete cds	
19841	2.6	X13482	Hs.80506	U2 SMALL NUCLEAR RIBONUCLEOPROTEIN A'	
7614	2.6	H59617	Hs.5169	ESTs Highly similar to UBIQUITIN-CONJUGATING ENZYME E2-17 KD [Drosophila melanogaster]	
11362	2.6	AA187579	Hs.102696	ESTs Weakly similar to Yel007c-ap [S. cerevisiae]	
13866	2.6	AA272261	Hs.20922	ESTs	
2993	2.6	AA476319	Hs.5327	ESTs	
12986	2.6	M64929	Hs.75200	Protein phosphatase 2 (formerly 2A) regulatory subunit B (PR 52) alpha isoform	
5932	2.5	AA430032	Hs.7487	ESTs Moderately similar to PTTG gene product [R. norvegicus]	
38434	2.5	X62153	Hs.82479	Minichromosome maintenance deficient (S. cerevisiae) 3	
39185	2.5	AA487013	Hs.142592	ESTs	
1424	2.5	AA487508	Hs.9877	Homo sapiens mRNA for KIAA0608 protein complete cds	
21876	2.5	J02645	Hs.81613	Eukaryotic translation initiation factor 2A	
6485	2.5	R43288	EST - RC_R43288		
7960	2.4	X92098	Hs.75914	H. sapiens mRNA for transmembrane protein mp24	
452	2.4	AA285277	Hs.8932	Homo sapiens brain expressed ring finger protein mRNA complete cds	
11701	2.4	D38076	Hs.24763	RAV binding protein 1	
36380	2.4	AA253031	Hs.31730	Homo sapiens RRM RNA binding protein Gyr-bp (GRY-RBP) mRNA complete cds	
14420	2.4	AA426291	Hs.108527	ESTs Weakly similar to No definition line found [C. elegans]	
6387	2.4	AA600322	Hs.19574	ESTs Highly similar to AAC-RICH MRNA CLONE AAC3 PROTEIN [Dictyostelium discoideum]	
1407	2.4	X85372	Hs.105465	H. sapiens mRNA for Sm protein F	
27872	2.4	J04088	Hs.3378	Topoisomerase (DNA) II alpha (170KD)	
8163	2.4	AA459254	Hs.46855	ESTs	
23065	2.4	AA357394	Hs.98073	ESTs	
20837	2.4	J23539	Hs.7165	ESTs Highly similar to zinc finger protein [M. musculus]	
	2.4	N69263	Hs.20524	ESTs Highly similar to HEXOKINASE TYPE I [Homo sapiens]	

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FIGURE 2 (CONT.)

17352	2.3	AA100925	Hs.20990	ESTs	EST - RC_D51272_s
28786	2.3	D51272	Hs.4310	ESTs	
26679	2.3	AA281733	Hs.14811	ESTs	Homo sapiens protein tyrosine phosphatase PIR1 mRNA complete cds
24092	2.3	W42845	Hs.83532	ESTs	Membrane cofactor protein (CD46) trophoblast-lymphocyte cross-reactive antigen
5875	2.3	X59405	Hs.7381	ESTs	Homo sapiens voltage dependent anion channel protein mRNA complete cds
7404	2.3	AA094989	Hs.77496	ESTs	H. sapiens mRNA for Sm protein G
6308	2.3	X63373	Hs.25863	ESTs	ESTs Weakly similar to retin [H.sapiens]
25050	2.3	AA011134	Hs.75761	ESTs	Human serine kinase mRNA complete cds
41935	2.3	T29681	Hs.21486	ESTs	SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 1-ALPHA/BETA
3343	2.3	M97936	Hs.80684	ESTs	High-mobility group (nonhistone chromosomal) protein 2
5937	2.2	X52534	Hs.71475	ESTs	
7387	2.2	AA093977	Hs.5683	ESTs	Homo sapiens mRNA for ATP-dependent RNA helicase #46 complete cds
20843	2.2	N69352	Hs.76887	ESTs	Human 26S proteasome-associated pad1 homolog (POH1) mRNA complete cds
28448	2.2	AA621752	Hs.103300	EST - D78129	
651	2.2	D78129	Hs.21214	ESTs	Homo sapiens diphthamide biosynthesis protein-2 (DPH2) mRNA complete cds
11688	2.2	AA252672	Hs.103300	ESTs	
11803	2.2	AA257971	Hs.21214	ESTs	
4046	2.2	U22376	Hs.1334	MYB PROTO-ONCOGENE PROTEIN	
20276	2.2	N32919	Hs.27931	ESTs	
34370	2.1	AA251829	Hs.104058	ESTs	ESTs Weakly similar to HYPOHETICAL 27.4 KD PROTEIN IN MET2-CPR7 INTERGENIC REGION [Saccharomyces cerevisiae]
14582	2.1	AA621340	Hs.10500	ESTs	ESTs Weakly similar to HYPOHETICAL 39.6 KD PROTEIN IN MTD1-NUP133 INTERGENIC REGION [Saccharomyces cerevisiae]
3461	2.1	S75256	EST - S75256	EST - HG1112-HT1112	
924	2.1	W86469	Hs.77699	EST - HG1112-HT1112	Tropomyosin alpha chain (skeletal muscle)
24348	2.1	AA112053	Hs.15313	ESTs	ESTs Weakly similar to PRE-MRNA SPLICING HELICASE BRR2 [S.cerevisiae]
10898	2.1	D28473	Hs.78770	ESTs	Isoludra-ORNA synthetase
381	2.1	AA236018	Hs.10724	ESTs	ESTs Weakly similar to unknown [S.cerevisiae]
11528	2.1	AA113149	Hs.8130	ESTs	Homo sapiens IPL (IPL) mRNA complete cds
25593	2.1	AA481403	Hs.107213	ESTs	
30040	2.1	U25312	Hs.83550	ESTs	Human heterochromatin protein HP1-Hs-gamma mRNA complete cds
4111	2.1	AC002115	Hs.83378	ESTs	Cytochrome c oxidase subunit Vb
61	2.0	D16611	Hs.89866	EST - D28423	Coproporphyrinogen oxidase (coproporphyrin harderoporphyria)
9112	2.0	D28423	EST - D28423	EST - D28364	
380	2.0	D28364	Hs.42582	ESTs	
377	2.0	AA609710	Hs.5950	ESTs	
29379	2.0	W72276	Hs.9564	ESTs	Human clone 121711 defective mariner transposon Hamar2 mRNA sequence
24230	2.0	H85535	Hs.104558	ESTs	
40212	2.0	AA328993			
8118	2.0				

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[illegible]

FIGURE 3 (CONT.)

25002	18	T60971	Hs 12513	ESTs	
25003	18	AA456432	Hs 123147	ESTs	
10510	18	AA584104	Hs 207177	ESTs	
25119	18	AA511283	Hs 133119	H sapiens mRNA for protein 2	
21	18	AB000965	Hs 133000	H sapiens histone H4 gene	
18797	18	F08438	Hs 124201	ESTs	
38221	18	AA621798	Hs 192236	Human sapiens protein phosphatase with 5'-flanking (PPP5C1) mRNA, complete cds	
25120	18	AA621799	Hs 192237	Human sapiens protein phosphatase with 5'-flanking (PPP5C1) mRNA, complete cds	
42902	18	W66433	Hs 125613	ESTs	
22372	18	R03231	Hs 203200	EST	
33115	18	AA532709	Hs 203203	ESTs	Weakly similar to HYPOTHETICAL BG 8 AD PROTEIN TOSHC7 IN CHROMOSOME 1 (C46948)
18810	18	AA532926	Hs 125849	ESTs	
29643	18	H15540	Hs 43116	ESTs	
36025	18	AA141526	Hs 125850	Human sapiens mRNA for KIAA0320 protein, partial cds	
15008	18	U32015	Hs 125851	Human sapiens mRNA for KIAA0320 protein, partial cds	
25122	18	AA541423	Hs 103448	ESTs	Human brain testis-specific histone H4C1i complementary (H4C1i) mRNA, complete cds
34581	18	AA338275	Hs 102118	ESTs	
40384	18	H33336	Hs 123237	ESTs	
10714	18	AA001207	Hs 59051	ESTs	
31684	18	AA532927	Hs 125852	ESTs	Human sapiens mRNA for KIAA0320 protein, partial cds
32904	18	D30822	Hs 107126	ESTs	
32064	18	N34658	Hs 7748	Human sapiens Gene 73815 mRNA, sequence	
36393	18	AA428333	Hs 863204	ESTs	
28011	18	AA428334	Hs 863205	ESTs	
32911	18	N28712	Hs 8890	ESTs	
338	18	D13645	Hs 133505	T-CELL SURFACE GLYCOPROTEIN CD1E PRECURSOR	
3673	18	X14873	Hs 87931	ESTs	
33659	18	AA410293	Hs 29494	Human brain secretory protein 18 kDa (Sp18) mRNA, complete cds	
5243	18	U35948	Hs 102503	ESTs	
32912	18	AA410294	Hs 102504	ESTs	
33788	18	AA410295	Hs 102505	ESTs	
3163	18	M44424	Hs 1335	Calnexin E	
22420	18	R04109	Hs 23457	ESTs	
29517	18	N03886	Hs 107747	ESTs	
39027	18	AA532333	Hs 113357	EST	
40913	18	AA532334	Hs 113358	EST	
3637	18	X58377	Hs 1721	Human mRNA for adipoquestin, inhibitory factor	
29351	18	H01134	Hs 141382	ESTs	
29329	18	F02202	Hs 100900	ESTs	
8155	18	X74331	Hs 24318	RNA domain polypeptide 2A (D502)	
3214	18	U35200	Hs 100901	Human testis-specific protein for granulosa cell-specific protein	
30746	18	AA410296	Hs 102506	ESTs	
40900	18	H49104	Hs 79108	NUCLEAR FACTOR RBP140	
31818	18	AA489954	Hs 104820	EST	
21861	18	AA324556	Hs 135196	EST	
22772	18	H48408	Hs 29410	ESTs	
37552	18	H07979	Hs 143279	ESTs	
31819	18	X58378	Hs 1721	Human mRNA for adipoquestin, inhibitory factor	
28311	18	H08116	Hs 3241	ESTs	Weakly similar to E2025.1 (C46948)
38318	18	AA492500	Hs 18747	Human testis ribonuclease P protein subunit p20 (RPP20) mRNA, complete cds	
37239	18	AA470004	Hs 95358	ESTs	
28170	18	U14518	Hs 1294	Chemokine protein A (CXCL1)	
3170	18	AA510951	Hs 123237	ESTs	
33006	18	W05876	Hs 52141	ESTs	
28188	18	AA502159	Hs 18349	Human sapiens KIAA0321 mRNA, partial cds	

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FIGURE 3 (CONT.)

30617	10	U02648	Hs 47083	EST	
30106	10	A0371581	Hs 143355	EST	Weakly similar to p27 (11 segments)
30190	10	H23264	Hs 44463	EST	
788	10	D08971	Hs 71851	Human mRNA for KIAA0271, gene product cts	
4388	10	U00022	Hs 21823	DNA repair protein, ERCC1	
31344	10	H07183	Hs 82010	EST	
4137	10	A040558	Hs 107811	Human cytochrome P-450 2C22 mRNA complete cds	29% (11 segments)
4137	10	U07811	Hs 107811	Human cytochrome P-450 2C22 mRNA complete cds	
2010	10	L37278	Hs 123074	Human aspartyl aminotransferase (P-450 2C22) mRNA complete cds	
2122	10	L40286	Hs 28956	Human aspartyl aminotransferase (P-450 2C22) mRNA complete cds	
28520	10	A0324202	Hs 48729	EST	
6479	10	H01853	Hs 21059	EST	
37995	10	A028570	Hs 21059	EST	
34004	10	A0321748	Hs 98719	EST	
35393	10	AA412530	Hs 97804	EST	
76644	10	D17183	Hs 103262	EST	
38184	10	AA07898	Hs 36932	EST	
42177	10	T73786	Hs 102582	EST	
3913	10	U10281	Hs 66376	Human PDL1 (p27) mRNA complete cds	
37138	10	T80313	Hs 18732	EST	
21238	10	R04584	Hs 51919	Phosphoglucomutase protein	
2637	10	M33597	Hs 31723	Fucosyltransferase 4 (alpha 1-3) (Lusitana) mRNA complete cds	
34518	10	A0378221	Hs 103104	EST	
19008	10	A017865	Hs 36251	Human aspartyl aminotransferase 2 (P-450 2C22) mRNA complete cds	
34048	10	H03781	Hs 28835	EST	
33060	10	D06831	Hs 128021	EST	
34105	10	T35331	Hs 141905	EST	
84121	10	A0207123	Hs 120857	EST	
30085	10	AA083724	Hs 108609	EST	PCNA40074
3196	10	F13635	Hs 85638	EST	Weakly similar to USAGL DNA GLO-COYLASE (PRECURSOR H. sapiens)
6723	10	M38817	Hs 143065	EST	Moderately similar to M3 ALU SUBFAMILY SBI WARRING ENTRY III (H. sapiens)
25713	10	A0325540	Hs 1255	ACQUILIPROTEIN REGULATORY PROTEIN-1	
7827	10	M29810	Hs 92223	Chondroitinase E	
32518	10	A0325540	Hs 1255	ACQUILIPROTEIN REGULATORY PROTEIN-1	
32518	10	N02044	Hs 20323	EST	Weakly similar to p27 (11 segments)
32518	10	R37272	Hs 29527	EST	
32518	10	N25115	Hs 44688	EST	
32518	10	R39427	Hs 46748	EST	
41878	10	R06073	Hs 144133	EST	
42392	10	A0371711	Hs 107479	EST	
38844	10	A020558	Hs 107479	EST	
35000	10	AA08715	Hs 107479	EST	
35000	10	L18920	Hs 20880	MELANOMA-ASSOCIATED ANTIGEN-2	
35218	10	AA02892	Hs 105465	EST	Weakly similar to Hs ALU SUBFAMILY J (H. sapiens)
35218	10	AA02892	Hs 105465	EST	Weakly similar to Hs ALU SUBFAMILY J (H. sapiens)
35218	10	AA02892	Hs 105465	EST	Weakly similar to Hs ALU SUBFAMILY J (H. sapiens)
41718	10	R06260	Hs 15108	EST	Weakly similar to p27 (11 segments)
39725	10	H11322	Hs 6733	EST	
27037	10	AA00188	Hs 83752	EST	
42877	10	H04031	Hs 40720	Human aspartyl aminotransferase, gene complete cds	
28349	10	AA153355	Hs 67132	Human aspartyl aminotransferase, gene complete cds	
3408	10	R06836	Hs 37104	SQUAMOUS CELL CARCINOMA ANTIGEN-1	
3375	10	S00233	Hs 108642	HNR.T1	

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FIGURE 3 (CONT.)

173	AA13707	Hs 90248	ESTs
174	AA139200	Hs 102223	ESTs
175	BS6432	Hs 26358	ESTs
176	CB3889	Hs 82292	Human mRNA for PMAO213 gene complete cds
177	AA134660	Hs 44511	ESTs
178	AA134660	Hs 44511	ESTs
179	AB0963	Hs 83794	Frp2p3 3' UTR cDNA
180	AA339828	Hs 50718	ESTs
181	N23870	Hs 44532	Marginalin mRNA for disialoglycophorin
182	U08087	Hs 47120	ESTs
183	U08087	Hs 47120	ESTs
184	AA134660	Hs 45023	Human beta-2-microglobulin mRNA for UDP-Galactose 4-epimerase
185	AA134660	Hs 45023	Human beta-2-microglobulin mRNA for UDP-Galactose 4-epimerase
186	AA134660	Hs 45023	Human beta-2-microglobulin mRNA for UDP-Galactose 4-epimerase
187	U11186	Hs 141802	ESTs
188	AA134660	Hs 141802	ESTs
189	AA134660	Hs 141802	ESTs
190	AA134660	Hs 141802	ESTs
191	AA134660	Hs 141802	ESTs
192	AA134660	Hs 141802	ESTs
193	AA134660	Hs 141802	ESTs
194	AA134660	Hs 141802	ESTs
195	AA134660	Hs 141802	ESTs
196	AA134660	Hs 141802	ESTs
197	AA134660	Hs 141802	ESTs
198	AA134660	Hs 141802	ESTs
199	AA134660	Hs 141802	ESTs
200	AA134660	Hs 141802	ESTs
201	AA134660	Hs 141802	ESTs
202	AA134660	Hs 141802	ESTs
203	AA134660	Hs 141802	ESTs
204	AA134660	Hs 141802	ESTs
205	AA134660	Hs 141802	ESTs
206	AA134660	Hs 141802	ESTs
207	AA134660	Hs 141802	ESTs
208	AA134660	Hs 141802	ESTs
209	AA134660	Hs 141802	ESTs
210	AA134660	Hs 141802	ESTs
211	AA134660	Hs 141802	ESTs
212	AA134660	Hs 141802	ESTs
213	AA134660	Hs 141802	ESTs
214	AA134660	Hs 141802	ESTs
215	AA134660	Hs 141802	ESTs
216	AA134660	Hs 141802	ESTs
217	AA134660	Hs 141802	ESTs
218	AA134660	Hs 141802	ESTs
219	AA134660	Hs 141802	ESTs
220	AA134660	Hs 141802	ESTs
221	AA134660	Hs 141802	ESTs
222	AA134660	Hs 141802	ESTs
223	AA134660	Hs 141802	ESTs
224	AA134660	Hs 141802	ESTs
225	AA134660	Hs 141802	ESTs
226	AA134660	Hs 141802	ESTs
227	AA134660	Hs 141802	ESTs
228	AA134660	Hs 141802	ESTs
229	AA134660	Hs 141802	ESTs
230	AA134660	Hs 141802	ESTs
231	AA134660	Hs 141802	ESTs
232	AA134660	Hs 141802	ESTs
233	AA134660	Hs 141802	ESTs
234	AA134660	Hs 141802	ESTs
235	AA134660	Hs 141802	ESTs
236	AA134660	Hs 141802	ESTs
237	AA134660	Hs 141802	ESTs
238	AA134660	Hs 141802	ESTs
239	AA134660	Hs 141802	ESTs
240	AA134660	Hs 141802	ESTs
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242	AA134660	Hs 141802	ESTs
243	AA134660	Hs 141802	ESTs
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245	AA134660	Hs 141802	ESTs
246	AA134660	Hs 141802	ESTs
247	AA134660	Hs 141802	ESTs
248	AA134660	Hs 141802	ESTs
249	AA134660	Hs 141802	ESTs
250	AA134660	Hs 141802	ESTs
251	AA134660	Hs 141802	ESTs
252	AA134660	Hs 141802	ESTs
253	AA134660	Hs 141802	ESTs
254	AA134660	Hs 141802	ESTs
255	AA134660	Hs 141802	ESTs
256	AA134660	Hs 141802	ESTs
257	AA134660	Hs 141802	ESTs
258	AA134660	Hs 141802	ESTs
259	AA134660	Hs 141802	ESTs
260	AA134660	Hs 141802	ESTs

FIGURE 3 (CONT.)

10	AA359543	Hs_141444	EST1	
11	U08108	Hs_29326	Human sapiens mRNA for TRAF5, complete cds	
12	R07437	Hs_2001	THROMBOXANE SYNTHASE	
13	R08118	Hs_20118	ESTs	
14	AA353400	Hs_104036	ESTs	
15	AA4400	Hs_123006	ESTs	
16	AA086905	Hs_123006	ESTs	
17	AA250841	Hs_41313	ESTs highly similar to N18 RIBOSOMAL PROTEIN L18 (Rblu1a noncsgu)	
18	U09060	Hs_41318	Human NAGE-5 antigen (NAGE5) gene complete cds	
19	R19383	Hs_102020	ESTs	
20	C1844	Hs_12136	ESTs	
21	AA086905	Hs_123006	ESTs	
22	AA086905	Hs_123006	ESTs	
23	AA086905	Hs_123006	ESTs	
24	AA086905	Hs_123006	ESTs	
25	AA086905	Hs_123006	ESTs	
26	AA086905	Hs_123006	ESTs	
27	AA086905	Hs_123006	ESTs	
28	AA086905	Hs_123006	ESTs	
29	AA086905	Hs_123006	ESTs	
30	AA086905	Hs_123006	ESTs	
31	AA086905	Hs_123006	ESTs	
32	AA086905	Hs_123006	ESTs	
33	AA086905	Hs_123006	ESTs	
34	AA086905	Hs_123006	ESTs	
35	AA086905	Hs_123006	ESTs	
36	AA086905	Hs_123006	ESTs	
37	AA086905	Hs_123006	ESTs	
38	AA086905	Hs_123006	ESTs	
39	AA086905	Hs_123006	ESTs	
40	AA086905	Hs_123006	ESTs	
41	AA086905	Hs_123006	ESTs	
42	AA086905	Hs_123006	ESTs	
43	AA086905	Hs_123006	ESTs	
44	AA086905	Hs_123006	ESTs	
45	AA086905	Hs_123006	ESTs	
46	AA086905	Hs_123006	ESTs	
47	AA086905	Hs_123006	ESTs	
48	AA086905	Hs_123006	ESTs	
49	AA086905	Hs_123006	ESTs	
50	AA086905	Hs_123006	ESTs	
51	AA086905	Hs_123006	ESTs	
52	AA086905	Hs_123006	ESTs	
53	AA086905	Hs_123006	ESTs	
54	AA086905	Hs_123006	ESTs	
55	AA086905	Hs_123006	ESTs	
56	AA086905	Hs_123006	ESTs	
57	AA086905	Hs_123006	ESTs	
58	AA086905	Hs_123006	ESTs	
59	AA086905	Hs_123006	ESTs	
60	AA086905	Hs_123006	ESTs	
61	AA086905	Hs_123006	ESTs	
62	AA086905	Hs_123006	ESTs	
63	AA086905	Hs_123006	ESTs	
64	AA086905	Hs_123006	ESTs	
65	AA086905	Hs_123006	ESTs	
66	AA086905	Hs_123006	ESTs	
67	AA086905	Hs_123006	ESTs	
68	AA086905	Hs_123006	ESTs	
69	AA086905	Hs_123006	ESTs	
70	AA086905	Hs_123006	ESTs	
71	AA086905	Hs_123006	ESTs	
72	AA086905	Hs_123006	ESTs	
73	AA086905	Hs_123006	ESTs	
74	AA086905	Hs_123006	ESTs	
75	AA086905	Hs_123006	ESTs	
76	AA086905	Hs_123006	ESTs	
77	AA086905	Hs_123006	ESTs	
78	AA086905	Hs_123006	ESTs	
79	AA086905	Hs_123006	ESTs	
80	AA086905	Hs_123006	ESTs	
81	AA086905	Hs_123006	ESTs	
82	AA086905	Hs_123006	ESTs	
83	AA086905	Hs_123006	ESTs	
84	AA086905	Hs_123006	ESTs	
85	AA086905	Hs_123006	ESTs	
86	AA086905	Hs_123006	ESTs	
87	AA086905	Hs_123006	ESTs	
88	AA086905	Hs_123006	ESTs	
89	AA086905	Hs_123006	ESTs	
90	AA086905	Hs_123006	ESTs	
91	AA086905	Hs_123006	ESTs	
92	AA086905	Hs_123006	ESTs	

FIGURE 3 (CONT.)

[illegible]

FIGURE 3 (CONT.)

34490	AA252354	Hs 111395	EST1	
34491	AA252355	Hs 102345	EST1	
34492	AA109440	Hs 5219	EST1	RC_M3344
34493	AA252356	Hs 102346	EST1	
34494	AA252357	Hs 102347	EST1	
34495	AA252358	Hs 102348	EST1	
34496	AA252359	Hs 102349	EST1	
34497	AA252360	Hs 102350	EST1	
34498	AA252361	Hs 102351	EST1	
34499	AA252362	Hs 102352	EST1	
34500	AA252363	Hs 102353	EST1	
34501	AA252364	Hs 102354	EST1	
34502	AA252365	Hs 102355	EST1	
34503	AA252366	Hs 102356	EST1	
34504	AA252367	Hs 102357	EST1	
34505	AA252368	Hs 102358	EST1	
34506	AA252369	Hs 102359	EST1	
34507	AA252370	Hs 102360	EST1	
34508	AA252371	Hs 102361	EST1	
34509	AA252372	Hs 102362	EST1	
34510	AA252373	Hs 102363	EST1	
34511	AA252374	Hs 102364	EST1	
34512	AA252375	Hs 102365	EST1	
34513	AA252376	Hs 102366	EST1	
34514	AA252377	Hs 102367	EST1	
34515	AA252378	Hs 102368	EST1	
34516	AA252379	Hs 102369	EST1	
34517	AA252380	Hs 102370	EST1	
34518	AA252381	Hs 102371	EST1	
34519	AA252382	Hs 102372	EST1	
34520	AA252383	Hs 102373	EST1	
34521	AA252384	Hs 102374	EST1	
34522	AA252385	Hs 102375	EST1	
34523	AA252386	Hs 102376	EST1	
34524	AA252387	Hs 102377	EST1	
34525	AA252388	Hs 102378	EST1	
34526	AA252389	Hs 102379	EST1	
34527	AA252390	Hs 102380	EST1	
34528	AA252391	Hs 102381	EST1	
34529	AA252392	Hs 102382	EST1	
34530	AA252393	Hs 102383	EST1	
34531	AA252394	Hs 102384	EST1	
34532	AA252395	Hs 102385	EST1	
34533	AA252396	Hs 102386	EST1	
34534	AA252397	Hs 102387	EST1	
34535	AA252398	Hs 102388	EST1	
34536	AA252399	Hs 102389	EST1	
34537	AA252400	Hs 102390	EST1	
34538	AA252401	Hs 102391	EST1	
34539	AA252402	Hs 102392	EST1	
34540	AA252403	Hs 102393	EST1	
34541	AA252404	Hs 102394	EST1	
34542	AA252405	Hs 102395	EST1	
34543	AA252406	Hs 102396	EST1	
34544	AA252407	Hs 102397	EST1	
34545	AA252408	Hs 102398	EST1	
34546	AA252409	Hs 102399	EST1	
34547	AA252410	Hs 102400	EST1	
34548	AA252411	Hs 102401	EST1	
34549	AA252412	Hs 102402	EST1	
34550	AA252413	Hs 102403	EST1	
34551	AA252414	Hs 102404	EST1	
34552	AA252415	Hs 102405	EST1	
34553	AA252416	Hs 102406	EST1	
34554	AA252417	Hs 102407	EST1	
34555	AA252418	Hs 102408	EST1	
34556	AA252419	Hs 102409	EST1	
34557	AA252420	Hs 102410	EST1	
34558	AA252421	Hs 102411	EST1	
34559	AA252422	Hs 102412	EST1	
34560	AA252423	Hs 102413	EST1	
34561	AA252424	Hs 102414	EST1	
34562	AA252425	Hs 102415	EST1	
34563	AA252426	Hs 102416	EST1	
34564	AA252427	Hs 102417	EST1	
34565	AA252428	Hs 102418	EST1	
34566	AA252429	Hs 102419	EST1	
34567	AA252430	Hs 102420	EST1	
34568	AA252431	Hs 102421	EST1	
34569	AA252432	Hs 102422	EST1	
34570	AA252433	Hs 102423	EST1	
34571	AA252434	Hs 102424	EST1	
34572	AA252435	Hs 102425	EST1	
34573	AA252436	Hs 102426	EST1	
34574	AA252437	Hs 102427	EST1	
34575	AA252438	Hs 102428	EST1	
34576	AA252439	Hs 102429	EST1	
34577	AA252440	Hs 102430	EST1	
34578	AA252441	Hs 102431	EST1	
34579	AA252442	Hs 102432	EST1	
34580	AA252443	Hs 102433	EST1	
34581	AA252444	Hs 102434	EST1	
34582	AA252445	Hs 102435	EST1	
34583	AA252446	Hs 102436	EST1	
34584	AA252447	Hs 102437	EST1	
34585	AA252448	Hs 102438	EST1	
34586	AA252449	Hs 102439	EST1	
34587	AA252450	Hs 102440	EST1	
34588	AA252451	Hs 102441	EST1	
34589	AA252452	Hs 102442	EST1	
34590	AA252453	Hs 102443	EST1	
34591	AA252454	Hs 102444	EST1	
34592	AA252455	Hs 102445	EST1	
34593	AA252456	Hs 102446	EST1	
34594	AA252457	Hs 102447	EST1	
34595	AA252458	Hs 102448	EST1	
34596	AA252459	Hs 102449	EST1	
34597	AA252460	Hs 102450	EST1	
34598	AA252461	Hs 102451	EST1	
34599	AA252462	Hs 102452	EST1	
34600	AA252463	Hs 102453	EST1	

FIGURE 3 (CONT.)

21	AA04354	Hs 89415 EST1	
22	U03833	Hs 29435 EST1	
23	AA05065	Hs 33744 EST1	
24	AA12894	Human spleen tissue B19p5.7 (B19p5.7) mRNA complete cds	
25	U03833	Hs 29435 EST1	
26	AA04482	Hs 12328 EST1	
27	AA04482	Hs 12328 EST1	
28	AA13590	Hs 81711 EST1	
29	U03833	Hs 29435 EST1	
30	AA13590	Hs 81711 EST1	
31	AA13590	Hs 81711 EST1	
32	AA13590	Hs 81711 EST1	
33	AA13590	Hs 81711 EST1	
34	AA13590	Hs 81711 EST1	
35	AA13590	Hs 81711 EST1	
36	AA13590	Hs 81711 EST1	
37	AA13590	Hs 81711 EST1	
38	AA13590	Hs 81711 EST1	
39	AA13590	Hs 81711 EST1	
40	AA13590	Hs 81711 EST1	
41	AA13590	Hs 81711 EST1	
42	AA13590	Hs 81711 EST1	
43	AA13590	Hs 81711 EST1	
44	AA13590	Hs 81711 EST1	
45	AA13590	Hs 81711 EST1	
46	AA13590	Hs 81711 EST1	
47	AA13590	Hs 81711 EST1	
48	AA13590	Hs 81711 EST1	
49	AA13590	Hs 81711 EST1	
50	AA13590	Hs 81711 EST1	
51	AA13590	Hs 81711 EST1	
52	AA13590	Hs 81711 EST1	
53	AA13590	Hs 81711 EST1	
54	AA13590	Hs 81711 EST1	
55	AA13590	Hs 81711 EST1	
56	AA13590	Hs 81711 EST1	
57	AA13590	Hs 81711 EST1	
58	AA13590	Hs 81711 EST1	
59	AA13590	Hs 81711 EST1	
60	AA13590	Hs 81711 EST1	
61	AA13590	Hs 81711 EST1	
62	AA13590	Hs 81711 EST1	
63	AA13590	Hs 81711 EST1	
64	AA13590	Hs 81711 EST1	
65	AA13590	Hs 81711 EST1	
66	AA13590	Hs 81711 EST1	
67	AA13590	Hs 81711 EST1	
68	AA13590	Hs 81711 EST1	
69	AA13590	Hs 81711 EST1	
70	AA13590	Hs 81711 EST1	
71	AA13590	Hs 81711 EST1	
72	AA13590	Hs 81711 EST1	
73	AA13590	Hs 81711 EST1	
74	AA13590	Hs 81711 EST1	
75	AA13590	Hs 81711 EST1	
76	AA13590	Hs 81711 EST1	
77	AA13590	Hs 81711 EST1	
78	AA13590	Hs 81711 EST1	
79	AA13590	Hs 81711 EST1	
80	AA13590	Hs 81711 EST1	
81	AA13590	Hs 81711 EST1	
82	AA13590	Hs 81711 EST1	
83	AA13590	Hs 81711 EST1	
84	AA13590	Hs 81711 EST1	
85	AA13590	Hs 81711 EST1	
86	AA13590	Hs 81711 EST1	
87	AA13590	Hs 81711 EST1	
88	AA13590	Hs 81711 EST1	
89	AA13590	Hs 81711 EST1	
90	AA13590	Hs 81711 EST1	
91	AA13590	Hs 81711 EST1	
92	AA13590	Hs 81711 EST1	
93	AA13590	Hs 81711 EST1	
94	AA13590	Hs 81711 EST1	
95	AA13590	Hs 81711 EST1	
96	AA13590	Hs 81711 EST1	
97	AA13590	Hs 81711 EST1	
98	AA13590	Hs 81711 EST1	
99	AA13590	Hs 81711 EST1	
100	AA13590	Hs 81711 EST1	

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FIGURE 3 (CONT.)

U00001	ACTA1	Actin	Actin	Cytoskeleton	
U00002	ACTA2	Actin	Actin	Cytoskeleton	
U00003	ACTA3	Actin	Actin	Cytoskeleton	
U00004	ACTA4	Actin	Actin	Cytoskeleton	
U00005	ACTA5	Actin	Actin	Cytoskeleton	
U00006	ACTA6	Actin	Actin	Cytoskeleton	
U00007	ACTA7	Actin	Actin	Cytoskeleton	
U00008	ACTA8	Actin	Actin	Cytoskeleton	
U00009	ACTA9	Actin	Actin	Cytoskeleton	
U00010	ACTA10	Actin	Actin	Cytoskeleton	
U00011	ACTA11	Actin	Actin	Cytoskeleton	
U00012	ACTA12	Actin	Actin	Cytoskeleton	
U00013	ACTA13	Actin	Actin	Cytoskeleton	
U00014	ACTA14	Actin	Actin	Cytoskeleton	
U00015	ACTA15	Actin	Actin	Cytoskeleton	
U00016	ACTA16	Actin	Actin	Cytoskeleton	
U00017	ACTA17	Actin	Actin	Cytoskeleton	
U00018	ACTA18	Actin	Actin	Cytoskeleton	
U00019	ACTA19	Actin	Actin	Cytoskeleton	
U00020	ACTA20	Actin	Actin	Cytoskeleton	
U00021	ACTA21	Actin	Actin	Cytoskeleton	
U00022	ACTA22	Actin	Actin	Cytoskeleton	
U00023	ACTA23	Actin	Actin	Cytoskeleton	
U00024	ACTA24	Actin	Actin	Cytoskeleton	
U00025	ACTA25	Actin	Actin	Cytoskeleton	
U00026	ACTA26	Actin	Actin	Cytoskeleton	
U00027	ACTA27	Actin	Actin	Cytoskeleton	
U00028	ACTA28	Actin	Actin	Cytoskeleton	
U00029	ACTA29	Actin	Actin	Cytoskeleton	
U00030	ACTA30	Actin	Actin	Cytoskeleton	
U00031	ACTA31	Actin	Actin	Cytoskeleton	
U00032	ACTA32	Actin	Actin	Cytoskeleton	
U00033	ACTA33	Actin	Actin	Cytoskeleton	
U00034	ACTA34	Actin	Actin	Cytoskeleton	
U00035	ACTA35	Actin	Actin	Cytoskeleton	
U00036	ACTA36	Actin	Actin	Cytoskeleton	
U00037	ACTA37	Actin	Actin	Cytoskeleton	
U00038	ACTA38	Actin	Actin	Cytoskeleton	
U00039	ACTA39	Actin	Actin	Cytoskeleton	
U00040	ACTA40	Actin	Actin	Cytoskeleton	
U00041	ACTA41	Actin	Actin	Cytoskeleton	
U00042	ACTA42	Actin	Actin	Cytoskeleton	
U00043	ACTA43	Actin	Actin	Cytoskeleton	
U00044	ACTA44	Actin	Actin	Cytoskeleton	
U00045	ACTA45	Actin	Actin	Cytoskeleton	
U00046	ACTA46	Actin	Actin	Cytoskeleton	
U00047	ACTA47	Actin	Actin	Cytoskeleton	
U00048	ACTA48	Actin	Actin	Cytoskeleton	
U00049	ACTA49	Actin	Actin	Cytoskeleton	
U00050	ACTA50	Actin	Actin	Cytoskeleton	
U00051	ACTA51	Actin	Actin	Cytoskeleton	
U00052	ACTA52	Actin	Actin	Cytoskeleton	
U00053	ACTA53	Actin	Actin	Cytoskeleton	
U00054	ACTA54	Actin	Actin	Cytoskeleton	
U00055	ACTA55	Actin	Actin	Cytoskeleton	
U00056	ACTA56	Actin	Actin	Cytoskeleton	
U00057	ACTA57	Actin	Actin	Cytoskeleton	
U00058	ACTA58	Actin	Actin	Cytoskeleton	
U00059	ACTA59	Actin	Actin	Cytoskeleton	
U00060	ACTA60	Actin	Actin	Cytoskeleton	
U00061	ACTA61	Actin	Actin	Cytoskeleton	
U00062	ACTA62	Actin	Actin	Cytoskeleton	
U00063	ACTA63	Actin	Actin	Cytoskeleton	
U00064	ACTA64	Actin	Actin	Cytoskeleton	
U00065	ACTA65	Actin	Actin	Cytoskeleton	
U00066	ACTA66	Actin	Actin	Cytoskeleton	
U00067	ACTA67	Actin	Actin	Cytoskeleton	
U00068	ACTA68	Actin	Actin	Cytoskeleton	
U00069	ACTA69	Actin	Actin	Cytoskeleton	
U00070	ACTA70	Actin	Actin	Cytoskeleton	
U00071	ACTA71	Actin	Actin	Cytoskeleton	
U00072	ACTA72	Actin	Actin	Cytoskeleton	
U00073	ACTA73	Actin	Actin	Cytoskeleton	
U00074	ACTA74	Actin	Actin	Cytoskeleton	
U00075	ACTA75	Actin	Actin	Cytoskeleton	
U00076	ACTA76	Actin	Actin	Cytoskeleton	
U00077	ACTA77	Actin	Actin	Cytoskeleton	
U00078	ACTA78	Actin	Actin	Cytoskeleton	
U00079	ACTA79	Actin	Actin	Cytoskeleton	
U00080	ACTA80	Actin	Actin	Cytoskeleton	
U00081	ACTA81	Actin	Actin	Cytoskeleton	
U00082	ACTA82	Actin	Actin	Cytoskeleton	
U00083	ACTA83	Actin	Actin	Cytoskeleton	
U00084	ACTA84	Actin	Actin	Cytoskeleton	
U00085	ACTA85	Actin	Actin	Cytoskeleton	
U00086	ACTA86	Actin	Actin	Cytoskeleton	
U00087	ACTA87	Actin	Actin	Cytoskeleton	
U00088	ACTA88	Actin	Actin	Cytoskeleton	
U00089	ACTA89	Actin	Actin	Cytoskeleton	
U00090	ACTA90	Actin	Actin	Cytoskeleton	
U00091	ACTA91	Actin	Actin	Cytoskeleton	
U00092	ACTA92	Actin	Actin	Cytoskeleton	
U00093	ACTA93	Actin	Actin	Cytoskeleton	
U00094	ACTA94	Actin	Actin	Cytoskeleton	
U00095	ACTA95	Actin	Actin	Cytoskeleton	
U00096	ACTA96	Actin	Actin	Cytoskeleton	
U00097	ACTA97	Actin	Actin	Cytoskeleton	
U00098	ACTA98	Actin	Actin	Cytoskeleton	
U00099	ACTA99	Actin	Actin	Cytoskeleton	
U00100	ACTA100	Actin	Actin	Cytoskeleton	

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FIGURE 3 (CONT.)

5	NC02011	Hs_13105	EST1	
6	NC02012	Hs_13106	EST1	
7	NC02013	Hs_13107	EST1	
8	NC02014	Hs_13108	EST1	
9	NC02015	Hs_13109	EST1	
10	NC02016	Hs_13110	EST1	
11	NC02017	Hs_13111	EST1	
12	NC02018	Hs_13112	EST1	
13	NC02019	Hs_13113	EST1	
14	NC02020	Hs_13114	EST1	
15	NC02021	Hs_13115	EST1	
16	NC02022	Hs_13116	EST1	
17	NC02023	Hs_13117	EST1	
18	NC02024	Hs_13118	EST1	
19	NC02025	Hs_13119	EST1	
20	NC02026	Hs_13120	EST1	
21	NC02027	Hs_13121	EST1	
22	NC02028	Hs_13122	EST1	
23	NC02029	Hs_13123	EST1	
24	NC02030	Hs_13124	EST1	
25	NC02031	Hs_13125	EST1	
26	NC02032	Hs_13126	EST1	
27	NC02033	Hs_13127	EST1	
28	NC02034	Hs_13128	EST1	
29	NC02035	Hs_13129	EST1	
30	NC02036	Hs_13130	EST1	
31	NC02037	Hs_13131	EST1	
32	NC02038	Hs_13132	EST1	
33	NC02039	Hs_13133	EST1	
34	NC02040	Hs_13134	EST1	
35	NC02041	Hs_13135	EST1	
36	NC02042	Hs_13136	EST1	
37	NC02043	Hs_13137	EST1	
38	NC02044	Hs_13138	EST1	
39	NC02045	Hs_13139	EST1	
40	NC02046	Hs_13140	EST1	
41	NC02047	Hs_13141	EST1	
42	NC02048	Hs_13142	EST1	
43	NC02049	Hs_13143	EST1	
44	NC02050	Hs_13144	EST1	
45	NC02051	Hs_13145	EST1	
46	NC02052	Hs_13146	EST1	
47	NC02053	Hs_13147	EST1	
48	NC02054	Hs_13148	EST1	
49	NC02055	Hs_13149	EST1	
50	NC02056	Hs_13150	EST1	
51	NC02057	Hs_13151	EST1	
52	NC02058	Hs_13152	EST1	
53	NC02059	Hs_13153	EST1	
54	NC02060	Hs_13154	EST1	
55	NC02061	Hs_13155	EST1	
56	NC02062	Hs_13156	EST1	
57	NC02063	Hs_13157	EST1	
58	NC02064	Hs_13158	EST1	
59	NC02065	Hs_13159	EST1	
60	NC02066	Hs_13160	EST1	
61	NC02067	Hs_13161	EST1	
62	NC02068	Hs_13162	EST1	
63	NC02069	Hs_13163	EST1	
64	NC02070	Hs_13164	EST1	
65	NC02071	Hs_13165	EST1	
66	NC02072	Hs_13166	EST1	
67	NC02073	Hs_13167	EST1	
68	NC02074	Hs_13168	EST1	
69	NC02075	Hs_13169	EST1	
70	NC02076	Hs_13170	EST1	
71	NC02077	Hs_13171	EST1	
72	NC02078	Hs_13172	EST1	
73	NC02079	Hs_13173	EST1	
74	NC02080	Hs_13174	EST1	
75	NC02081	Hs_13175	EST1	
76	NC02082	Hs_13176	EST1	
77	NC02083	Hs_13177	EST1	
78	NC02084	Hs_13178	EST1	
79	NC02085	Hs_13179	EST1	
80	NC02086	Hs_13180	EST1	
81	NC02087	Hs_13181	EST1	
82	NC02088	Hs_13182	EST1	
83	NC02089	Hs_13183	EST1	
84	NC02090	Hs_13184	EST1	
85	NC02091	Hs_13185	EST1	
86	NC02092	Hs_13186	EST1	
87	NC02093	Hs_13187	EST1	
88	NC02094	Hs_13188	EST1	
89	NC02095	Hs_13189	EST1	
90	NC02096	Hs_13190	EST1	
91	NC02097	Hs_13191	EST1	
9				

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FIGURE 3 (CONT.)

[illegible]

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FIGURE 3 (CONT.)

[illegible]

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FIGURE 3 (CONT.)

41	D31145	Hs.61332	Proteoglycan 2 Glycosyltransferase	
42	A4218406	Hs.19347	EST1	
43	H08161	Hs.86597	EST1	
44	H05408	Hs.39704	EST1	
45	H05778	Hs.13331	EST1	
46	A4218093	Hs.108642	HsCR.71	
47	U78247	Hs.90790	Human clone 23509 mRNA, sequence	
48	A436220	Hs.86553	EST1	
49	A4218094	Hs.86554	EST1	
50	A4218095	Hs.86555	EST1	
51	U42451	Hs.82260	EST1	
52	A436065	Hs.56159	EST1	Weakly similar to EMB49.2 gene product [C. elegans]
53	H10643	Hs.42932	EST	
54	H08163	Hs.78802	EST	
55	F03115	Hs.89403	Homo sapiens protein tyrosine kinase EPHB2 (EPH2B) mRNA, complete cds	
56	A4443221	Hs.101110	EST1	
57	A4471863	Hs.96914	EST1	Human sapiens mRNA for KIA04052 protein, partial cds
58	A4471864	Hs.96915	EST1	Human sapiens protein tyrosine kinase EPHB2 (EPH2B) mRNA, complete cds
59	U42021	Hs.90713	EST1	EST1 highly similar to PUFATIVE UBIQUITIN CARBOXY-TERMINAL HYDROLASE C13A11.6AC [Schistosoma mansoni, partial]
60	A4119313	Hs.43232	EST1	U42021 highly similar to PUFATIVE UBIQUITIN CARBOXY-TERMINAL HYDROLASE C13A11.6AC [Schistosoma mansoni, partial]
61	A4119314	Hs.43233	EST1	U42021 highly similar to PUFATIVE UBIQUITIN CARBOXY-TERMINAL HYDROLASE C13A11.6AC [Schistosoma mansoni, partial]
62	A4119315	Hs.43234	EST1	U42021 highly similar to PUFATIVE UBIQUITIN CARBOXY-TERMINAL HYDROLASE C13A11.6AC [Schistosoma mansoni, partial]
63	A4119316	Hs.43235	EST1	U42021 highly similar to PUFATIVE UBIQUITIN CARBOXY-TERMINAL HYDROLASE C13A11.6AC [Schistosoma mansoni, partial]
64	A4119317	Hs.43236	EST1	U42021 highly similar to PUFATIVE UBIQUITIN CARBOXY-TERMINAL HYDROLASE C13A11.6AC [Schistosoma mansoni, partial]
65	A4119318	Hs.43237	EST1	U42021 highly similar to PUFATIVE UBIQUITIN CARBOXY-TERMINAL HYDROLASE C13A11.6AC [Schistosoma mansoni, partial]
66	A4119319	Hs.43238	EST1	U42021 highly similar to PUFATIVE UBIQUITIN CARBOXY-TERMINAL HYDROLASE C13A11.6AC [Schistosoma mansoni, partial]
67	A4119320	Hs.43239	EST1	U42021 highly similar to PUFATIVE UBIQUITIN CARBOXY-TERMINAL HYDROLASE C13A11.6AC [Schistosoma mansoni, partial]
68	A4119321	Hs.43240	EST1	U42021 highly similar to PUFATIVE UBIQUITIN CARBOXY-TERMINAL HYDROLASE C13A11.6AC [Schistosoma mansoni, partial]
69	A4119322	Hs.43241	EST1	U42021 highly similar to PUFATIVE UBIQUITIN CARBOXY-TERMINAL HYDROLASE C13A11.6AC [Schistosoma mansoni, partial]
70	A4119323	Hs.43242	EST1	U42021 highly similar to PUFATIVE UBIQUITIN CARBOXY-TERMINAL HYDROLASE C13A11.6AC [Schistosoma mansoni, partial]
71	A4119324	Hs.43243	EST1	U42021 highly similar to PUFATIVE UBIQUITIN CARBOXY-TERMINAL HYDROLASE C13A11.6AC [Schistosoma mansoni, partial]
72	A4119325	Hs.43244	EST1	U42021 highly similar to PUFATIVE UBIQUITIN CARBOXY-TERMINAL HYDROLASE C13A11.6AC [Schistosoma mansoni, partial]
73	A4119326	Hs.43245	EST1	U42021 highly similar to PUFATIVE UBIQUITIN CARBOXY-TERMINAL HYDROLASE C13A11.6AC [Schistosoma mansoni, partial]
74	A4119327	Hs.43246	EST1	U42021 highly similar to PUFATIVE UBIQUITIN CARBOXY-TERMINAL HYDROLASE C13A11.6AC [Schistosoma mansoni, partial]
75	A4119328	Hs.43247	EST1	U42021 highly similar to PUFATIVE UBIQUITIN CARBOXY-TERMINAL HYDROLASE C13A11.6AC [Schistosoma mansoni, partial]
76	A4119329	Hs.43248	EST1	U42021 highly similar to PUFATIVE UBIQUITIN CARBOXY-TERMINAL HYDROLASE C13A11.6AC [Schistosoma mansoni, partial]
77	A4119330	Hs.43249	EST1	U42021 highly similar to PUFATIVE UBIQUITIN CARBOXY-TERMINAL HYDROLASE C13A11.6AC [Schistosoma mansoni, partial]
78	A4119331	Hs.43250	EST1	U42021 highly similar to PUFATIVE UBIQUITIN CARBOXY-TERMINAL HYDROLASE C13A11.6AC [Schistosoma mansoni, partial]
79	A4119332	Hs.43251	EST1	U42021 highly similar to PUFATIVE UBIQUITIN CARBOXY-TERMINAL HYDROLASE C13A11.6AC [Schistosoma mansoni, partial]
80	A4119333	Hs.43252	EST1	U42021 highly similar to PUFATIVE UBIQUITIN CARBOXY-TERMINAL HYDROLASE C13A11.6AC [Schistosoma mansoni, partial]
81	A4119334	Hs.43253	EST1	U42021 highly similar to PUFATIVE UBIQUITIN CARBOXY-TERMINAL HYDROLASE C13A11.6AC [Schistosoma mansoni, partial]
82	A4119335	Hs.43254	EST1	U42021 highly similar to PUFATIVE UBIQUITIN CARBOXY-TERMINAL HYDROLASE C13A11.6AC [Schistosoma mansoni, partial]
83	A4119336	Hs.43255	EST1	U42021 highly similar to PUFATIVE UBIQUITIN CARBOXY-TERMINAL HYDROLASE C13A11.6AC [Schistosoma mansoni, partial]
84	A4119337	Hs.43256	EST1	U42021 highly similar to PUFATIVE UBIQUITIN CARBOXY-TERMINAL HYDROLASE C13A11.6AC [Schistosoma mansoni, partial]
85	A4119338	Hs.43257	EST1	U42021 highly similar to PUFATIVE UBIQUITIN CARBOXY-TERMINAL HYDROLASE C13A11.6AC [Schistosoma mansoni, partial]
86	A4119339	Hs.43258	EST1	U42021 highly similar to PUFATIVE UBIQUITIN CARBOXY-TERMINAL HYDROLASE C13A11.6AC [Schistosoma mansoni, partial]
87	A4119340	Hs.43259	EST1	U42021 highly similar to PUFATIVE UBIQUITIN CARBOXY-TERMINAL HYDROLASE C13A11.6AC [Schistosoma mansoni, partial]
88	A4119341	Hs.43260	EST1	U42021 highly similar to PUFATIVE UBIQUITIN CARBOXY-TERMINAL HYDROLASE C13A11.6AC [Schistosoma mansoni, partial]
89	A4119342	Hs.43261	EST1	U42021 highly similar to PUFATIVE UBIQUITIN CARBOXY-TERMINAL HYDROLASE C13A11.6AC [Schistosoma mansoni, partial]
90	A4119343	Hs.43262	EST1	U42021 highly similar to PUFATIVE UBIQUITIN CARBOXY-TERMINAL HYDROLASE C13A11.6AC [Schistosoma mansoni, partial]
91	A4119344	Hs.43263	EST1	U42021 highly similar to PUFATIVE UBIQUITIN CARBOXY-TERMINAL HYDROLASE C13A11.6AC [Schistosoma mansoni, partial]
92	A4119345	Hs.43264	EST1	U42021 highly similar to PUFATIVE UBIQUITIN CARBOXY-TERMINAL HYDROLASE C13A11.6AC [Schistosoma mansoni, partial]
93	A4119346	Hs.43265	EST1	

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FIGURE 3 (CONT.)

[illegible]

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FIGURE 3 (CONT.)

13018	AA163302	Hs 31005	ESTs	
13019	AA117289	Hs 07832	MAQ105170	
13020	AA191489	Hs 72614	Human high-affinity copper uptake protein (HCTR1) mRNA, complete cds	
13021	D14320	Hs 81728	Basic transcription element binding protein 2	
13022	U09844	Hs 363	Zinc finger protein 139 (clone pZ1.37)	
13023	AA152018	Hs 30514	ESTs	
13024	AA152019	Hs 30514	ESTs	
13025	AA152020	Hs 30514	ESTs	
13026	AA152021	Hs 30514	ESTs	
13027	AA152022	Hs 30514	ESTs	
13028	AA152023	Hs 30514	ESTs	
13029	AA152024	Hs 30514	ESTs	
13030	AA152025	Hs 30514	ESTs	
13031	AA152026	Hs 30514	ESTs	
13032	AA152027	Hs 30514	ESTs	
13033	AA152028	Hs 30514	ESTs	
13034	AA152029	Hs 30514	ESTs	
13035	AA152030	Hs 30514	ESTs	
13036	AA152031	Hs 30514	ESTs	
13037	AA152032	Hs 30514	ESTs	
13038	AA152033	Hs 30514	ESTs	
13039	AA152034	Hs 30514	ESTs	
13040	AA152035	Hs 30514	ESTs	
13041	AA152036	Hs 30514	ESTs	
13042	AA152037	Hs 30514	ESTs	
13043	AA152038	Hs 30514	ESTs	
13044	AA152039	Hs 30514	ESTs	
13045	AA152040	Hs 30514	ESTs	
13046	AA152041	Hs 30514	ESTs	
13047	AA152042	Hs 30514	ESTs	
13048	AA152043	Hs 30514	ESTs	
13049	AA152044	Hs 30514	ESTs	
13050	AA152045	Hs 30514	ESTs	
13051	AA152046	Hs 30514	ESTs	
13052	AA152047	Hs 30514	ESTs	
13053	AA152048	Hs 30514	ESTs	
13054	AA152049	Hs 30514	ESTs	
13055	AA152050	Hs 30514	ESTs	
13056	AA152051	Hs 30514	ESTs	
13057	AA152052	Hs 30514	ESTs	
13058	AA152053	Hs 30514	ESTs	
13059	AA152054	Hs 30514	ESTs	
13060	AA152055	Hs 30514	ESTs	
13061	AA152056	Hs 30514	ESTs	
13062	AA152057	Hs 30514	ESTs	
13063	AA152058	Hs 30514	ESTs	
13064	AA152059	Hs 30514	ESTs	
13065	AA152060	Hs 30514	ESTs	
13066	AA152061	Hs 30514	ESTs	
13067	AA152062	Hs 30514	ESTs	
13068	AA152063	Hs 30514	ESTs	
13069	AA152064	Hs 30514	ESTs	
13070	AA152065	Hs 30514	ESTs	
13071	AA152066	Hs 30514	ESTs	
13072	AA152067	Hs 30514	ESTs	
13073	AA152068	Hs 30514	ESTs	
13074	AA152069	Hs 30514	ESTs	
13075	AA152070	Hs 30514	ESTs	
13076	AA152071	Hs 30514	ESTs	
13077	AA152072	Hs 30514	ESTs	
13078	AA152073	Hs 30514	ESTs	
13079	AA152074	Hs 30514	ESTs	
13080	AA152075	Hs 30514	ESTs	
13081	AA152076	Hs 30514	ESTs	
13082	AA152077	Hs 30514	ESTs	
13083	AA152078	Hs 30514	ESTs	
13084	AA152079	Hs 30514	ESTs	
13085	AA152080	Hs 30514	ESTs	
13086	AA152081	Hs 30514	ESTs	
13087	AA152082	Hs 30514	ESTs	
13088	AA152083	Hs 30514	ESTs	
13089	AA152084	Hs 30514	ESTs	
13090	AA152085	Hs 30514	ESTs	
13091	AA152086	Hs 30514	ESTs	
13092	AA152087	Hs 30514	ESTs	
13093	AA152088	Hs 30514	ESTs	
13094	AA152089	Hs 30514	ESTs	
13095	AA152090	Hs 30514	ESTs	
13096	AA152091	Hs 30514	ESTs	
13097	AA152092	Hs 30514	ESTs	
13098	AA152093	Hs 30514	ESTs	
13099	AA152094	Hs 30514	ESTs	
13100	AA152095	Hs 30514	ESTs	
13101	AA152096	Hs 30514	ESTs	
13102	AA152097	Hs 30514	ESTs	
13103	AA152098	Hs 30514	ESTs	
13104	AA152099	Hs 30514	ESTs	
13105	AA152100	Hs 30514	ESTs	
13106	AA152101	Hs 30514	ESTs	
13107	AA152102	Hs 30514	ESTs	
13108	AA152103	Hs 30514	ESTs	
13109	AA152104	Hs 30514	ESTs	
13110	AA152105	Hs 30514	ESTs	
13111	AA152106	Hs 30514	ESTs	
13112	AA152107	Hs 30514	ESTs	
13113	AA152108	Hs 30514	ESTs	
13114	AA152109	Hs 30514	ESTs	
13115	AA152110	Hs 30514	ESTs	
13116	AA152111	Hs 30514	ESTs	
13117	AA152112	Hs 30514	ESTs	
13118	AA152113	Hs 30514	ESTs	
13119	AA152114	Hs 30514	ESTs	
13120	AA152115	Hs 30514	ESTs	
13121	AA152116	Hs 30514	ESTs	
13122	AA152117	Hs 30514	ESTs	
13123	AA152118	Hs 30514	ESTs	
13124	AA152119	Hs 30514	ESTs	
13125	AA152120	Hs 30514	ESTs	
13126	AA152121	Hs 30514	ESTs	
13127	AA152122	Hs 30514	ESTs	
13128	AA152123	Hs 30514	ESTs	
13129	AA152124	Hs 30514	ESTs	
13130	AA152125	Hs 30514	ESTs	
13131	AA152126	Hs 30514	ESTs	
13132	AA152127	Hs 30514	ESTs	
13133	AA152128	Hs 30514	ESTs	
13134	AA152129	Hs 30514	ESTs	
13135	AA152130	Hs 30514	ESTs	
13136	AA152131	Hs 30514	ESTs	
13137	AA152132	Hs 30514	ESTs	
13138	AA152133	Hs 30514	ESTs	
13139	AA152134	Hs 30514	ESTs	
13140	AA152135	Hs 30514	ESTs	
13141	AA152136	Hs 30514	ESTs	
13142	AA152137	Hs 30514	ESTs	
13143	AA152138	Hs 30514	ESTs	
13144	AA152139	Hs 30514	ESTs	
13145	AA152140	Hs 30514	ESTs	
13146	AA152141	Hs 30514	ESTs	
13147	AA152142	Hs 30514	ESTs	
13148	AA152143	Hs 30514	ESTs	
13149	AA152144	Hs 30514	ESTs	
13150	AA152145	Hs 30514	ESTs	
13151	AA152146	Hs 30514	ESTs	
13152	AA152147	Hs 30514	ESTs	
13153	AA152148	Hs 30514	ESTs	
13154	AA152149	Hs 30514	ESTs	
13155	AA152150	Hs 30514	ESTs	
13156	AA152151	Hs 30514	ESTs	
13157	AA152152	Hs 30514	ESTs	
13158	AA152153	Hs 30514	ESTs	
13159	AA152154	Hs 30514	ESTs	
13160	AA152155	Hs 30514	ESTs	
13161	AA152156	Hs 30514	ESTs	
13162	AA152157	Hs 30514	ESTs	
13163	AA152158	Hs 30514	ESTs	
13164	AA152159	Hs 30514	ESTs	
13165	AA152160	Hs 30514	ESTs	
13166	AA152161	Hs 30514	ESTs	
13167	AA152162	Hs 30514	ESTs	
13168	AA152163	Hs 30514	ESTs	
13169	AA152164	Hs 30514	ESTs	
13170	AA152165	Hs 30514	ESTs	
13171	AA152166	Hs 30514	ESTs	
13172	AA152167	Hs 30514	ESTs	
13173	AA152168	Hs 30514	ESTs	
13174	AA152169	Hs 30514	ESTs	
13175	AA152170	Hs 30514	ESTs	
13176	AA152171	Hs 30514	ESTs	
13177	AA152172	Hs 30514	ESTs	
13178	AA152173	Hs 30514	ESTs	
13179	AA152174	Hs 30514	ESTs	
13180	AA152175	Hs 30514	ESTs	
13181	AA152176	Hs 30514	ESTs	
13182	AA152177	Hs 30514	ESTs	
13183	AA152178	Hs 30514	ESTs	
13184	AA152179	Hs 30514	ESTs	
13185	AA152180	Hs 30514	ESTs	
13186	AA152181	Hs 30514	ESTs	
13187	AA152182	Hs 30514	ESTs	
13188	AA152183	Hs 30514	ESTs	
13189	AA152184	Hs 30514	ESTs	
13190	AA152185	Hs 30514	ESTs	
13191	AA152186	Hs 30514	ESTs	
13192	AA152187	Hs 30514	ESTs	
13193	AA152188	Hs 30514	ESTs	
13194	AA152189	Hs 30514	ESTs	
13195	AA152190	Hs 30514	ESTs	
13196	AA152191	Hs 30514	ESTs	
13197	AA152192	Hs 30514	ESTs	
13198	AA152193	Hs 30514	ESTs	
13199	AA152194	Hs 30514	ESTs	
13200	AA152195	Hs 30514	ESTs	
13201	AA152196	Hs 30514	ESTs	
13202	AA152197	Hs 30514	ESTs	
13203	AA152198	Hs 30514	ESTs	
13204	AA152199	Hs 30514	ESTs	
13205	AA152200	Hs 30514	ESTs	
13206	AA152201	Hs 30514	ESTs	
13207	AA152202	Hs 30514	ESTs	
13208	AA152203	Hs 30514	ESTs	
13209	AA152204	Hs 30514	ESTs	
13210	AA152205	Hs 30514	ESTs	
13211	AA152206	Hs 30514	ESTs	
13212	AA152207	Hs 30514	ESTs	
13213	AA152208	Hs 30514	ESTs	
13214	AA152209	Hs 30514	ESTs	
13215	AA152210	Hs 30514	ESTs	
13216	AA152211	Hs 30514	ESTs	
13217	AA152212	Hs 30514	ESTs	
13218	AA152213	Hs 30514	ESTs	
13219	AA152214	Hs 30514	ESTs	
13220	AA152215	Hs 30514	ESTs	
13221	AA152216	Hs 30514	ESTs	
13222	AA152217	Hs 30514	ESTs	
13223	AA152218	Hs 30514	ESTs	
13224	AA152219	Hs 30514	ESTs	
13225	AA152220	Hs 30514	ESTs	
13226	AA152221	Hs 30514	ESTs	
13227	AA152222	Hs 30514	ESTs	
13228	AA152223	Hs 30514	ESTs	
13229	AA152224	Hs 30514	ESTs	
13230	AA152225	Hs 30514	ESTs	
13231	AA152226	Hs 30514	ESTs	
13232	AA152227	Hs 30514	ESTs	
13233	AA152228	Hs 30514	ESTs	
13234	AA152229	Hs 30514	ESTs	
13235	AA152230	Hs 30514	ESTs	
13236	AA152231	Hs 30514	ESTs	
13237	AA152232	Hs 30514	ESTs	
13238	AA152233	Hs 30514	ESTs	
13239	AA152234	Hs 30514	ESTs	
13240	AA152235	Hs 30514	ESTs	
13241	AA152236	Hs 30514	ESTs	
13242	AA152237	Hs 30514	ESTs	
13243	AA152238	Hs 30514	ESTs	
13244	AA152239	Hs 30514	ESTs	
13245	AA152240	Hs 30514	ESTs	
13246	AA152241	Hs 30514	ESTs	
13247	AA152242	Hs 30514	ESTs	
13248	AA152243	Hs 30514	ESTs	
13249	AA152244	Hs 30514	ESTs	
13250	AA152245	Hs 30514	ESTs	
13251	AA152246	Hs 30514	ESTs	
13252	AA152247	Hs 30514	ESTs	
13253	AA152248	Hs 30514	ESTs	
13254	AA152249	Hs 30514	ESTs	
13255	AA152250	Hs 30514	ESTs	
13256	AA152251	Hs 30514	ESTs	
13				

FIGURE 3 (CONT.)

[illegible]

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FIGURE 3 (CONT.)

[illegible]

FIGURE 3 (CONT.)

1742	27	A4123841	Hs 414155	EST1. Moderately similar to C-1, TETRAHYDROPTERIN SYNTHASE (CYP4B1) NCBI (H sapien)
8731	37	A4123841	Hs 414155	EST1. Moderately similar to C-1, TETRAHYDROPTERIN SYNTHASE (CYP4B1) NCBI (H sapien)
41428	37	A414984	Hs 108187	EST1. Moderately similar to C-1, TETRAHYDROPTERIN SYNTHASE (CYP4B1) NCBI (H sapien)
17032	37	A4078515	Hs 142190	EST1. Moderately similar to C-1, TETRAHYDROPTERIN SYNTHASE (CYP4B1) NCBI (H sapien)
24142	37	A4075550	Hs 142190	EST1. Moderately similar to C-1, TETRAHYDROPTERIN SYNTHASE (CYP4B1) NCBI (H sapien)
24142	37	A4075550	Hs 142190	EST1. Moderately similar to C-1, TETRAHYDROPTERIN SYNTHASE (CYP4B1) NCBI (H sapien)
3183	37	U81710	Hs 108187	EST1. Moderately similar to C-1, TETRAHYDROPTERIN SYNTHASE (CYP4B1) NCBI (H sapien)
23637	37	H64418	Hs 417020	EST1. Moderately similar to C-1, TETRAHYDROPTERIN SYNTHASE (CYP4B1) NCBI (H sapien)
15743	37	A4017802	Hs 873508	EST1. Moderately similar to C-1, TETRAHYDROPTERIN SYNTHASE (CYP4B1) NCBI (H sapien)
19594	37	H85100	Hs 333377	EST1. Moderately similar to C-1, TETRAHYDROPTERIN SYNTHASE (CYP4B1) NCBI (H sapien)
41816	37	286120	Hs 333377	EST1. Moderately similar to C-1, TETRAHYDROPTERIN SYNTHASE (CYP4B1) NCBI (H sapien)
81916	37	286120	Hs 333377	EST1. Moderately similar to C-1, TETRAHYDROPTERIN SYNTHASE (CYP4B1) NCBI (H sapien)
8740	37	278627	Hs 255058	EST1. Moderately similar to C-1, TETRAHYDROPTERIN SYNTHASE (CYP4B1) NCBI (H sapien)
42116	37	189274	Hs 871201	EST1. Moderately similar to C-1, TETRAHYDROPTERIN SYNTHASE (CYP4B1) NCBI (H sapien)
17701	37	A4015533	Hs 871201	EST1. Moderately similar to C-1, TETRAHYDROPTERIN SYNTHASE (CYP4B1) NCBI (H sapien)
17958	37	A4117805	Hs 232857	EST1. Moderately similar to C-1, TETRAHYDROPTERIN SYNTHASE (CYP4B1) NCBI (H sapien)
42534	37	Q07118	Hs 894923	EST1. Moderately similar to C-1, TETRAHYDROPTERIN SYNTHASE (CYP4B1) NCBI (H sapien)
23838	37	A409458	Hs 852655	EST1. Moderately similar to C-1, TETRAHYDROPTERIN SYNTHASE (CYP4B1) NCBI (H sapien)
10316	37	FR8282	Hs 107373	EST1. Moderately similar to C-1, TETRAHYDROPTERIN SYNTHASE (CYP4B1) NCBI (H sapien)
12139	37	S54641	Hs 73103	EST1. Moderately similar to C-1, TETRAHYDROPTERIN SYNTHASE (CYP4B1) NCBI (H sapien)
32981	37	A032046	Hs 71493	EST1. Moderately similar to C-1, TETRAHYDROPTERIN SYNTHASE (CYP4B1) NCBI (H sapien)
10160	37	A032046	Hs 71493	EST1. Moderately similar to C-1, TETRAHYDROPTERIN SYNTHASE (CYP4B1) NCBI (H sapien)
32983	37	121897	Hs 21605	EST1. Moderately similar to C-1, TETRAHYDROPTERIN SYNTHASE (CYP4B1) NCBI (H sapien)
34562	37	A4261768	Hs 7323	EST1. Moderately similar to C-1, TETRAHYDROPTERIN SYNTHASE (CYP4B1) NCBI (H sapien)
13773	37	A4443770	Hs 7531	EST1. Moderately similar to C-1, TETRAHYDROPTERIN SYNTHASE (CYP4B1) NCBI (H sapien)
8494	37	A4443460	Hs 34705	EST1. Moderately similar to C-1, TETRAHYDROPTERIN SYNTHASE (CYP4B1) NCBI (H sapien)
10400	37	A4067234	Hs 300268	EST1. Moderately similar to C-1, TETRAHYDROPTERIN SYNTHASE (CYP4B1) NCBI (H sapien)
1130	37	C3132-RT3306	EST1 - (C3132-RT3306	EST1. Moderately similar to C-1, TETRAHYDROPTERIN SYNTHASE (CYP4B1) NCBI (H sapien)
3379	37	H61937	Hs 85197	EST1. Moderately similar to C-1, TETRAHYDROPTERIN SYNTHASE (CYP4B1) NCBI (H sapien)
18906	37	F10088	Hs 48151	EST1. Moderately similar to C-1, TETRAHYDROPTERIN SYNTHASE (CYP4B1) NCBI (H sapien)
24190	37	A4291251	Hs 97101	EST1. Moderately similar to C-1, TETRAHYDROPTERIN SYNTHASE (CYP4B1) NCBI (H sapien)
2009	37	132881	Hs 15804	EST1. Moderately similar to C-1, TETRAHYDROPTERIN SYNTHASE (CYP4B1) NCBI (H sapien)
33688	37	232501	Hs 8789	EST1. Moderately similar to C-1, TETRAHYDROPTERIN SYNTHASE (CYP4B1) NCBI (H sapien)
1385	37	G884-H1184	EST1 - (G884-H1184	EST1. Moderately similar to C-1, TETRAHYDROPTERIN SYNTHASE (CYP4B1) NCBI (H sapien)
24758	37	240515	Hs 27599	EST1. Moderately similar to C-1, TETRAHYDROPTERIN SYNTHASE (CYP4B1) NCBI (H sapien)
24758	37	A4174264	Hs 82868	EST1. Moderately similar to C-1, TETRAHYDROPTERIN SYNTHASE (CYP4B1) NCBI (H sapien)
21566	37	R29185	Hs 108187	EST1. Moderately similar to C-1, TETRAHYDROPTERIN SYNTHASE (CYP4B1) NCBI (H sapien)
40328	37	R31255	Hs 108187	EST1. Moderately similar to C-1, TETRAHYDROPTERIN SYNTHASE (CYP4B1) NCBI (H sapien)
22585	37	A4045803	Hs 77119	EST1. Moderately similar to C-1, TETRAHYDROPTERIN SYNTHASE (CYP4B1) NCBI (H sapien)
8390	37	D31715	Hs 10724	EST1. Moderately similar to C-1, TETRAHYDROPTERIN SYNTHASE (CYP4B1) NCBI (H sapien)
13114	37	A4281216	Hs 267550	EST1. Moderately similar to C-1, TETRAHYDROPTERIN SYNTHASE (CYP4B1) NCBI (H sapien)
31544	37	4452121	Hs 105282	EST1. Moderately similar to C-1, TETRAHYDROPTERIN SYNTHASE (CYP4B1) NCBI (H sapien)
7383	37	A4093354	Hs 109573	EST1. Moderately similar to C-1, TETRAHYDROPTERIN SYNTHASE (CYP4B1) NCBI (H sapien)
1623	37	L23608	Hs 18165	EST1. Moderately similar to C-1, TETRAHYDROPTERIN SYNTHASE (CYP4B1) NCBI (H sapien)
24908	37	241840	Hs 8517	EST1. Moderately similar to C-1, TETRAHYDROPTERIN SYNTHASE (CYP4B1) NCBI (H sapien)
34007	37	A158893	Hs 48372	EST1. Moderately similar to C-1, TETRAHYDROPTERIN SYNTHASE (CYP4B1) NCBI (H sapien)
25040	37	A401797	Hs 333378	EST1. Moderately

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25	Hs14907	Hs12003	ES11	
26	Hs14908	Hs15034	ES11	
27	Hs14909	Hs15035	ES11	
28	Hs14910	Hs15036	ES11	
29	Hs14911	Hs15037	ES11	
30	Hs14912	Hs15038	ES11	
31	Hs14913	Hs15039	ES11	
32	Hs14914	Hs15040	ES11	
33	Hs14915	Hs15041	ES11	
34	Hs14916	Hs15042	ES11	
35	Hs14917	Hs15043	ES11	
36	Hs14918	Hs15044	ES11	
37	Hs14919	Hs15045	ES11	
38	Hs14920	Hs15046	ES11	
39	Hs14921	Hs15047	ES11	
40	Hs14922	Hs15048	ES11	
41	Hs14923	Hs15049	ES11	
42	Hs14924	Hs15050	ES11	
43	Hs14925	Hs15051	ES11	
44	Hs14926	Hs15052	ES11	
45	Hs14927	Hs15053	ES11	
46	Hs14928	Hs15054	ES11	
47	Hs14929	Hs15055	ES11	
48	Hs14930	Hs15056	ES11	
49	Hs14931	Hs15057	ES11	
50	Hs14932	Hs15058	ES11	
51	Hs14933	Hs15059	ES11	
52	Hs14934	Hs15060	ES11	
53	Hs14935	Hs15061	ES11	
54	Hs14936	Hs15062	ES11	
55	Hs14937	Hs15063	ES11	
56	Hs14938	Hs15064	ES11	
57	Hs14939	Hs15065	ES11	
58	Hs14940	Hs15066	ES11	
59	Hs14941	Hs15067	ES11	
60	Hs14942	Hs15068	ES11	
61	Hs14943	Hs15069	ES11	
62	Hs14944	Hs15070	ES11	
63	Hs14945	Hs15071	ES11	
64	Hs14946	Hs15072	ES11	
65	Hs14947	Hs15073	ES11	
66	Hs14948	Hs15074	ES11	
67	Hs14949	Hs15075	ES11	
68	Hs14950	Hs15076	ES11	
69	Hs14951	Hs15077	ES11	
70	Hs14952	Hs15078	ES11	
71	Hs14953	Hs15079	ES11	
72	Hs14954	Hs15080	ES11	
73	Hs14955	Hs15081	ES11	
74	Hs14956	Hs15082	ES11	
75	Hs14957	Hs15083	ES11	
76	Hs14958	Hs15084	ES11	
77	Hs14959	Hs15085	ES11	
78	Hs14960	Hs15086	ES11	
79	Hs14961	Hs15087	ES11	
80	Hs14962	Hs15088	ES11	
81	Hs14963	Hs15089	ES11	
82	Hs14964	Hs15090	ES11	
83	Hs14965	Hs15091	ES11	
84	Hs14966	Hs15092	ES11	
85	Hs14967	Hs15093	ES11	
86	Hs14968	Hs15094	ES11	
87	Hs14969	Hs15095	ES11	
88	Hs14970	Hs15096	ES11	
89	Hs14971	Hs15097	ES11	
90	Hs14972	Hs15098	ES11	
91	Hs14973	Hs15099	ES11	
92	Hs14974	Hs15100	ES11	
93	Hs14975	Hs15101	ES11	
94	Hs14976	Hs15102	ES11	
95	Hs14977	Hs15103	ES11	
96	Hs14978	Hs15104	ES11	
97	Hs14979	Hs15105	ES11	
98	Hs14980	Hs15106	ES11	
99	Hs14981	Hs15107	ES11	
100	Hs14982	Hs15108	ES11	

FIGURE 3 (CONT.)

[illegible]

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FIGURE 3 (CONT.)

29550	24	N24932	Hs 88245	Homo sapiens mRNA for E1B-55kDa-associated protein
8396	24	AA098179	Hs 104615	ESTs Weakly similar to Sema-4 in 5' untranslated region
21018	24	AA027283	Hs 1295	Human terminal transferase mRNA, complete cds
22121	24	AA043851	Hs 13082	ESTs
19823	24	AA043851	Hs 13082	ESTs
26163	24	AA079708	Hs 68063	ESTs
22142	24	R51382	Hs 124275	Homo sapiens mRNA for HAAK53 protein partial cds
13333	24	AA045807	Hs 81114	ESTs highly similar to HYPOTHETICAL 622 NO PROTEIN K224.3 IN CHROMOSOME III (Carson-Ackis et al)
11334	24	AA036223	Hs 8145	ESTs
8331	24	AA036223	Hs 8145	ESTs
2302	24	AA036223	Hs 8145	ESTs
22387	24	AA036223	Hs 8145	ESTs
22371	24	AA036223	Hs 8145	ESTs
22366	24	AA036223	Hs 8145	ESTs
8054	24	AA036223	Hs 8145	ESTs
12233	24	AA036223	Hs 8145	ESTs
22394	24	AA036223	Hs 8145	ESTs
14371	24	AA036223	Hs 8145	ESTs
13101	24	AA036223	Hs 8145	ESTs
26186	24	AA036223	Hs 8145	ESTs
20524	24	AA036223	Hs 8145	ESTs
18201	24	AA036223	Hs 8145	ESTs
7813	24	AA036223	Hs 8145	ESTs
13171	24	AA036223	Hs 8145	ESTs
8174	24	AA036223	Hs 8145	ESTs
41537	24	AA036223	Hs 8145	ESTs
17332	24	AA036223	Hs 8145	ESTs
18814	24	AA036223	Hs 8145	ESTs
28880	24	AA036223	Hs 8145	ESTs
30176	24	AA036223	Hs 8145	ESTs
22191	24	AA036223	Hs 8145	ESTs
4788	24	AA036223	Hs 8145	ESTs
60817	24	AA036223	Hs 8145	ESTs
13637	24	AA036223	Hs 8145	ESTs
24532	24	AA036223	Hs 8145	ESTs
38333	24	AA036223	Hs 8145	ESTs
41221	24	AA036223	Hs 8145	ESTs
8532	24	AA036223	Hs 8145	ESTs
28579	24	AA036223	Hs 8145	ESTs
17855	24	AA036223	Hs 8145	ESTs
31858	24	AA036223	Hs 8145	ESTs
24592	24	AA036223	Hs 8145	ESTs
18759	24	AA036223	Hs 8145	ESTs
7861	24	AA036223	Hs 8145	ESTs
3360	24	AA036223	Hs 8145	ESTs
40288	24	AA036223	Hs 8145	ESTs
18428	24	AA036223	Hs 8145	ESTs
30680	24	AA036223	Hs 8145	ESTs
27264	24	AA036223	Hs 8145	ESTs
13800	24	AA036223	Hs 8145	ESTs

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FIGURE 3 (CONT.)

22	AA14943	Hs 29311	EST5	Modestly similar to Y11-actin and factor 2 (H sapiens)	
23	U87538	Hs 59726	EST5	Modestly similar to Y11-actin and factor 2 (H sapiens)	
24	A437374	Hs 142437	EST5		
25	A434146	Hs 90337	EST1		
26	U87538	Hs 59726	EST5		
27	U87538	Hs 59726	EST5		
28	U87538	Hs 59726	EST5		
29	U87538	Hs 59726	EST5		
30	U87538	Hs 59726	EST5		
31	U87538	Hs 59726	EST5		
32	U87538	Hs 59726	EST5		
33	U87538	Hs 59726	EST5		
34	U87538	Hs 59726	EST5		
35	U87538	Hs 59726	EST5		
36	U87538	Hs 59726	EST5		
37	U87538	Hs 59726	EST5		
38	U87538	Hs 59726	EST5		
39	U87538	Hs 59726	EST5		
40	U87538	Hs 59726	EST5		
41	U87538	Hs 59726	EST5		
42	U87538	Hs 59726	EST5		
43	U87538	Hs 59726	EST5		
44	U87538	Hs 59726	EST5		
45	U87538	Hs 59726	EST5		
46	U87538	Hs 59726	EST5		
47	U87538	Hs 59726	EST5		
48	U87538	Hs 59726	EST5		
49	U87538	Hs 59726	EST5		
50	U87538	Hs 59726	EST5		
51	U87538	Hs 59726	EST5		
52	U87538	Hs 59726	EST5		
53	U87538	Hs 59726	EST5		
54	U87538	Hs 59726	EST5		
55	U87538	Hs 59726	EST5		
56	U87538	Hs 59726	EST5		
57	U87538	Hs 59726	EST5		
58	U87538	Hs 59726	EST5		
59	U87538	Hs 59726	EST5		
60	U87538	Hs 59726	EST5		
61	U87538	Hs 59726	EST5		
62	U87538	Hs 59726	EST5		
63	U87538	Hs 59726	EST5		
64	U87538	Hs 59726	EST5		
65	U87538	Hs 59726	EST5		
66	U87538	Hs 59726	EST5		
67	U87538	Hs 59726	EST5		
68	U87538	Hs 59726	EST5		
69	U87538	Hs 59726	EST5		
70	U87538	Hs 59726	EST5		
71	U87538	Hs 59726	EST5		
72	U87538	Hs 59726	EST5		
73	U87538	Hs 59726	EST5		
74	U87538	Hs 59726	EST5		
75	U87538	Hs 59726	EST5		
76	U87538	Hs 59726	EST5		
77	U87538	Hs 59726	EST5		
78	U87538	Hs 59726	EST5		
79	U87538	Hs 59726	EST5		
80	U87538	Hs 59726	EST5		
81	U87538	Hs 59726	EST5		
82	U87538	Hs 59726	EST5		
83	U87538	Hs 59726	EST5		
84	U87538	Hs 59726	EST5		
85	U87538	Hs 59726	EST5		
86	U87538	Hs 59726	EST5		
87	U87538	Hs 59726	EST5		
88	U87538	Hs 59726	EST5		
89	U87538	Hs 59726	EST5		
90	U87538	Hs 59726	EST5		
91	U87538	Hs 59726	EST5		
92	U87538	Hs 59726	EST5		
93	U87538	Hs 59726	EST5		
94	U87538	Hs 59726	EST5		
95	U87538	Hs 59726	EST5		
96	U87538	Hs 59726	EST5		
97	U87538	Hs 59726	EST5		
98	U87538	Hs 59726	EST5		
99	U87538	Hs 59726	EST5		
100	U87538	Hs 59726	EST5		

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FIGURE 3 (CONT.)

22022	22	H93005	EST - RC_93305	
31231	22	AA451898	Hs 89250	EST
32174	22	AA452079	Hs 89151	EST
32175	22	AA452080	Hs 89152	EST
31767	22	A24941	Hs 77550	CD226 protein kinase 1
40334	22	U71958	Hs 60879	Nuclein transcription initiation factor 1F10 subunit 1A1031 mRNA complete cds
36222	22	U71958	Hs 60879	Nuclein transcription initiation factor 1F10 subunit 1A1031 mRNA complete cds
18567	22	AA421181	Hs 89134	EST
4271	22	AA421181	Hs 89134	EST
32028	22	U26596	Hs 82731	Human mRNA for KIAA03139 gene complete cds
20222	22	U26596	Hs 82731	Human mRNA for KIAA03139 gene complete cds
8714	22	U26596	Hs 82731	Human mRNA for KIAA03139 gene complete cds
18249	22	U26596	Hs 82731	Human mRNA for KIAA03139 gene complete cds
11868	22	U26596	Hs 82731	Human mRNA for KIAA03139 gene complete cds
21530	22	U26596	Hs 82731	Human mRNA for KIAA03139 gene complete cds
42632	22	U26596	Hs 82731	Human mRNA for KIAA03139 gene complete cds
4963	22	U26596	Hs 82731	Human mRNA for KIAA03139 gene complete cds
32778	22	U26596	Hs 82731	Human mRNA for KIAA03139 gene complete cds
32341	22	U26596	Hs 82731	Human mRNA for KIAA03139 gene complete cds
11803	22	U26596	Hs 82731	Human mRNA for KIAA03139 gene complete cds
36248	22	U26596	Hs 82731	Human mRNA for KIAA03139 gene complete cds
40608	22	U26596	Hs 82731	Human mRNA for KIAA03139 gene complete cds
11800	22	U26596	Hs 82731	Human mRNA for KIAA03139 gene complete cds
5051	22	U26596	Hs 82731	Human mRNA for KIAA03139 gene complete cds
33917	22	U26596	Hs 82731	Human mRNA for KIAA03139 gene complete cds
22614	22	U26596	Hs 82731	Human mRNA for KIAA03139 gene complete cds
32115	22	U26596	Hs 82731	Human mRNA for KIAA03139 gene complete cds
32114	22	U26596	Hs 82731	Human mRNA for KIAA03139 gene complete cds
24111	22	U26596	Hs 82731	Human mRNA for KIAA03139 gene complete cds
4733	22	U26596	Hs 82731	Human mRNA for KIAA03139 gene complete cds
4911	22	U26596	Hs 82731	Human mRNA for KIAA03139 gene complete cds
32115	22	U26596	Hs 82731	Human mRNA for KIAA03139 gene complete cds
32115	22	U26596	Hs 82731	Human mRNA for KIAA03139 gene complete cds
34618	22	U26596	Hs 82731	Human mRNA for KIAA03139 gene complete cds
32541	22	U26596	Hs 82731	Human mRNA for KIAA03139 gene complete cds
1518	22	U26596	Hs 82731	Human mRNA for KIAA03139 gene complete cds
15105	22	U26596	Hs 82731	Human mRNA for KIAA03139 gene complete cds
19131	22	U26596	Hs 82731	Human mRNA for KIAA03139 gene complete cds
4136	22	U26596	Hs 82731	Human mRNA for KIAA03139 gene complete cds
20278	22	U26596	Hs 82731	Human mRNA for KIAA03139 gene complete cds
13272	22	U26596	Hs 82731	Human mRNA for KIAA03139 gene complete cds
22606	22	U26596	Hs 82731	Human mRNA for KIAA03139 gene complete cds
8255	22	U26596	Hs 82731	Human mRNA for KIAA03139 gene complete cds
31827	22	U26596	Hs 82731	Human mRNA for KIAA03139 gene complete cds
34138	22	U26596	Hs 82731	Human mRNA for KIAA03139 gene complete cds
34648	22	U26596	Hs 82731	Human mRNA for KIAA03139 gene complete cds
3790	22	U26596	Hs 82731	Human mRNA for KIAA03139 gene complete cds
3790	22	U26596	Hs 82731	Human mRNA for KIAA03139 gene complete cds
3790	22	U26596	Hs 82731	Human mRNA for KIAA03139 gene complete cds
4187	22	U26596	Hs 82731	Human mRNA for KIAA03139 gene complete cds
13904	22	U26596	Hs 82731	Human mRNA for KIAA03139 gene complete cds
34552	22	U26596	Hs 82731	Human mRNA for KIAA03139 gene complete cds
13306	22	U26596	Hs 82731	Human mRNA for KIAA03139 gene complete cds

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FIGURE 3 (CONT.)

[illegible]

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FIGURE 3 (CONT.)

[illegible]

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FIGURE 4

Primary Key	Accession	Unigene	Unigene Description
32916	U02778	Hs.55279	Protease inhibitor 3 (trypsin)
34197	U02778	Hs.12640	Human spleen clone 23707 and 23317 mRNA part cds
18187	U02778	Hs.31656	ESTs
8125	U02778	Hs.62911	Human protein-tyrosine phosphatase (Hs pp-1) mRNA partial sequence
18362	U02778	Hs.12013	Ribonuclease L (2S -oligoadenylate synthetase dependent) inhibitor
39925	U02778	Hs.109240	EST
19228	U02778	Hs.27835	ESTs
19228	U02778	Hs.72202	Human mRNA for transcriptional activator HNF2B complete cds
38456	U02778	Hs.10707	ESTs
17659	U02778	Hs.71190	ESTs
8106	U02778	Hs.83484	SRV (as determined region Y) box 4
8948	U02778	Hs.69433	Human spleen clone protease (ms1) mRNA complete cds
5918	U02778	Hs.2711	HISTONE H2A.X
5903	U02778	Hs.75581	Transcription factor 1
37877	U02778	Hs.96384	Human spleen clone protein-coupled receptor HCN3 mRNA complete cds
11581	U02778	Hs.19222	E4-1
16430	U02778	Hs.91533	ESTs
32240	U02778	Hs.12013	Ribonuclease L (2S -oligoadenylate synthetase dependent) inhibitor
12465	U02778	Hs.6880	Human spleen U-methyl-lysine-associated cytoplasm (Hs-Cy) mRNA complete cds
2144	U02778	Hs.74074	Proteinase C beta 4
1143	U02778	Hs.10707	ESTs
33035	U02778	Hs.110709	ESTs (likely similar to ZK1038.5 (C-terminus))
30355	U02778	Hs.32930	Human mRNA for NFKB2 protein-coupled protein
6449	U02778	Hs.95513	ESTs
37653	U02778	Hs.110736	Human bumblebee-like Na-K-Cl cotransporter (Hs-GC1) mRNA complete cds
4178	U02778	Hs.121541	TRANSLATIONAL INITIATION FACTOR 2 GAMMA SUBUNIT
1983	U02778	Hs.37362	ESTs
19787	U02778	Hs.24550	ESTs
8272	U02778	Hs.31853	ESTs
6747	U02778	Hs.6585	Human spleen clone 23592 mRNA sequence
63191	U02778	Hs.65668	ESTs
33191	U02778	Hs.2841	NEURONEIN-28 PRECURSOR
13136	U02778	Hs.7327	ESTs
59613	U02778	Hs.2877	Cadherin 3 (p-cadherin)
38179	U02778	Hs.78272	Human spleen clone 23592 mRNA sequence
30238	U02778	Hs.84686	Cathepsin B
17887	U02778	Hs.72853	ESTs
36895	U02778	Hs.98786	ESTs
10233	U02778	Hs.10091	ESTs (likely similar to PHEVULANLYL-TRNA SYNTHETASE ALPHA CHAIN CYTOSOLIC [Saccharomyces cerevisiae])
38300	U02778	Hs.112227	ESTs
10489	U02778	Hs.131815	EST - Hs.131815
38492	U02778	Hs.93393	Cell division cycle 2 C1 b5.5 and C2.10 M
5510	U02778	Hs.73826	Protein tyrosine phosphatase non-receptor type 4
3021	U02778	Hs.64880	ESTs
17734	U02778	Hs.109761	ESTs
36371	U02778	Hs.425017	ESTs
459	U02778	D3893	Human mRNA for cathepsin-like protein complete cds
17419	U02778	AA113349	EST
14054	U02778	AA485223	Human putative ATPGIP-binding protein (Hs-AB) mRNA complete cds
5021	U02778	U7324	ESTs
4964	U02778	Hs.12045	Human C2 mRNA complete cds

FIGURE 4 (CONT.)

23935	AA256379	Hs 90291	ESTs	
4445	U09844	Hs 14732	MALATE OXIDOREDUCTASE	
10748	AA055692	Hs 14543	ESTs	
8111	AA323787	Hs 4770	ESTs	
19289	H20185	Hs 31734	EST	
32195	H43471	Hs 22355	ESTs	Weakly similar to ORF YOR259a (S cerevisiae)
21519	R77975	EST - HC_R27975		
6197	R77975	Hs 17013	Ribonuclease L (2S of poliovirus RNA synthesis-dependent) inhibitor	
5986	RG1634	Hs 17070	ESTs	
41107	AA324063	Hs 17070	ESTs	Putative cytosolic sulfotransferase type 1
17070	U57341	Hs 18989	ESTs	Highly similar to GONADOTROPIN-RELEASING HORMONE RECEPTOR (Rattus norvegicus)
18076	FR0222	Hs 27895	ESTs	
24197	V07277	Hs 17568	ESTs	
4713	U57771	Hs 81771	Human L-lysine hydrolase mRNA complete cds	
38460	AA504462	Hs 105730	ESTs	
18330	AA318722	Hs 54481	Human mRNA for apolipoprotein E receptor 2 complete cds	
18782	F09739	Hs 12300	ESTs	
42768	Z093394	Hs 84432	ESTs	Moderately similar to H1ALU SUBFAMILY SP REPEATING ENTRY (H1H apes)
34014	AA191348	Hs 80178	ESTs	
18833	AA054585	Hs 81771	ESTs	
21163	HC2003	Hs 42106	ESTs	
11160	AA184589	Hs 26009	ESTs	
11168	HQ3044173521	EST - HQ3344-H1351		
11813	AA059168	Hs 22153	ESTs	
10992	AA112523	Hs 22900	Human apolipoprotein BAC clone RG11602 from Tg15	
5788	X54925	Hs 83169	Human metallothionein 1 (intracellular)	
18993	AA055300	Hs 75337	Human mRNA for KIAA0025 gene partial cds	
17854	AA133350	Hs 07180	ESTs	
39436	D26927	Hs 74374	Human C/EBP-dependent enhancer protein for secretion mRNA complete cds	
19727	R27622	Hs 35581	ESTs	
4381	R27622	Hs 31748	Human mRNA for IRE5	
35708	R79111	Hs 29398	ESTs	
33980	AA06209	Hs 104746	ESTs	
37084	AA180223	Hs 8414	CAMP-DEPENDENT PROTEIN KINASE TYPE II-ALPHA REGULATORY CHAIN	
29935	AA464869	Hs 170179	Human insulin-like growth factor protein 2 (IGF2) mRNA partial cds	
2188	AA347159	Hs 77831	ESTs	Weakly similar to NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4 (Caenorhabditis elegans)
4362	L47276	EST - L47276		
9127	U09617	Hs 30829	Bloom syndrome	
20914	D30037	Hs 91447	PHOSPHATIDYLINOSITOL	
5952	R19230	Hs 18937	ESTs	
3368	U07144	Hs 17070	ESTs	Similar to G185, a protein involved in
37445	U01157	Hs 10991	Human insulin-like growth factor protein 2 (IGF2) mRNA partial cds	
37445	Z38482	Hs 185	Glucagon-like peptide-1 receptor	
10840	AA454932	Hs 12403	ESTs	
23179	AA084104	Hs 123157	ESTs	
21	AB007265	Hs 30177	ESTs	
18782	F09458	Hs 113379	Human insulin-like growth factor protein 2	
32232	AA051409	Hs 143080	Human insulin-like growth factor protein 2	
42602	R05423	Hs 17421	ESTs	
23772	R05423	Hs 117908	ESTs	
18410	AA053079	Hs 20390	EST	
23845	AA053036	Hs 20960	ESTs	Weakly similar to HYPOTHETICAL 60.5 KD PROTEIN 105110.7 IN CHROMOSOME II (C. elegans)
	Hs 58410	Hs 12940	ESTs	
		Hs 42116	ESTs	

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FIGURE 4 (CONT.)

36405	AA426406	Hs 10801	Homo sapiens mRNA for KIAA0530 protein partial cds
4029	U21099	Hs 74590	Human DNA polymerase delta small subunit mRNA complete cds
15006	U30746	Hs 110729	Human tumour necrosis factor alpha K/C coding region (RCC1) mRNA complete cds
40594	N35388	Hs 11227	ESTs
31484	N69496	Hs 49933	ESTs
36201	AA396735	Hs 109041	ESTs
36202	AA396736	Hs 109042	ESTs
36203	AA396737	Hs 109043	ESTs
36204	AA396738	Hs 109044	ESTs
36205	AA396739	Hs 109045	ESTs
36206	AA396740	Hs 109046	ESTs
36207	AA396741	Hs 109047	ESTs
36208	AA396742	Hs 109048	ESTs
36209	AA396743	Hs 109049	ESTs
36210	AA396744	Hs 109050	ESTs
36211	AA396745	Hs 109051	ESTs
36212	AA396746	Hs 109052	ESTs
36213	AA396747	Hs 109053	ESTs
36214	AA396748	Hs 109054	ESTs
36215	AA396749	Hs 109055	ESTs
36216	AA396750	Hs 109056	ESTs
36217	AA396751	Hs 109057	ESTs
36218	AA396752	Hs 109058	ESTs
36219	AA396753	Hs 109059	ESTs
36220	AA396754	Hs 109060	ESTs
36221	AA396755	Hs 109061	ESTs
36222	AA396756	Hs 109062	ESTs
36223	AA396757	Hs 109063	ESTs
36224	AA396758	Hs 109064	ESTs
36225	AA396759	Hs 109065	ESTs
36226	AA396760	Hs 109066	ESTs
36227	AA396761	Hs 109067	ESTs
36228	AA396762	Hs 109068	ESTs
36229	AA396763	Hs 109069	ESTs
36230	AA396764	Hs 109070	ESTs
36231	AA396765	Hs 109071	ESTs
36232	AA396766	Hs 109072	ESTs
36233	AA396767	Hs 109073	ESTs
36234	AA396768	Hs 109074	ESTs
36235	AA396769	Hs 109075	ESTs
36236	AA396770	Hs 109076	ESTs
36237	AA396771	Hs 109077	ESTs
36238	AA396772	Hs 109078	ESTs
36239	AA396773	Hs 109079	ESTs
36240	AA396774	Hs 109080	ESTs
36241	AA396775	Hs 109081	ESTs
36242	AA396776	Hs 109082	ESTs
36243	AA396777	Hs 109083	ESTs
36244	AA396778	Hs 109084	ESTs
36245	AA396779	Hs 109085	ESTs
36246	AA396780	Hs 109086	ESTs
36247	AA396781	Hs 109087	ESTs
36248	AA396782	Hs 109088	ESTs
36249	AA396783	Hs 109089	ESTs
36250	AA396784	Hs 109090	ESTs
36251	AA396785	Hs 109091	ESTs
36252	AA396786	Hs 109092	ESTs
36253	AA396787	Hs 109093	ESTs
36254	AA396788	Hs 109094	ESTs
36255	AA396789	Hs 109095	ESTs
36256	AA396790	Hs 109096	ESTs
36257	AA396791	Hs 109097	ESTs
36258	AA396792	Hs 109098	ESTs
36259	AA396793	Hs 109099	ESTs
36260	AA396794	Hs 109100	ESTs
36261	AA396795	Hs 109101	ESTs
36262	AA396796	Hs 109102	ESTs
36263	AA396797	Hs 109103	ESTs
36264	AA396798	Hs 109104	ESTs
36265	AA396799	Hs 109105	ESTs
36266	AA396800	Hs 109106	ESTs
36267	AA396801	Hs 109107	ESTs
36268	AA396802	Hs 109108	ESTs
36269	AA396803	Hs 109109	ESTs
36270	AA396804	Hs 109110	ESTs
36271	AA396805	Hs 109111	ESTs
36272	AA396806	Hs 109112	ESTs
36273	AA396807	Hs 109113	ESTs
36274	AA396808	Hs 109114	ESTs
36275	AA396809	Hs 109115	ESTs
36276	AA396810	Hs 109116	ESTs
36277	AA396811	Hs 109117	ESTs
36278	AA396812	Hs 109118	ESTs
36279	AA396813	Hs 109119	ESTs
36280	AA396814	Hs 109120	ESTs
36281	AA396815	Hs 109121	ESTs
36282	AA396816	Hs 109122	ESTs
36283	AA396817	Hs 109123	ESTs
36284	AA396818	Hs 109124	ESTs
36285	AA396819	Hs 109125	ESTs
36286	AA396820	Hs 109126	ESTs
36287	AA396821	Hs 109127	ESTs
36288	AA396822	Hs 109128	ESTs
36289	AA396823	Hs 109129	ESTs
36290	AA396824	Hs 109130	ESTs
36291	AA396825	Hs 109131	ESTs
36292	AA396826	Hs 109132	ESTs
36293	AA396827	Hs 109133	ESTs
36294	AA396828	Hs 109134	ESTs
36295	AA396829	Hs 109135	ESTs
36296	AA396830	Hs 109136	ESTs
36297	AA396831	Hs 109137	ESTs
36298	AA396832	Hs 109138	ESTs
36299	AA396833	Hs 109139	ESTs
36300	AA396834	Hs 109140	ESTs
36301	AA396835	Hs 109141	ESTs
36302	AA396836	Hs 109142	ESTs
36303	AA396837	Hs 109143	ESTs
36304	AA396838	Hs 109144	ESTs
36305	AA396839	Hs 109145	ESTs
36306	AA396840	Hs 109146	ESTs
36307	AA396841	Hs 109147	ESTs
36308	AA396842	Hs 109148	ESTs
36309	AA396843	Hs 109149	ESTs
36310	AA396844	Hs 109150	ESTs
36311	AA396845	Hs 109151	ESTs
36312	AA396846	Hs 109152	ESTs
36313	AA396847	Hs 109153	ESTs
36314	AA396848	Hs 109154	ESTs
36315	AA396849	Hs 109155	ESTs
36316	AA396850	Hs 109156	ESTs
36317	AA396851	Hs 109157	ESTs
36318	AA396852	Hs 109158	ESTs
36319	AA396853	Hs 109159	ESTs
36320	AA396854	Hs 109160	ESTs
36321	AA396855	Hs 109161	ESTs
36322	AA396856	Hs 109162	ESTs
36323	AA396857	Hs 109163	ESTs
36324	AA396858	Hs 109164	ESTs
36325	AA396859	Hs 109165	ESTs
36326	AA396860	Hs 109166	ESTs
36327	AA396861	Hs 109167	ESTs
36328	AA396862	Hs 109168	ESTs
36329	AA396863	Hs 109169	ESTs
36330	AA396864	Hs 109170	ESTs
36331	AA396865	Hs 109171	ESTs
36332	AA396866	Hs 109172	ESTs
36333	AA396867	Hs 109173	ESTs
36334	AA396868	Hs 109174	ESTs
36335	AA396869	Hs 109175	ESTs
36336	AA396870	Hs 109176	ESTs
36337	AA396871	Hs 109177	ESTs
36338	AA396872	Hs 109178	ESTs
36339	AA396873	Hs 109179	ESTs
36340	AA396874	Hs 109180	ESTs
36341	AA396875	Hs 109181	ESTs
36342	AA396876	Hs 109182	ESTs
36343	AA396877	Hs 109183	ESTs
36344	AA396878	Hs 109184	ESTs
36345	AA396879	Hs 109185	ESTs
36346	AA396880	Hs 109186	ESTs
36347	AA396881	Hs 109187	ESTs
36348	AA396882	Hs 109188	ESTs
36349	AA396883	Hs 109189	ESTs
36350	AA396884	Hs 109190	ESTs
36351	AA396885	Hs 109191	ESTs
36352	AA396886	Hs 109192	ESTs
36353	AA396887	Hs 109193	ESTs
36354	AA396888	Hs 109194	ESTs
36355	AA396889	Hs 109195	ESTs
36356	AA396890	Hs 109196	ESTs
36357	AA396891	Hs 109197	ESTs
36358	AA396892	Hs 109198	ESTs
36359	AA396893	Hs 109199	ESTs
36360	AA396894	Hs 109200	ESTs
36361	AA396895	Hs 109201	ESTs
36362	AA396896	Hs 109202	ESTs
36363	AA396897	Hs 109203	ESTs
36364	AA396898	Hs 109204	ESTs
36365	AA396899	Hs 109205	ESTs
36366	AA396900	Hs 109206	ESTs
36367	AA396901	Hs 109207	ESTs
36368	AA396902	Hs 109208	ESTs
36369	AA396903	Hs 109209	ESTs
36370	AA396904	Hs 109210	ESTs
36371	AA396905	Hs 109211	ESTs
36372	AA396906	Hs 109212	ESTs
36373	AA396907	Hs 109213	ESTs
36374	AA396908	Hs 109214	ESTs
36375	AA396909	Hs 109215	ESTs
36376	AA396910	Hs 109216	ESTs
36377	AA396911	Hs 109217	ESTs
36378	AA396912	Hs 109218	ESTs
36379	AA396913	Hs 109219	ESTs
36380	AA396914	Hs 109220	ESTs
36381	AA396915	Hs 109221	ESTs
36382	AA396916	Hs 109222	ESTs
36383	AA396917	Hs 109223	ESTs
36384	AA396918	Hs 109224	ESTs
36385	AA396919	Hs 109225	ESTs
36386	AA396920	Hs 109226	ESTs
36387	AA396921	Hs 109227	ESTs
36388	AA396922	Hs 109228	ESTs
36389	AA396923	Hs 109229	ESTs
36390	AA396924	Hs 109230	ESTs
36391	AA396925	Hs 109231	ESTs
36392	AA396926	Hs 109232	ESTs
36393	AA396927	Hs 109233	ESTs
36394	AA396928	Hs 109234	ESTs
36395	AA396929	Hs 109235	ESTs
36396	AA396930	Hs 109236	ESTs
36397	AA396931	Hs 109237	ESTs
36398	AA396932	Hs 109238	ESTs
36399	AA396933	Hs 109239	ESTs
36400	AA396934	Hs 109240	ESTs
36401	AA396935	Hs 109241	ESTs
36402	AA396936	Hs 109242	ESTs
36403	AA396937	Hs 109243	ESTs
36404	AA396938	Hs 109244	ESTs
36405	AA396939	Hs 109245	ESTs
36406	AA396940	Hs 109246	ESTs
36407	AA396941	Hs 109247	ESTs
36408	AA396942	Hs 109248	ESTs
36409	AA396943	Hs 109249	ESTs
36410	AA396944	Hs 109250	ESTs
36411	AA396945	Hs 109251	ESTs
36412	AA396946	Hs 109252	ESTs
36413	AA396947	Hs 109253	ESTs
36414	AA396948	Hs 109254	ESTs
36415	AA396949	Hs 109255	ESTs
36416	AA396950	Hs 109256	ESTs
36417	AA396951	Hs 109257	ESTs
36418	AA396952	Hs 109258	ESTs
36419	AA396953	Hs 109259	ESTs
36420	AA396954	Hs 109260	ESTs
36421	AA396955	Hs 109261	ESTs
36422	AA396956	Hs 109262	ESTs
36423	AA396957	Hs 109263	ESTs
36424	AA396958	Hs 109264	ESTs
36425	AA396959	Hs 109265	ESTs
36426	AA396960	Hs 109266	ESTs
36427	AA396961	Hs 109267	ESTs
36428	AA396962	Hs 109268	ESTs
36429	AA396963	Hs 109269	ESTs
36430	AA396964	Hs 109270	ESTs
36431	AA396965	Hs 109271	ESTs
36432	AA396966	Hs 109272	ESTs
36433	AA396967	Hs 109273	ESTs
36434	AA396968	Hs 109274	ESTs
36435	AA396969	Hs 109275	ESTs
36436	AA396970	Hs 109276	ESTs
36437	AA396971	Hs 109277	ESTs
36438	AA396972	Hs 109278	ESTs
36439	AA396973	Hs 109279	ESTs
36440	AA396974	Hs 109280	ESTs
36441	AA396975	Hs 109281	ESTs
36442	AA396976	Hs 109282	ESTs
36443	AA396977	Hs 109283	ESTs
36444	AA396978	Hs 109284	ESTs
36445	AA396979	Hs 109285	ESTs
36446	AA396980	Hs 109286	ESTs
36447	AA396981	Hs 109287	ESTs
36448	AA396982	Hs 109288	ESTs
36449	AA396983	Hs 109289	ESTs
36450			

FIGURE 4 (CONT.)

2659	U04313	Hs 55270	Protease inhibitor 2 (mucopl)
17051	AA070801	Hs 51015	ESTs
19203	H11593	Hs 20110	ESTs
20791	H60657	Hs 90357	Homo sapiens telomeric repeat binding factor (TRF1) mRNA complete cds
24215	W69425	Hs 15767	ESTs
6746	AA449211	Hs 90658	Homo sapiens mitotic checkpoint protein kinase (BUB1) mRNA complete cds
6780	Y12394	Hs 3306	Homo sapiens importin alpha homolog (STP1 gamma) mRNA complete cds
2506	AA148007	Hs 103971	EST
3007	AA424803	Hs 98474	EST
3007	AA011031	Hs 11002	ESTs
3243	U05048	Hs 11045	ESTs
3243	X55330	Hs 11061	transglutaminase
5799	T84047	Hs 15476	ESTs
29523	H83533	Hs 10312	ESTs
26291	AA334422	Hs 14219	ESTs
33831	AA410261	Hs 14121	ESTs
40084	H12283	Hs 39463	Human mRNA for KIAA035 gene partial cds
29795	N20641	Hs 48230	ESTs highly similar to HYPOTHETICAL MYELOID CELL LINE PROTEIN 3 (Homo sapiens)
5920	X53575	Hs 89512	ATPase Ca++ transporting plasma membrane 2 (NOTE: translation of symbol)
37111	AA458209	Hs 52070	Human signaling lymphocyte activation molecule (SLAM) mRNA complete cds
37111	AA458210	Hs 10565	ESTs
37166	AA44772	Hs 126139	EST
38433	D57037	Hs 35950	Human Bromodomain kinase 2 (TIC2) mRNA complete cds
1970	K01363	EST - K01363	EST - K01363
30817	I50948	Hs 47003	ESTs
35105	AA371581	Hs 142355	EST Weakly similar to putative p150 (H sapiens)
789	D96971	Hs 78851	Human mRNA for KIAA0317 gene partial cds
4306	U40922	Hs 21573	DNA repair protein XRCC4
31944	K05183	Hs 80310	ESTs
4537	AA443371	Hs 42493	ESTs Weakly similar to Hs ALU SUBFAMILY 7 WARNING ENTRY III (H sapiens)
4537	K05181	Hs 78797	Human cytoskeleton associated protein 40 kDa (CAP40) mRNA complete cds
2123	L40198	Hs 28958	Homo sapiens (clone 42271) cDNA fragment
20926	AA344402	Hs 48729	EST - X51653
5479	X91653	Hs 24098	ESTs
11859	AA700970	Hs 102948	ESTs
37601	AA458364	Hs 103202	ESTs
28644	D12163	Hs 103202	ESTs
40604	N38933	Hs 28578	Homo sapiens KIAA0428 mRNA complete cds
3913	U10261	Hs 66576	Human MDA-7 (mda-7) mRNA complete cds
23759	T00313	Hs 10732	ESTs
2857	X58537	Hs 21723	Fosdyshenase 4 (alpha 13) fosdyshenase myeloid specific
2857	AA443411	Hs 30557	Homo sapiens clone 24749 and 24750 mRNA sequences
18298	AA171895	Hs 29855	ESTs
19091	D06531	Hs 129021	ESTs
39468	T18531	Hs 141905	ESTs
23360	AA207123	Hs 130657	EST - RC_AA45724
34105	AA485724	Hs 130657	EST - RC_AA45724
20603	F13855	Hs 65933	ESTs Moderately similar to Hs ALU SUBFAMILY 591 WARNING ENTRY III (H sapiens)
8723	L44542	Hs 129923	ESTs
25215	AA035540	Hs 125	AROPROTEIN A REGULATORY PROTEIN-1
32118	AA021390	Hs 114851	ESTs
32118	H05048	Hs 114851	ESTs
32113	Z39427	Hs 65749	ESTs Weakly similar to putative p150 (H sapiens)
18192	AA227151	Hs 55896	ESTs
42390	W40150	Hs 24485	Homo sapiens chromosome associated polypeptide (HCAP) mRNA complete cds

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FIGURE 4 (CONT.)

5693	AA05465	Hs 92864	EST1: weakly similar to similar to complete beta-specific protein (C elegans)
3559	AA00716	Hs 10749	ESTs
1896	L18920	Hs 30880	MELANOMA-ASSOCIATED ANTIGEN 2
38259	AA423962	Hs 10845	ESTs: weakly similar to Hs 10845 SUBFAMILY J WARRING ENTRY III (H sapiens)
37065	AA46317	Hs 21143	ESTs: weakly similar to Hs 1410 CLASS C VARIANTS ENTRY III (H sapiens)
33020	W66091	Hs 59668	ESTs: weakly similar to polypeptide N-acetylglucosaminyltransferase (H sapiens)
27027	AA000169	Hs 83753	ESTs
40027	H64051	Hs 49520	Home sapiens Werner syndrome gene complete cds
3375	550223	Hs 108642	HsR-11
37310	AA43727	Hs 69240	ESTs
38235	AA460030	Hs 108220	ESTs
22258	H65024	Hs 108220	ESTs
5246	AA436188	Hs 10302	ESTs
38320	AA596538	Hs 50216	ESTs
30207	H33270	Hs 44532	H sapiens mRNA for diubiquitin
6484	X29859	Hs 55823	H sapiens mRNA for UDP-GalNAc 4-epimerase N-acetylglucosaminyl transferase
38288	AA414502	Hs 68402	ESTs
37548	AA459641	Hs 99433	ESTs
4183	U31116	Hs 77501	Human beta-sarcoglycan A3b mRNA complete cds
37777	AA445960	Hs 115541	Human beta-sarcoglycan A3b mRNA complete cds
38390	AA449791	Hs 115541	Human beta-sarcoglycan A3b mRNA complete cds
2943	A13313	Hs 79308	Catalytic translation initiation factor 4E
38043	AA400377	Hs 10314	ESTs
38235	AA463237	Hs 11114	ESTs
3432	S56267	Hs 74101	Synten lysine kinase
22362	R59187	Hs 21320	ESTs
32740	T62550	Hs 91077	ESTs
37057	AA446131	Hs 124918	ESTs
34107	AA209458	Hs 90297	ESTs
34391	AA232703	Hs 58174	ESTs
33301	W73583	Hs 495	Prostaglandin G/H synthase 3 (subtype EP3) (alternative product)
7785	D96596	Hs 495	Prostaglandin G/H synthase 3 (subtype EP3) (alternative product)
38390	AA443375	Hs 6592	ESTs
38041	AA443375	Hs 6592	ESTs
38390	X97155	Hs 75530	MITOCHONDRIAL KINESIN-LIKE PROTEIN 1
38390	HUNTERPRA11537	Hs 75530	MITOCHONDRIAL KINESIN-LIKE PROTEIN 1
35377	AA338530	Hs 97265	ESTs
28059	AA338655	Hs 58940	ESTs
25801	AA144530	Hs 28434	ESTs
37258	R55923	Hs 80961	DNA polymerase gamma
34554	AA380216	Hs 55209	ESTs: moderately similar to DNR-19 PROTEIN (H sapiens)
32034	H69828	Hs 77256	Human epsilon of zeta homolog 2 (E2f2) mRNA complete cds
4787	U07541	Hs 9968	Human epsilon of zeta homolog 2 (E2f2) mRNA complete cds
1084	U07541	Hs 9968	Human epsilon of zeta homolog 2 (E2f2) mRNA complete cds
18719	U07541	Hs 9968	Human epsilon of zeta homolog 2 (E2f2) mRNA complete cds
37057	U07541	Hs 9968	Human epsilon of zeta homolog 2 (E2f2) mRNA complete cds
3263	U07541	Hs 9968	Human epsilon of zeta homolog 2 (E2f2) mRNA complete cds
4308	U07541	Hs 9968	Human epsilon of zeta homolog 2 (E2f2) mRNA complete cds
38311	AA488687	Hs 14777	Home sapiens p115del-G1-PLC mRNA complete cds
6418	X93298	Hs 142639	ESTs
38580	AA528545	Hs 78853	URACIL DNA GLYCOSYLASE 1 PRECURSOR
4845	U83108	Hs 141444	ESTs
41854	R76437	Hs 29736	Home sapiens mRNA for TRAF5 complete cds
34400	R08178	Hs 2001	THROMBOPLASTIN SYNTHASE
35522	AA334400	Hs 70116	ESTs
		Hs 104286	ESTs
		Hs 104706	ESTs

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FIGURE 4 (CONT.)

26528	10	A4278541	Hs 40128 ESTs highly similar to GDS RIBOSOMAL PROTEIN L30 [ratia nervogica]
40704	10	H48396	EST - RC_H48396
19164	10	H10395	EST
26240	10	A432382	Human mRNA for KIAA0152 gene complete cds
8663	10	U55437	AFK-HUMIT RPRM1507_M
33327	10	A4328710	Hs 87195 Hs sapiens RNA for CLON5
27293	10	H48396	EST - H48396
36052	10	A441707	EST - H48396
26514	10	A4278504	Hs 104787 EST
31197	10	A4328120	Hs 597604 ESTs
37978	10	A4179285	Hs 108200 ESTs highly similar to RING CANAL PROTEIN [Drosophila melanogaster]
4862	10	U55437	Hs 85838 Human homeodomain-containing protein [HNF] cDNA complete cds
26700	10	A4328197	Hs 85002 EST
35049	10	A4328057	Hs 27507 ESTs
40063	10	H72456	Hs 76086 MITOCHONDRIAL GDS RIBOSOMAL PROTEIN L3
17841	10	A4127459	Hs 130789 ESTs
17841	10	U55437	Hs 116115 ESTs highly similar to H48396
4477	10	U55437	Hs 42778 ESTs
26916	10	A4331363	Hs 102524 ESTs
34188	10	A4278630	Hs 30232 Human mRNA for KIAA0186 gene complete cds
29229	10	H48396	EST - YEL0192AM321
42773	10	R43183	EST - RC_AA435910
32189	10	A4135810	EST
26739	10	H56931	Hs 42959 EST
26545	10	A4278979	Hs 85547 ESTs
21822	10	R43022	Hs 22091 EST
26545	10	A4278979	Hs 28497 ESTs highly similar to CYCLIC AMP DEPENDENT TRANSCRIPTION FACTOR ATF-2 [H. sapiens]
22044	10	H56931	Hs 33782 EST - H48396
1346	10	H48396	EST - H48396
218	10	D13540	Hs 22989 PROTEIN-TYROSINE PHOSPHATASE 7C
26100	10	A4278335	Hs 5917 Human mRNA for KIAA0337 gene complete cds
41583	10	R41129	Hs 141745 ESTs
42700	10	T81105	Hs 142670 ESTs
6713	10	Y08564	Hs 42836 ESTs highly similar to F46B17 [C. elegans]
33037	10	H61219	Hs 52273 ESTs
31819	10	N73449	Hs 40407 ESTs
26718	10	A4328256	Hs 104807 Human AT 6 mRNA complete cds
27008	10	H72456	Hs 13266 ESTs
40113	10	A4280285	Hs 9722 ESTs highly similar to PROBABLE UBICUITIN CARBOXYL-TERMINAL HYDROLASE 9 [H. sapiens]
10801	10	A4280285	Hs 97630 ESTs highly similar to CHROMOSOME CONDENSATION PROTEIN DPK-27 [Caenorhabditis elegans]
37491	10	A4455239	Hs 81892 Human mRNA for KIAA0101 gene complete cds
254	10	D14627	Hs 42453 ESTs
26893	10	H97819	Hs 43881 ESTs
21523	10	A4278392	Hs 19114 Homo sapiens mRNA for high mobility group protein HMG2a
13110	10	A4435840	Hs 89041 EST
34863	10	A4278979	Hs 82265 Phosphoribosylglycylamide synthetase phosphoribosylglycylamide synthetase phosphoribosylglycylamide synthetase
31402	10	D51691	Hs 11024 ESTs
21522	10	N71274	Hs 13308 ESTs
20342	10	A4278392	Hs 13308 ESTs
4476	10	U55437	Hs 78619 Homo sapiens gamma-glutamyl hydrolase [GGH] mRNA complete cds
34363	10	A4351587	Hs 10901 Homo sapiens mRNA for KIAA0330 protein partial cds
35094	10	A4351587	Hs 112264 ESTs
3888	10	U15128	Hs 35573 Human beta-12-N-acetylglucosaminyltransferase II [MGAT2] gene complete cds

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FIGURE 4 (CONT.)

32386	012184	Hs 3350	ESTs	Hs 3350	ESTs	
3189	U17599	Hs 121479	Human 5P prostaglandin receptor (PTGDR) mRNA partial cds			
4597	U17599	Hs 24852	Human putative calcium efflux channel (hce3) mRNA complete cds			
35606	AA02227	Hs 97345	ESTs Moderately similar to N-tubulin-like 1 (N-tubulin-like 1) [Homo sapiens]			
18219	Hs 58113	Hs 37629	ESTs			
14837	T40145	Hs 21821	ESTs			
17336	AA09955	Hs 41175	ESTs			
29406	Hs 54324	Hs 40972	ESTs			
92	Hs 42993	ESTs Moderately similar to 11L ALU SUBFAMILY J MEMBER ENTRY III [Homo sapiens]				
17697	AA106833	Hs 72535	ESTs			
13893	AA106833	Hs 34027	ESTs Moderately similar to 11L ALU SUBFAMILY J MEMBER ENTRY III [Homo sapiens]			
26339	Hs 80572	Hs 80572	ESTs			
11	AA02702	Hs 80569	ESTs			
60	Hs 83369	ESTs				
903	Hs 30945	ESTs				
27674	Hs 8037	ESTs				
15244	AA029457	Hs 82489	ESTs			
18263	Hs 33947	ESTs				
19662	Hs 81564	ESTs				
2348	Hs 109931	Human tyrosine tRNA synthetase mRNA complete cds				
7736	AA032121	Hs 109931	Human tyrosine tRNA synthetase mRNA complete cds			
39926	Hs 109931	Human tyrosine tRNA synthetase mRNA complete cds				
25111	Hs 109931	Human tyrosine tRNA synthetase mRNA complete cds				
2174	Hs 109931	Human tyrosine tRNA synthetase mRNA complete cds				
27024	Hs 109931	Human tyrosine tRNA synthetase mRNA complete cds				
4999	Hs 109931	Human tyrosine tRNA synthetase mRNA complete cds				
2316	Hs 109931	Human tyrosine tRNA synthetase mRNA complete cds				
37253	Hs 109931	Human tyrosine tRNA synthetase mRNA complete cds				
38624	Hs 109931	Human tyrosine tRNA synthetase mRNA complete cds				
23213	Hs 109931	Human tyrosine tRNA synthetase mRNA complete cds				
2790	Hs 109931	Human tyrosine tRNA synthetase mRNA complete cds				
32478	Hs 109931	Human tyrosine tRNA synthetase mRNA complete cds				
19681	Hs 109931	Human tyrosine tRNA synthetase mRNA complete cds				
2174	Hs 109931	Human tyrosine tRNA synthetase mRNA complete cds				
14723	Hs 109931	Human tyrosine tRNA synthetase mRNA complete cds				
31764	Hs 109931	Human tyrosine tRNA synthetase mRNA complete cds				
6069	Hs 109931	Human tyrosine tRNA synthetase mRNA complete cds				
7465	Hs 109931	Human tyrosine tRNA synthetase mRNA complete cds				
16501	Hs 109931	Human tyrosine tRNA synthetase mRNA complete cds				
34327	Hs 109931	Human tyrosine tRNA synthetase mRNA complete cds				
6700	Hs 109931	Human tyrosine tRNA synthetase mRNA complete cds				
7632	Hs 109931	Human tyrosine tRNA synthetase mRNA complete cds				
11188	Hs 109931	Human tyrosine tRNA synthetase mRNA complete cds				
42793	Hs 109931	Human tyrosine tRNA synthetase mRNA complete cds				
17330	Hs 109931	Human tyrosine tRNA synthetase mRNA complete cds				
23371	Hs 109931	Human tyrosine tRNA synthetase mRNA complete cds				
17508	Hs 109931	Human tyrosine tRNA synthetase mRNA complete cds				
18497	Hs 109931	Human tyrosine tRNA synthetase mRNA complete cds				
235	Hs 109931	Human tyrosine tRNA synthetase mRNA complete cds				
24525	Hs 109931	Human tyrosine tRNA synthetase mRNA complete cds				
7626	Hs 109931	Human tyrosine tRNA synthetase mRNA complete cds				
37142	Hs 109931	Human tyrosine tRNA synthetase mRNA complete cds				
39007	Hs 109931	Human tyrosine tRNA synthetase mRNA complete cds				
6235	Hs 109931	Human tyrosine tRNA synthetase mRNA complete cds				
24317	Hs 109931	Human tyrosine tRNA synthetase mRNA complete cds				
38344	Hs 109931	Human tyrosine tRNA synthetase mRNA complete cds				

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FIGURE 4 (CONT.)

1	Hs02890	EST1	18	Hs02890	EST1
2	Hs02891	EST1	19	Hs02891	EST1
3	Hs02892	EST1	20	Hs02892	EST1
4	Hs02893	EST1	21	Hs02893	EST1
5	Hs02894	EST1	22	Hs02894	EST1
6	Hs02895	EST1	23	Hs02895	EST1
7	Hs02896	EST1	24	Hs02896	EST1
8	Hs02897	EST1	25	Hs02897	EST1
9	Hs02898	EST1	26	Hs02898	EST1
10	Hs02899	EST1	27	Hs02899	EST1
11	Hs02900	EST1	28	Hs02900	EST1
12	Hs02901	EST1	29	Hs02901	EST1
13	Hs02902	EST1	30	Hs02902	EST1
14	Hs02903	EST1	31	Hs02903	EST1
15	Hs02904	EST1	32	Hs02904	EST1
16	Hs02905	EST1	33	Hs02905	EST1
17	Hs02906	EST1	34	Hs02906	EST1
18	Hs02907	EST1	35	Hs02907	EST1
19	Hs02908	EST1	36	Hs02908	EST1
20	Hs02909	EST1	37	Hs02909	EST1
21	Hs02910	EST1	38	Hs02910	EST1
22	Hs02911	EST1	39	Hs02911	EST1
23	Hs02912	EST1	40	Hs02912	EST1
24	Hs02913	EST1	41	Hs02913	EST1
25	Hs02914	EST1	42	Hs02914	EST1
26	Hs02915	EST1	43	Hs02915	EST1
27	Hs02916	EST1	44	Hs02916	EST1
28	Hs02917	EST1	45	Hs02917	EST1
29	Hs02918	EST1	46	Hs02918	EST1
30	Hs02919	EST1	47	Hs02919	EST1
31	Hs02920	EST1	48	Hs02920	EST1
32	Hs02921	EST1	49	Hs02921	EST1
33	Hs02922	EST1	50	Hs02922	EST1
34	Hs02923	EST1	51	Hs02923	EST1
35	Hs02924	EST1	52	Hs02924	EST1
36	Hs02925	EST1	53	Hs02925	EST1
37	Hs02926	EST1	54	Hs02926	EST1
38	Hs02927	EST1	55	Hs02927	EST1
39	Hs02928	EST1	56	Hs02928	EST1
40	Hs02929	EST1	57	Hs02929	EST1
41	Hs02930	EST1	58	Hs02930	EST1
42	Hs02931	EST1	59	Hs02931	EST1
43	Hs02932	EST1	60	Hs02932	EST1
44	Hs02933	EST1	61	Hs02933	EST1
45	Hs02934	EST1	62	Hs02934	EST1
46	Hs02935	EST1	63	Hs02935	EST1
47	Hs02936	EST1	64	Hs02936	EST1
48	Hs02937	EST1	65	Hs02937	EST1
49	Hs02938	EST1	66	Hs02938	EST1
50	Hs02939	EST1	67	Hs02939	EST1
51	Hs02940	EST1	68	Hs02940	EST1
52	Hs02941	EST1	69	Hs02941	EST1
53	Hs02942	EST1	70	Hs02942	EST1
54	Hs02943	EST1	71	Hs02943	EST1
55	Hs02944	EST1	72	Hs02944	EST1
56	Hs02945	EST1	73	Hs02945	EST1
57	Hs02946	EST1	74	Hs02946	EST1
58	Hs02947	EST1	75	Hs02947	EST1
59	Hs02948	EST1	76	Hs02948	EST1
60	Hs02949	EST1	77	Hs02949	EST1
61	Hs02950	EST1	78	Hs02950	EST1
62	Hs02951	EST1	79	Hs02951	EST1
63	Hs02952	EST1	80	Hs02952	EST1
64	Hs02953	EST1	81	Hs02953	EST1
65	Hs02954	EST1	82	Hs02954	EST1
66	Hs02955	EST1	83	Hs02955	EST1
67	Hs02956	EST1	84	Hs02956	EST1
68	Hs02957	EST1	85	Hs02957	EST1
69	Hs02958	EST1	86	Hs02958	EST1
70	Hs02959	EST1	87	Hs02959	EST1
71	Hs02960	EST1	88	Hs02960	EST1
72	Hs02961	EST1	89	Hs02961	EST1
73	Hs02962	EST1	90	Hs02962	EST1
74	Hs02963	EST1			

1	Hs02890	EST1	18	Hs02890	EST1
2	Hs02891	EST1	19	Hs02891	EST1
3	Hs02892	EST1	20	Hs02892	EST1
4	Hs02893	EST1	21	Hs02893	EST1
5	Hs02894	EST1	22	Hs02894	EST1
6	Hs02895	EST1	23	Hs02895	EST1
7	Hs02896	EST1	24	Hs02896	EST1
8	Hs02897	EST1	25	Hs02897	EST1
9	Hs02898	EST1	26	Hs02898	EST1
10	Hs02899	EST1	27	Hs02899	EST1
11	Hs02900	EST1	28	Hs02900	EST1
12	Hs02901	EST1	29	Hs02901	EST1
13	Hs02902	EST1	30	Hs02902	EST1
14	Hs02903	EST1	31	Hs02903	EST1
15	Hs02904	EST1	32	Hs02904	EST1
16	Hs02905	EST1	33	Hs02905	EST1
17	Hs02906	EST1	34	Hs02906	EST1
18	Hs02907	EST1	35	Hs02907	EST1
19	Hs02908	EST1	36	Hs02908	EST1
20	Hs02909	EST1	37	Hs02909	EST1
21	Hs02910	EST1	38	Hs02910	EST1
22	Hs02911	EST1	39	Hs02911	EST1
23	Hs02912	EST1	40	Hs02912	EST1
24	Hs02913	EST1	41	Hs02913	EST1
25	Hs02914	EST1	42	Hs02914	EST1
26	Hs02915	EST1	43	Hs02915	EST1
27	Hs02916	EST1	44	Hs02916	EST1
28	Hs02917	EST1	45	Hs02917	EST1
29	Hs02918	EST1	46	Hs02918	EST1
30	Hs02919	EST1	47	Hs02919	EST1
31	Hs02920	EST1	48	Hs02920	EST1
32	Hs02921	EST1	49	Hs02921	EST1
33	Hs02922	EST1	50	Hs02922	EST1
34	Hs02923	EST1	51	Hs02923	EST1
35	Hs02924	EST1	52	Hs02924	EST1
36	Hs02925	EST1	53	Hs02925	EST1
37	Hs02926	EST1	54	Hs02926	EST1
38	Hs02927	EST1	55	Hs02927	EST1
39	Hs02928	EST1	56	Hs02928	EST1
40	Hs02929	EST1	57	Hs02929	EST1
41	Hs02930	EST1	58	Hs02930	EST1
42	Hs02931	EST1	59	Hs02931	EST1
43	Hs02932	EST1	60	Hs02932	EST1
44	Hs02933	EST1	61	Hs02933	EST1
45	Hs02934	EST1	62	Hs02934	EST1
46	Hs02935	EST1	63	Hs02935	EST1
47	Hs02936	EST1	64	Hs02936	EST1
48	Hs02937	EST1	65	Hs02937	EST1
49	Hs02938	EST1	66	Hs02938	EST1
50	Hs02939	EST1	67	Hs02939	EST1
51	Hs02940	EST1	68	Hs02940	EST1
52	Hs02941	EST1	69	Hs02941	EST1
53	Hs02942	EST1	70	Hs02942	EST1
54	Hs02943	EST1	71	Hs02943	EST1
55	Hs02944	EST1	72	Hs02944	EST1
56	Hs02945	EST1	73	Hs02945	EST1
57	Hs02946	EST1	74	Hs02946	EST1
58	Hs02947	EST1	75	Hs02947	EST1
59	Hs02948	EST1	76	Hs02948	EST1
60	Hs02949	EST1	77	Hs02949	EST1
61	Hs02950	EST1	78	Hs02950	EST1
62	Hs02951	EST1	79	Hs02951	EST1
63	Hs02952	EST1	80	Hs02952	EST1
64	Hs02953	EST1	81	Hs02953	EST1
65	Hs02954	EST1	82	Hs02954	EST1
66	Hs02955	EST1	83	Hs02955	EST1
67	Hs02956	EST1	84	Hs02956	EST1
68	Hs02957	EST1	85	Hs02957	EST1
69	Hs02958	EST1	86	Hs02958	EST1
70	Hs02959	EST1	87	Hs02959	EST1
71	Hs02960	EST1	88	Hs02960	EST1
72	Hs02961	EST1	89	Hs02961	EST1
73	Hs02962	EST1	90	Hs02962	EST1
74	Hs02963	EST1			

1	Hs02890	EST1	18	Hs02890	EST1
2	Hs02891	EST1	19	Hs02891	EST1
3	Hs02892	EST1	20	Hs02892	EST1
4	Hs02893	EST1	21	Hs02893	EST1
5	Hs02894	EST1	22	Hs02894	EST1
6	Hs02895	EST1	23	Hs02895	EST1
7	Hs02896	EST1	24	Hs02896	EST1
8	Hs02897	EST1	25	Hs02897	EST1
9	Hs02898	EST1	26	Hs02898	EST1
10	Hs02899	EST1	27	Hs02899	EST1
11	Hs02900	EST1	28	Hs02900	EST1
12	Hs02901	EST1	29	Hs02901	EST1
13	Hs02902	EST1	30	Hs02902	EST1
14	Hs02903	EST1	31	Hs02903	EST1
15	Hs02904	EST1	32	Hs02904	EST1
16	Hs02905	EST1	33	Hs02905	EST1
17	Hs02906	EST1	34	Hs02906	EST1
18	Hs02907	EST1	35	Hs02907	EST1
19	Hs02908	EST1	36	Hs02908	EST1
20	Hs02909	EST1	37	Hs02909	EST1
21	Hs02910	EST1	38	Hs02910	EST1
22	Hs02911	EST1	39	Hs02911	EST1
23	Hs02912	EST1	40	Hs02912	EST1
24	Hs02913	EST1	41	Hs02913	EST1
25	Hs02914	EST1	42	Hs02914	EST1
26	Hs02915	EST1	43	Hs02915	EST1
27	Hs02916	EST1	44	Hs02916	EST1
28	Hs02917	EST1	45	Hs02917	EST1
29	Hs02918	EST1	46	Hs02918	EST1
30	Hs02919	EST1	47	Hs02919	EST1
31	Hs02920	EST1	48	Hs02920	EST1
32	Hs02921	EST1	49	Hs02921	EST1
33	Hs02922	EST1	50	Hs02922	EST1
34	Hs02923	EST1	51	Hs02923	EST1
35	Hs02924	EST1	52	Hs02924	EST1
36	Hs02925	EST1	53	Hs02925	EST1
37	Hs02926	EST1	54	Hs02926	EST1
38	Hs02927	EST1	55	Hs02927	EST1
39	Hs02928	EST1	56	Hs02928	EST1
40	Hs02929	EST1	57	Hs02929	EST1
41	Hs02930	EST1	58	Hs02930	EST1
42	Hs02931	EST1	59	Hs02931	EST1
43	Hs02932	EST1	60	Hs02932	EST1
44	Hs02933	EST1	61	Hs02933	EST1
45	Hs02934	EST1	62	Hs02934	EST1
46	Hs02935	EST1	63	Hs02935	EST1
47	Hs02936	EST1	64	Hs02936	EST1
48	Hs02937	EST1	65	Hs02937	EST1
49	Hs02938	EST1	66	Hs02938	EST1
50	Hs02939	EST1	67	Hs02939	EST1
51	Hs02940	EST1	68	Hs02940	EST1
52	Hs02941	EST1	69	Hs02941	EST1
53	Hs02942	EST1	70	Hs02942	EST1
54	Hs02943	EST1	71	Hs02943	EST1
55	Hs02944	EST1	72	Hs02944	EST1
56	Hs02945	EST1	73	Hs02945	EST1
57	Hs02946	EST1	74	Hs02946	EST1
58	Hs02947	EST1	75	Hs02947	EST1
59	Hs02948	EST1	76	Hs02948	EST1
60	Hs02949	EST1	77	Hs02949	EST1
61	Hs02950	EST1	78	Hs02950	EST1
62	Hs02951	EST1	79	Hs02951	EST1
63	Hs02952	EST1	80	Hs02952	EST1
64	Hs02953	EST1	81	Hs02953	EST1
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68	Hs02957	EST1	85	Hs02957	EST1
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70	Hs02959	EST1	87	Hs02959	EST1
71	Hs02960	EST1	88	Hs02960	EST1
72	Hs02961	EST1	89	Hs02961	EST1
73	Hs02962	EST1	90	Hs02962	EST1
74	Hs02963	EST1			

1	Hs02890	EST1	18	Hs02890	EST1
2	Hs02891	EST1	19	Hs02891	EST1
3	Hs02892	EST1	20	Hs02892	EST1
4	Hs02893	EST1	21	Hs02893	EST1
5	Hs02894	EST1	22	Hs02894	EST1
6	Hs02895	EST1	23	Hs02895	EST1
7	Hs02896	EST1	24	Hs02896	EST1
8	Hs02897	EST1	25	Hs02897	EST1
9	Hs02898	EST1</			

FIGURE 4 (CONT.)

2545	W25753	Hs.22960	Cyclin B1
3352	W63127	Hs.69422	ESTs
28443	D60252	Hs.110819	ESTs
6160	X74794	Hs.88906	CDK21 HOMOLOG
42515	W72110	Hs.100333	Homo sapiens clone 23522 mRNA sequence
3327	U25222	Hs.84713	Human histone H4 interacting protein (HIF2) mRNA complete cds
3328	U25222	Hs.84713	Human histone H4 interacting protein (HIF2) mRNA complete cds
20320	A439214	Hs.63370	ESTs
746	D84454	Hs.21890	Human mRNA for UDP-glucanase pseudocatalytic complex cds
3117	M81182	Hs.71781	Functional membrane protein 1 (FMP1) cDNA sequence
21257	R09186	Hs.20321	ESTs Moderately similar to M-phase phosphoprotein 11 (H. sapiens)
31487	M69507	Hs.129649	ESTs
28954	F03153	Hs.90383	ESTs
38928	A4609565	Hs.106960	ESTs
29603	N33366	Hs.63664	EST
28209	A4691250	Hs.54990	ESTs
8470	H46817	EST - H46817	
9215	H46817	EST - H46817	
21411	A428137	Hs.69434	EST - H46817
30015	M92546	Hs.47076	ESTs
29934	N24194	Hs.43531	ESTs
1084	HQ2845-HT293	Hs.25740	EST - HQ2845-HT293
11232	AA188904	Hs.53442	ESTs
26343	AA287450	Hs.53442	ESTs
8035	AA305119	EST - AA305119	
19293	H15054	Hs.22184	ESTs
24596	C28010	Hs.27194	ESTs
24596	C21245	Hs.11171	H. sapiens mRNA for cyclin specific protein
6960	X71785	Hs.100333	Homo sapiens cyclin specific protein 6
30710	N51781	Hs.42338	EST
28360	A4258460	Hs.46810	ESTs
2351	M15798	Hs.78996	Proliferating cell nuclear antigen
30292	N35065	Hs.44890	Homo sapiens clone 21739 mRNA sequence
41792	T03886	Hs.100265	ESTs
36710	AA434411	Hs.88906	ESTs
42185	T79951	Hs.118035	ESTs
35148	F09134	Hs.12036	ESTs
29593	AA400003	Hs.88906	ESTs
29593	AA426868	Hs.86178	H. sapiens mRNA for M-phase phosphoprotein mp29
2117	AA403298	Hs.81178	ESTs
30458	W68835	Hs.14159	Homo sapiens mRNA for KAP635 protein complete cds
26893	AA282120	Hs.88975	EST
12659	AA417330	Hs.5101	Homo sapiens protein regulating cyclinase 1 (PRC1) mRNA complete cds
29701	H97970	Hs.42476	EST
34628	AA322436	Hs.27021	Homo sapiens semaphorin F homolog mRNA complete cds
14985	U15128	Hs.30373	Human beta-12-N-acetylglucosaminyltransferase II (MGAT2) gene complete cds
34781	AA287833	Hs.89908	ESTs
23211	T68819	Hs.8329	ESTs
40811	N07136	Hs.100794	Homo sapiens mRNA for KAP635 protein complete cds
17281	AA128395	Hs.11139	EST
18712	F04877	Hs.17381	ESTs
30709	N51752	Hs.47334	ESTs Weakly similar to synaptonemal complex protein tag7-1 (D. melanogaster)
34179	AA327963	Hs.41127	ESTs Highly similar to GTP-BINDING PROTEIN LEPA [Pseudomonas fluorescens]
1285	HQ4157-HT4427	EST - HQ4157-HT4427	

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FIGURE 4 (CONT.)

1109	41	HC2261-UT3127	EST - JAC384-UT3127
34367	41	Hs 40323	Homo sapiens spleen mitotic checkpoint BUB3 (BUB3) mRNA complete cds
34802	41	Hs 81504	ESTs
11595	41	Hs 32339	ESTs
8295	41	Hs 125014	ESTs
17622	41	Hs 11435	ESTs Weakly similar to SOF1 PROTEIN [Saccharomyces cerevisiae]
34754	41	Hs 81948	Human mRNA for KIAA0278 gene complete cds
31687	41	Hs 11065	ESTs Highly similar to 60S RIBOSOMAL PROTEIN L26 [Rattus norvegicus]
38622	41	Hs 141862	ESTs
25038	41	Hs 82758	CC28 protein kinase 2
32503	41	Hs 80393	Collagen type I alpha 2
3278	41	Hs 54769	SODIUM CHANNEL PROTEIN BRIAN II ALPHA SUBUNIT
3278	41	Hs 54769	SODIUM CHANNEL PROTEIN BRIAN II ALPHA SUBUNIT
35367	41	Hs 86438	Human transferrin receptor protein 1
31381	41	Hs 49397	ESTs
26723	41	Hs 95321	ESTs Highly similar to PRE-MRNA SPLICING FACTOR RNA HELICASE PRP20 [Saccharomyces cerevisiae]
30584	41	Hs 48024	ESTs
38286	41	Hs 12019	ESTs Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (Nucleobase co-antigen)
14474	41	Hs 24184	ESTs Moderately similar to RII ALU SUBFAMILY SC VARIING ENTRY III (H sapiens)
5312	41	Hs 79187	Human cell surface protein HCAR mRNA complete cds
35588	41	Hs 97343	EST
29738	41	Hs 42710	EST
7733	41	Hs 89403	ESTs
32290	41	Hs 52954	ESTs
8965	41	Hs 10584	ESTs Weakly similar to LITHOSTATHINE-1 BETA PRECURSOR (H sapiens)
224	41	Hs 77685	Human mRNA for KIAA0008 gene complete cds
33658	41	Hs 50582	ESTs
34065	41	Hs 111650	ESTs Weakly similar to RII ALU SUBFAMILY J VARIING ENTRY III (H sapiens)
8028	41	Hs 80011	Adenylsuccinate synthase
4106	41	Hs 106102	Cytidine B501
41069	41	Hs 81107	H sapiens mRNA for Hsf1 protein
8264	41	Hs 106941	ESTs
27588	41	Hs 41181	ESTs
32026	41	Hs 105518	Human histone H4C12 core particle (H4C12) mRNA complete cds
18931	41	Hs 10708	Homo sapiens mRNA for nucleolar protein hNgp56
11379	41	Hs 24841	ESTs
35223	41	Hs 110042	ESTs Highly similar to DOUCMYL-PHOSPHATE BETA-GLUCOSYLTRANSFERASE [Saccharomyces cerevisiae]
8771	41	Hs 82273	ESTs
7888	41	Hs 81634	ESTs
19902	41	Hs 34180	ESTs
10716	41	Hs 9951	ESTs
13193	41	Hs 20483	ESTs Highly similar to G2/MITOTIC-SPECIFIC CYCLIN B2 [Mus musculus]
9593	41	Hs 118538	NUCLEOSIDE DIPHOSPHATE KINASE A
31889	41	Hs 50482	ESTs
31889	41	Hs 50482	ESTs
28231	41	Hs 82453	EST
28248	41	Hs 71969	ESTs
33036	41	Hs 39572	ESTs Weakly similar to Transposon LRE2 reverse transcriptase homolog (H sapiens)
28106	41	Hs 110462	ESTs
38690	41	Hs 114687	ESTs
20203	41	Hs 5558	ESTs Moderately similar to RII ALU SUBFAMILY SC VARIING ENTRY III (H sapiens)
10251	41	Hs 18171	ESTs Weakly similar to Cdh67 (C elegans)
31586	41	Hs 57413	Neural resistance-associated macrophage protein 2
1572	41	EST - K01884	

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FIGURE 4 (CONT.)

39242	AA421523	Hs.110032 ESTs	Hs.110032 ESTs
27354	AA425221	Hs.81008 ESTs	Hs.81008 ESTs
4332	U98189	Hs.78279 Human placenta (CH25) mRNA complete cds	Hs.78279 Human placenta (CH25) mRNA complete cds
10135	AA434718	Hs.110070 Human testis (CH25) mRNA partial cds	Hs.110070 Human testis (CH25) mRNA partial cds
10134	AA434709	EST - RC_A003607	EST - RC_A003607
42463	U98180	Hs.103130 ESTs	Hs.103130 ESTs
867		Hs.100315 Human mRNA for KIAA2007 gene partial cds	Hs.100315 Human mRNA for KIAA2007 gene partial cds
31795	N80703	Hs.50473 ESTs	Hs.50473 ESTs
27828	R98192	Hs.35678 ESTs	Hs.35678 ESTs
25240	AA439713	Hs.110400 ESTs	Hs.110400 ESTs
4341	U39545	Hs.82507 Human ARF-activated phosphatidylinositol-specific phospholipase D1a (pILD1) mRNA complete cds	Hs.82507 Human ARF-activated phosphatidylinositol-specific phospholipase D1a (pILD1) mRNA complete cds
17483	AA122147	Hs.84691 ESTs	Hs.84691 ESTs
16854	AA55552	Hs.71622 ESTs	Hs.71622 ESTs
3709	U07550	Hs.11187 Head shock 10 KD protein 1 (phaucoron 10)	Hs.11187 Head shock 10 KD protein 1 (phaucoron 10)
808	U00205	Hs.11120 KERNATIN TYPE II CYTOSKELETAL 8D	Hs.11120 KERNATIN TYPE II CYTOSKELETAL 8D
4018	AA439713	Hs.11120 Human RNA binding protein C1-3 mRNA complete cds	Hs.11120 Human RNA binding protein C1-3 mRNA complete cds
20418	AA48200	Hs.32171 ESTs	Hs.32171 ESTs
27695	AA470155	Hs.75807 Homo sapiens codonless protein (COPA) mRNA complete cds	Hs.75807 Homo sapiens codonless protein (COPA) mRNA complete cds
7971	AA287423	Hs.126399 ESTs	Hs.126399 ESTs
27600	AA437193	Hs.64761 ESTs	Hs.64761 ESTs
24677	Z39338	Hs.21201 ESTs	Hs.21201 ESTs
9278	DE5818	Hs.33886 Homo sapiens importin-alpha homolog (SRP1) gamma1 mRNA complete cds	Hs.33886 Homo sapiens importin-alpha homolog (SRP1) gamma1 mRNA complete cds
17678	AA134275	Hs.134510 Human IVF1 late element modulatory factor mRNA sequence from chromosome 3	Hs.134510 Human IVF1 late element modulatory factor mRNA sequence from chromosome 3
36709	AA421205	Hs.13889 ESTs	Hs.13889 ESTs
20094	H99053	Hs.10908 ESTs	Hs.10908 ESTs
9713	L44338	Hs.78494 Homo sapiens mRNA for KIAA0225 protein partial cds	Hs.78494 Homo sapiens mRNA for KIAA0225 protein partial cds
28922	U11637	Hs.22846 ESTs	Hs.22846 ESTs
28922	U11637	Hs.22846 ESTs	Hs.22846 ESTs
29004	AA148985	Hs.111740 ESTs	Hs.111740 ESTs
2402	M23865	Hs.18484 Tumor protein p53 (L-Franchet syndrome)	Hs.18484 Tumor protein p53 (L-Franchet syndrome)
14804	T83389	Hs.107147 ESTs	Hs.107147 ESTs
22075	AA043785	Hs.54649 H sapiens R1-1 mRNA for putative nucleic acid binding protein	Hs.54649 H sapiens R1-1 mRNA for putative nucleic acid binding protein
13606	AA459437	Hs.20386 ESTs	Hs.20386 ESTs
42307	T90585	EST - RC_T00355	EST - RC_T00355
1544	A05568	Hs.2017 TRANSCOBALANIN PRECURSOR	Hs.2017 TRANSCOBALANIN PRECURSOR
42311	T97237	Hs.84500 ESTs	Hs.84500 ESTs
4013	U48020	Hs.3025 INITIATION FACTOR IF-2 MITOCHONDRIAL PRECURSOR	Hs.3025 INITIATION FACTOR IF-2 MITOCHONDRIAL PRECURSOR
33737	U48020	Hs.3025 Human testis (CH25) mRNA complete cds	Hs.3025 Human testis (CH25) mRNA complete cds
17220	AA055070	Hs.3281 Neuronal perlecanin II	Hs.3281 Neuronal perlecanin II
24322	W85782	Hs.18328 ESTs	Hs.18328 ESTs
32587	AA412057	Hs.68117 ESTs	Hs.68117 ESTs
8338	AA417152	Hs.5101 Homo sapiens protein regulating cytokinesis 1 (PRC1) mRNA complete cds	Hs.5101 Homo sapiens protein regulating cytokinesis 1 (PRC1) mRNA complete cds
387	O25589	EST - D26559	EST - D26559
12310	AA398109	Hs.20990 ESTs	Hs.20990 ESTs
15643	W95247	Hs.27437 ESTs	Hs.27437 ESTs
12118	AA180488	Hs.33746 ESTs	Hs.33746 ESTs
18339	AA025206	Hs.11511 Human mRNA for KIAA0073 gene partial cds	Hs.11511 Human mRNA for KIAA0073 gene partial cds
12320	U48020	Hs.97711 ESTs	Hs.97711 ESTs
22595	AA425242	Hs.107092 Hs.107092	Hs.107092 Hs.107092
34078	AA181488	Hs.75814 Human high-affinity copper uptake protein (ICTR1) mRNA complete cds	Hs.75814 Human high-affinity copper uptake protein (ICTR1) mRNA complete cds
251	D14520	Hs.84728 Basic transcription element binding protein 2	Hs.84728 Basic transcription element binding protein 2
3778	U09548	Hs.303 Zinc finger protein 139 (zfp139)	Hs.303 Zinc finger protein 139 (zfp139)
24535	Z38409	Hs.8053 ESTs	Hs.8053 ESTs
18127	AA060690	Hs.39441 ESTs	Hs.39441 ESTs

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FIGURE 4 (CONT.)

26146	3.4	AA250824	Hs 60478	ESTs Weakly similar to ZINC FINGER PROTEIN 91 [H sapiens]
4011	3.4	U75535	Hs 3280	Human cysteine protease MO2 mRNA alpha (MO2) mRNA complete cds
5660	3.4	X15294	Hs 31721	NAD(P)-DEPENDENT METHYLENE TETRAHYDROFOLATE DEHYDROGENASE
76270	3.4	AA242600	Hs 47222	ESTs
30227	3.4	AA242606	Hs 98395	ESTs
141716	3.4	U75535	Hs 3280	Human cysteine protease MO2 mRNA alpha (MO2) mRNA complete cds
17261	3.4	AA101381	Hs 68900	ESTs
15098	3.3	W16684	Hs 74284	ESTs. Modestly similar to similar to 5 carboxylate hydrolase protein L3111 [H sapiens]
17675	3.3	AA134064	Hs 44045	ESTs
10009	3.3	N81193	Hs 43133	Human aspartic protease for <I>A</I>AD28 protein complete cds
33885	3.3	AA181560	Hs 61890	Human aspartic protease beta subunit mRNA complete cds
6270	3.3	H85189	Hs 24937	Human aspartic protease beta subunit mRNA complete cds
37351	3.3	AA458079	Hs 72508	ESTs
18367	3.3	AA224150	Hs 103332	ESTs. Modestly similar to overexpression protein [H sapiens]
14310	3.3	AA588412	Hs 6739	ESTs. Highly similar to HYPOXEMIA-TRIP-ASP REPEATS CONTAINING PROTEIN IN PMT&PCT INTERGENIC REGION [Saccharomyces cerevisiae]
18220	3.3	H12534	Hs 8104	ESTs
144626	3.3	AA458079	Hs 72508	ESTs
21551	3.3	R33073	Hs 24568	ESTs
13767	3.3	AA463234	Hs 119087	ESTs
4739	3.3	U53768	Hs 75801	Human FX protein mRNA complete cds
7258	3.3	AA075427	Hs 17798	ESTs
17041	3.3	AA070364	Hs 44131	ESTs
16214	3.3	W23862	Hs 86081	ESTs
16504	3.3	AA196835	Hs 35987	Human translation initiation factor eIF3 p80 subunit mRNA complete cds
7401	3.3	AA064800	Hs 17215	Human aspartic protease 28071 subunit mRNA partial cds
10912	3.3	U75535	Hs 3280	Human cysteine protease MO2 mRNA alpha (MO2) mRNA complete cds
144626	3.3	AA458079	Hs 72508	ESTs
9410	3.3	H26443	Hs 31748	Human mRNA for TRES
2148	3.2	L41390	EST - L41390	
16883	3.2	F04258	Hs 36454	ESTs. Highly similar to NORGANIC PYROPHOSPHATASE [Bos taurus]
33891	3.2	X76944	Hs 91378	PTB ASSOCIATED SPLICING FACTOR
15840	3.2	K82439	Hs 87157	130 KD LEUCINE-RICH PROTEIN
3258	3.2	U41387	Hs 5122	Human O6 protein mRNA partial cds
4400	3.2	R15848	Hs 21730	ESTs
21350	3.2	AA380925	Hs 24297	ESTs
11881	3.2	H12534	Hs 8104	ESTs
22390	3.2	AA380925	Hs 24297	ESTs
144626	3.2	AA458079	Hs 72508	ESTs
13484	3.2	AA453431	Hs 21043	ESTs
12908	3.2	AA427578	Hs 8047	ESTs
31309	3.1	N65818	Hs 42179	ESTs
31192	3.1	N64408	Hs 54174	ESTs
11288	3.1	AA195512	Hs 23916	ESTs
172	3.1	D03356	Hs 82962	Thymidylate synthase
26105	3.1	AA243133	Hs 48915	Human aspartic serine/threonine kinase (HAK) mRNA complete cds
11059	3.1	AA251809	Hs 32708	Human aspartic serine/threonine kinase (HAK) protein kinase mRNA complete cds
19177	3.1	H10534	Hs 12338	ESTs
17380	3.1	AA458079	Hs 72508	ESTs
42136	3.1	U42046	Hs 10304	ESTs
18335	3.1	W64028	Hs 63320	ESTs. Weakly similar to CA BINDING PROTEIN BEA-2 (CABP2) [H sapiens]
3195	3.1	W64028	Hs 131801	PERUVIAN DEHYDROGENASE E1 COMPLEX (HAK) ALPHA SUBUNIT. TEST IS SPECIFIC FORM PREDICTION
17499	3.1	AA112979	Hs 48290	Human aspartic protease beta subunit mRNA complete cds
14130	3.1	AA468041	Hs 15140	ESTs
14134	3.1	AA468041	Hs 3266	ESTs. Highly similar to phosphorylation regulatory protein HP-12 [H sapiens]
42421	3.1	W45491	Hs 108835	ESTs. Weakly similar to T23517 [C elegans]
15723	3.1	W79260	Hs 5337	ESTs. Highly similar to ribosome-binding protein p34 [H sapiens]

FIGURE 4 (CONT.)

11140	31	AA158132	Hs11817 ESTs Highly similar to YSA1 PROTEIN [Sclerodermatolysis associated]
14322	31	AA158133	Hs27883 ESTs Highly similar to YSA1 PROTEIN [Sclerodermatolysis associated]
15962	31	Z11406	Hs30019 ESTs
17150	31	AA158134	Hs15818 ESTs
22113	31	AA158135	Hs15819 ESTs
33528	31	AA158136	Hs15820 ESTs
17825	31	AA158137	Hs15821 ESTs
5053	31	AA158138	Hs15822 ESTs
15090	31	U54899	Hs71134 Human TGF- β 1 mRNA complete cds
17757	31	AA147224	Hs93121 Human LCN protein mRNA complete cds
28330	31	AA278650	Hs71814 EST
22660	31	T10272	Hs73291 ESTs
4298	31	U96448	Hs43287 ESTs
7445	31	AA110048	Hs74374 Human Cdc-2-related esterase protein for secretion mRNA complete cds
7535	31	AA110049	Hs110048 ESTs
7537	31	AA110050	Hs110049 ESTs
806	31	AA110051	Hs110050 ESTs
38447	31	AA110052	Hs110051 ESTs
41464	31	AA110053	Hs110052 ESTs
9607	31	AA110054	Hs110053 ESTs
13174	31	AA110055	Hs110054 ESTs
33820	31	AA110056	Hs110055 ESTs
1930	31	AA110057	Hs110056 ESTs
32159	31	AA110058	Hs110057 ESTs
13617	31	AA110059	Hs110058 ESTs
11889	31	AA110060	Hs110059 ESTs
6059	31	AA110061	Hs110060 ESTs
1605	31	AA110062	Hs110061 ESTs
4536	31	AA110063	Hs110062 ESTs
10173	31	AA110064	Hs110063 ESTs
21009	31	AA110065	Hs110064 ESTs
38200	31	AA110066	Hs110065 ESTs
38209	31	AA110067	Hs110066 ESTs
1864	31	AA110068	Hs110067 ESTs
1865	31	AA110069	Hs110068 ESTs
5928	31	AA110070	Hs110069 ESTs
18190	31	AA110071	Hs110070 ESTs
19887	31	AA110072	Hs110071 ESTs
6681	31	AA110073	Hs110072 ESTs
5254	31	AA110074	Hs110073 ESTs
13579	31	AA110075	Hs110074 ESTs
38495	31	AA110076	Hs110075 ESTs
2028	31	AA110077	Hs110076 ESTs
27374	31	AA110078	Hs110077 ESTs
20126	31	AA110079	Hs110078 ESTs
18128	31	AA110080	Hs110079 ESTs
18129	31	AA110081	Hs110080 ESTs
357	31	AA110082	Hs110081 ESTs
28045	31	AA110083	Hs110082 ESTs
8059	31	AA110084	Hs110083 ESTs
21358	31	AA110085	Hs110084 ESTs
3572	31	AA110086	Hs110085 ESTs
11877	31	AA110087	Hs110086 ESTs
35830	31	AA110088	Hs110087 ESTs

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FIGURE 4 (CONT.)

26	U27855	Hs 0831	homo sapiens clone 14D3 unknown protein mRNA partial cds
27	U27855	EST: RC_AA09287	
28	AA236927	Hs 118726	ESTs
29	AA236927	Hs 35459	EST
30	AA236927	Hs 63273	ESTs
31	AA236927	Hs 98150	ESTs
32	AA236927	Hs 42118	ESTs
33	AA236927	Hs 28553	ESTs
34	AA236927	EST: RC_AA23294	
35	AA236927	Hs 75337	human mRNA for KIA0035 gene partial cds
36	AA236927	Hs 84974	h-spleen mRNA for lcn protein
37	AA236927	Hs 95187	EST
38	AA236927	Hs 06180	Replication protein A (E col) RecA homologous (noncoding)
39	AA236927	Hs 5158	ESTs
40	AA236927	Hs 21700	ESTs
41	AA236927	Hs 86248	ESTs
42	AA236927	Hs 27047	ESTs
43	AA236927	Hs 20153	Western BDM RNA binding protein Cyt-4p (Cyt4-RBP) mRNA complete cds
44	AA236927	Hs 20153	Western BDM RNA binding protein Cyt-4p (Cyt4-RBP) mRNA complete cds
45	AA236927	Hs 44155	ESTs Weakly similar to C.1:1ETB47DPC/PLATE SYNTHASE CYP145AC (H. sapiens)
46	AA236927	Hs 2758	human reticulocytos binding protein (RbAp48) mRNA complete cds
47	AA236927	Hs 108182	ESTs
48	AA236927	Hs 4214	Homo sapiens TLR-5 associated protein TLR-5 mRNA complete cds
49	AA236927	Hs 90556	ESTs
50	AA236927	Hs 90077	h-spleen mRNA for TGF protein
51	AA236927	Hs 15066	h-spleen mRNA for TGF protein
52	AA236927	EST: RC_AA09284	
53	AA236927	Hs 97101	ESTs
54	AA236927	Hs 22357	ESTs
55	AA236927	Hs 89403	Homo sapiens protein-tyrosine kinase EphA2 (EPH2) mRNA complete cds
56	AA236927	Hs 42946	ESTs
57	AA236927	Hs 97361	ESTs
58	AA236927	Hs 21603	human mRNA for KIA0038 gene complete cds
59	AA236927	Hs 7551	ESTs
60	AA236927	Hs 3430	ESTs
61	AA236927	U27855	U27855
62	AA236927	U27855	U27855
63	AA236927	Hs 6719	human bone tissue c1 protein mRNA complete cds
64	AA236927	Hs 6671	human S10 domain-containing protein S10P16 (human cytochrome c2)
65	AA236927	Hs 97101	ESTs
66	AA236927	Hs 8766	ESTs Weakly similar to PHO8A/E ES PROTEIN (human cytochrome c2)
67	AA236927	Hs 13904	Homo sapiens mRNA for KIA0037 protein complete cds
68	AA236927	Hs 96013	Homo sapiens mRNA for KIA0054 protein complete cds
69	AA236927	Hs 10724	ESTs Weakly similar to unknown (S. cerevisiae)
70	AA236927	Hs 10724	ESTs Weakly similar to unknown (S. cerevisiae)
71	AA236927	Hs 10992	ESTs Weakly similar to unknown (S. cerevisiae)
72	AA236927	Hs 1695	homo sapiens mRNA for KIA0037 protein complete cds
73	AA236927	Hs 46372	ESTs
74	AA236927	Hs 44439	ESTs
75	AA236927	Hs 12063	ESTs
76	AA236927	Hs 85634	ESTs
77	AA236927	Hs 105478	human mRNA for KIA0061 gene KIA0051 protein
78	AA236927	Hs 24928	ESTs
79	AA236927	Hs 24928	ESTs Weakly similar to tubulin (H. musculus)
80	AA236927	Hs 93341	homo sapiens mRNA complete cds
81	AA236927	Hs 63136	ESTs
82	AA236927	Hs 20178	ESTs Weakly similar to RAR (H. nonnegligi)
83	AA236927	Hs 15288	ESTs

FIGURE 4 (CONT.)

2332	191715	Hs 14374	EST1a Highly similar to HYPOTHETICAL 103.6 NO PROTEIN IN COUS88 PH28 INTERGENIC REGION [Saccharomyces cerevisiae]
10961	AA128719	Hs 23382	EST1a
29881	AA202659	Hs 03887	EST1a
7199	AA215299	Hs 70830	Homo sapiens chromosome 19 contig R10703
11308	AA207114	Hs 27147	EST1a
4206	AA217014	Hs 11171	Human anterior regulatory factor-1 mRNA complete cds
11819	AA219038	Hs 32471	EST1a
37433	AA454103	Hs 11001	EST1a
5507	X13482	Hs 80008	U2 SMALL NUCLEAR RIBONUCLEOPROTEIN A'
19841	H03617	Hs 5109	EST1a Highly similar to Y607c-tp [S. cerevisiae]
12655	AA240882	Hs 10290	EST1a
31574	H71303	Hs 50015	EST1a
7814	AA107279	Hs 10208	EST1a Weakly similar to Y607c-tp [S. cerevisiae]
7050	AA009913	Hs 10300	Homo sapiens epithelial dehydratase protease-2 (DPH2) mRNA complete cds
24219	H05900	Hs 19416	EST1a
19070	AA136369	Hs 13308	Human clone Z1020 mRNA sequence
17116	AA136369	Hs 14299	EST1a
12132	AA136369	Hs 31921	Homo sapiens mRNA for KIAA0649 protein partial cds
8613	AA159455	Hs 5307	EST1a
13966	AA178319	Hs 75574	PUTATIVE 60S RIBOSOMAL PROTEIN
30552	R03653	Hs 84162	Human chromosome 3p21.1 gene sequence complete cds
1799	L13434	Hs 90315	Human mRNA for KIAA0007 gene partial cds
14746	D60354	Hs 75200	Protein phosphatase 2 (formerly 2A) regulatory subunit B (PR 52) alpha isoform
2953	MA4829	Hs 7487	EST1a Moderately similar to PTTG gene product [R. norvegicus]
17899	AA430032	Hs 70960	EST1a
18003	AA171692	Hs 10239	EST1a
42633	V02703	Hs 10239	EST1a
15254	AA226185	Hs 10239	EST1a Weakly similar to CSUF 4.12 [C. elegans]
26113	AA213705	Hs 70791	EST1a
15437	V07560	Hs 90718	EST1a
27146	AA453159	Hs 41723	Human braininhibin a spinin protein (INSP) mRNA complete cds
32315	R05540	Hs 70189	EST1a Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOGY (Nystanov coupling)
23310	AA048745	Hs 110457	EST1a
9658	L10991	Hs 79006	Deoxythymidylase kinase
12210	AA293774	Hs 21261	EST1a Weakly similar to PROBABLE TRYPTOPHANYL-TRNA SYNTHETASE MITOCHONDRIAL [C. elegans]
33828	V02091	Hs 20330	Human mRNA for breast-related protein partial cds
9652	L37747	Hs 09487	LAMIN B1
27862	AA455296	Hs 50683	EST1a
10896	AA219038	Hs 11001	EST1a
9889	N05443	Hs 11449	EST1a Highly similar to HYPOTHETICAL 30.3 NO PROTEIN IN APE104-CPY1 INTERGENIC REGION [Saccharomyces cerevisiae]
5932	X07453	Hs 82478	Mitochondrion encodes a protein deficient (S. cerevisiae) 3
26834	AA287139	Hs 59346	EST1a Weakly similar to ASPARTYL-TRNA SYNTHETASE [Thermus aquaticus thermophilus]
5157	U80034	Hs 68585	Human mitochondrial intermedial peptide precursor (MPEP) mRNA mitochondrial gene encoding mitochondrial protein complete cds
39434	AA497013	Hs 14292	EST1a
7590	AA173505	Hs 35353	EST1a
14960	U05337	Hs 99872	Human fetal AL-50-reactive clone 1 (FAC1) mRNA complete cds
13585	AA455099	Hs 32151	EST1a Highly similar to NEUROLYSIN PRECURSOR [Rue scrofa]
33193	AA487208	Hs 08877	Homo sapiens mRNA for KIAA0638 protein complete cds
34078	AA284744	Hs 72910	Artemis XI (58KD subdomain)
47474	AA284744	Hs 72910	Artemis XI (58KD subdomain)
21474	AA284744	Hs 72910	Artemis XI (58KD subdomain)
34720	AA284744	Hs 72910	Artemis XI (58KD subdomain)
16109	AA180861	Hs 58169	Homo sapiens neuroblastoma associated protein hNC mRNA complete cds
8465	X92098	Hs 72914	H. sapiens mRNA for transmembrane protein mp2.4
27444	AA430160	Hs 42785	EST1a Weakly similar to F25197 [C. elegans]

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FIGURE 4 (CONT.)

3007	35	N27409	Hs 51652 EST	Hs 51652 EST
27602	35	AA443302	Hs 29635 EST	Weakly similar to W02B12.7 [C. elegans]
3390	35	S59184	Hs 79350 PTK	receptor like tyrosine kinase
25042	35	AA5010188	Hs 102303 EST	
40477	34	N24096	Hs 95048 Homo sapiens DAC gene	RG30622 from 7c21-c31.1
18620	34	F27560	Hs 9417 EST	
15120	34	U73524	Hs 67465 Human pituitary A1P1 (P) binding protein (HEAB) mRNA	complete cds
26813	34	D59257	Hs 91181 Human C-1 mRNA	containing cds
34723	34	AA287115	Hs 60597 EST	
7993	34	AA453277	Hs 8027 Homo sapiens brain expressed ring finger protein mRNA	complete cds
18217	34	U11087	Hs 12344 EST	
25033	34	AA453011	Hs 80777 EST	
452	34	AA453011	Hs 80777 EST	
11701	34	AA453011	Hs 80777 EST	
12672	34	AA453011	Hs 80777 EST	
4330	34	AA453011	Hs 80777 EST	
42300	34	AA453011	Hs 80777 EST	
28395	34	AA453011	Hs 80777 EST	
36390	34	AA453011	Hs 80777 EST	
12916	34	AA453011	Hs 80777 EST	
30766	34	AA453011	Hs 80777 EST	
14426	34	AA453011	Hs 80777 EST	
6307	34	AA453011	Hs 80777 EST	
11342	34	AA453011	Hs 80777 EST	
1497	34	AA453011	Hs 80777 EST	
11454	34	AA453011	Hs 80777 EST	
35976	34	AA453011	Hs 80777 EST	
27872	34	AA453011	Hs 80777 EST	
11623	34	AA453011	Hs 80777 EST	
11570	34	AA453011	Hs 80777 EST	
13533	34	AA453011	Hs 80777 EST	
6231	34	AA453011	Hs 80777 EST	
24371	34	AA453011	Hs 80777 EST	
25266	34	AA453011	Hs 80777 EST	
8163	34	AA453011	Hs 80777 EST	
12233	34	AA453011	Hs 80777 EST	
14371	34	AA453011	Hs 80777 EST	
26169	34	AA453011	Hs 80777 EST	
23065	34	AA453011	Hs 80777 EST	
20594	34	AA453011	Hs 80777 EST	
20837	34	AA453011	Hs 80777 EST	
11745	34	AA453011	Hs 80777 EST	
13737	34	AA453011	Hs 80777 EST	
17352	34	AA453011	Hs 80777 EST	
11914	34	AA453011	Hs 80777 EST	
20796	34	AA453011	Hs 80777 EST	
22491	34	AA453011	Hs 80777 EST	
40847	34	AA453011	Hs 80777 EST	
42022	34	AA453011	Hs 80777 EST	
8053	34	AA453011	Hs 80777 EST	
383	34	AA453011	Hs 80777 EST	
20796	34	AA453011	Hs 80777 EST	
31852	34	AA453011	Hs 80777 EST	
24092	34	AA453011	Hs 80777 EST	

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FIGURE 4 (CONT.)

23	H22940	Hs 31842	EST	
23	A416380	Hs 42210	EST	
23	AA45296	Hs 32794	EST	
23	AA454943	Hs 28911	EST	
23	A2370774	Hs 142497	EST	
23	U03237	Hs 05872	Human fetal AL-3; rat-delta clone 1 (FAC1) mRNA, complete cds	
23	A238710	Hs 17823	EST	
23	AB05316	Hs 66093	EST	
23	U63037	Hs 63337	EST	
23	U67010	Hs 108703	Recombinant protein L37	
23	U59405	Hs 63263	EST Moderately similar to the ALU SURFAMILY 5X WARNING ENTRY, 1p (H sapiens)	
23	U59405	Hs 63532	Membrane cofactor protein (CD46) transmembrane alpha cross-reactive antigen	
23	U79100	Hs 63190	EST	
23	A11987	Hs 108678	EST	
23	F04320	Hs 325120	Replication factor C 3.7.10 subunit	
23	A059496	Hs 7301	Home sapiens voltage dependent anion channel protein mRNA, complete cds	
23	AB05313	Hs 74290	Home sapiens voltage dependent anion channel protein mRNA, complete cds	
23	U63037	Hs 63337	EST	
23	U67010	Hs 108703	EST	
23	AB05316	Hs 66093	EST	
23	U63037	Hs 63337	EST	
23	U67010	Hs 108703	EST	
23	U59405	Hs 63263	EST Moderately similar to the ALU SURFAMILY 5X WARNING ENTRY, 1p (H sapiens)	
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23	U79100	Hs 63190	EST	
23	A11987	Hs 108678	EST	
23	F04320	Hs 325120	Replication factor C 3.7.10 subunit	
23	A059496	Hs 7301	Home sapiens voltage dependent anion channel protein mRNA, complete cds	
23	AB05313	Hs 74290	Home sapiens voltage dependent anion channel protein mRNA, complete cds	
23	U63037	Hs 63337	EST	
23	U67010	Hs 108703	EST	
23	AB05316	Hs 66093	EST	
23	U63037	Hs 63337	EST	
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23	AB05313	Hs 74290	Home sapiens voltage dependent anion channel protein mRNA, complete cds	
23	U63037	Hs 63337	EST	
23	U67010	Hs 108703	EST	
23	AB05316	Hs 66093	EST	
23	U63037	Hs 63337	EST	
23	U67010	Hs 108703	EST	
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23	U79100	Hs 63190	EST	
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23	U67010	Hs 108703	EST	
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23	A11987	Hs 108678	EST	
23	F04320	Hs 325120	Replication factor C 3.7.10 subunit	
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23	AB05313	Hs 74290	Home sapiens voltage dependent anion channel protein mRNA, complete cds	
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23	U67010	Hs 108703	EST	
23	AB05316	Hs 66093	EST	
23	U63037	Hs 63337	EST	
23	U67010	Hs 108703	EST	
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23	U79100	Hs 63190	EST	
23	A11987	Hs 108678	EST	
23	F04320	Hs 325120	Replication factor C 3.7.10 subunit	
23	A059496	Hs 7301	Home sapiens voltage dependent anion channel protein mRNA, complete cds	
23	AB05313	Hs 74290	Home sapiens voltage dependent anion channel protein mRNA, complete cds	
23	U63037	Hs 63337	EST	
23	U67010	Hs 108703	EST	
23	AB05316	Hs 66093	EST	
23	U63037	Hs 63337	EST	
23	U67010	Hs 108703	EST	
23	U59405	Hs 63263	EST Moderately similar to the ALU SURFAMILY 5X WARNING ENTRY, 1p (H sapiens)	
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23	U79100	Hs 63190	EST	
23	A11987	Hs 108678	EST	
23	F04320	Hs 325120	Replication factor C 3.7.10 subunit	
23	A059496	Hs 7301	Home sapiens voltage dependent anion channel protein mRNA, complete cds	
23	AB05313	Hs 74290	Home sapiens voltage dependent anion channel protein mRNA, complete cds	
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23	U67010	Hs 108703	EST	
23	AB05316	Hs 66093	EST	
23	U63037	Hs 63337	EST	
23	U67010	Hs 108703	EST	
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23	U79100	Hs 63190	EST	
23	A11987	Hs 108678	EST	
23	F04320	Hs 325120	Replication factor C 3.7.10 subunit	
23	A059496	Hs 7301	Home sapiens voltage dependent anion channel protein mRNA, complete cds	
23	AB05313	Hs 74290	Home sapiens voltage dependent anion channel protein mRNA, complete cds	
23	U63037	Hs 63337	EST	
23	U67010	Hs 108703	EST	
23	AB05316	Hs 66093	EST	
23	U63037	Hs 63337	EST	
23	U67010	Hs 108703	EST	
23	U59405	Hs 63263	EST Moderately similar to the ALU SURFAMILY 5X WARNING ENTRY, 1p (H sapiens)	
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23	A11987	Hs 108678	EST	
23	F04320	Hs 325120	Replication factor C 3.7.10 subunit	
23	A059496	Hs 7301	Home sapiens voltage dependent anion channel protein mRNA, complete cds	
23	AB05313	Hs 74290	Home sapiens voltage dependent anion channel protein mRNA, complete cds	
23	U63037	Hs 63337	EST	
23	U67010	Hs 108703	EST	
23	AB05316	Hs 66093	EST	
23	U63037	Hs 63337	EST	
23	U67010	Hs 108703	EST	
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23	A11987	Hs 108678	EST	
23	F04320	Hs 325120	Replication factor C 3.7.10 subunit	
23	A059496	Hs 7301	Home sapiens voltage dependent anion channel protein mRNA, complete cds	
23	AB05313	Hs 74290	Home sapiens voltage dependent anion channel protein mRNA, complete cds	
23	U63037	Hs 63337	EST	
23	U67010	Hs 108703	EST	
23	AB05316	Hs 66093	EST	
23	U63037	Hs 63337	EST	
23	U67010	Hs 108703	EST	
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23	A11987	Hs 108678	EST	
23	F04320	Hs 325120	Replication factor C 3.7.10 subunit	
23	A059496	Hs 7301	Home sapiens voltage dependent anion channel protein mRNA, complete cds	
23	AB05313	Hs 74290	Home sapiens voltage dependent anion channel protein mRNA, complete cds	
23	U63037	Hs 63337	EST	
23	U67010	Hs 108703	EST	
23	AB05316	Hs 66093	EST	
23	U63037	Hs 63337	EST	
23	U67010	Hs 108703	EST	
23	U59405	Hs 63263	EST Moderately similar to the ALU SURFAMILY 5X WARNING ENTRY, 1p (H sapiens)	
23	U59405	Hs 63532	Membrane cofactor protein (CD46) transmembrane alpha cross-reactive antigen	
23	U79100	Hs 63190	EST	
23	A11987	Hs 108678	EST	
23	F04320	Hs 325120	Replication factor C 3.7.10 subunit	
23	A059496	Hs 7301	Home sapiens voltage dependent anion channel protein mRNA, complete cds	
23	AB05313	Hs 74290	Home sapiens voltage dependent anion channel protein mRNA, complete cds	
23	U63037	Hs 63337	EST	
23	U67010	Hs 108703	EST	
23	AB05316	Hs 66093	EST	
23	U63037	Hs 63337	EST	
23	U67010	Hs 108703	EST	
23	U59405	Hs 63263	EST Moderately similar to the ALU SURFAMILY 5X WARNING ENTRY, 1p (H sapiens)	
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23	U79100	Hs 63190	EST	
23	A11987	Hs 108678	EST	
23	F04320	Hs 325120	Replication factor C 3.7.10 subunit	
23	A059496	Hs 7301	Home sapiens voltage dependent anion channel protein mRNA, complete cds	
23	AB05313	Hs 74290	Home sapiens voltage dependent anion channel protein mRNA, complete cds	
23	U63037	Hs 63337	EST	
23	U67010	Hs 108703	EST	
23	AB05316	Hs 66093	EST	
23	U63037	Hs 63337	EST	
23	U67010	Hs 108703	EST	
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23	U79100	Hs 63190	EST	
23	A11987	Hs 108678	EST	
23	F04320	Hs 325120	Replication factor C 3.7.10 subunit	
23	A059496	Hs 7301	Home sapiens voltage dependent anion channel protein mRNA, complete cds	
23	AB05313	Hs 74290	Home sapiens voltage dependent anion channel protein mRNA, complete cds	
23	U63037	Hs 63337	EST	
23	U67010	Hs 108703	EST	
23	AB05316	Hs 66093	EST	
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23	U79100	Hs 63190	EST	
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23	U63037	Hs 63337	EST	
23	U67010	Hs 108703	EST	
23	AB05316	Hs 66093	EST	
23	U63037	Hs 63337	EST	
23	U67010	Hs 108703	EST	
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23	U59405	Hs 63532	Membrane cofactor protein (CD46) transmembrane alpha cross-reactive antigen	
23	U79100	Hs 63190	EST	
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23	A059496	Hs 7301	Home sapiens voltage dependent anion channel protein mRNA, complete cds	
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23	U63037	Hs 63337	EST	
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23	U63037	Hs 63337	EST	
23	U67010	Hs 108703	EST	
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23	U59405	Hs 63532	Membrane cofactor protein (CD46) transmembrane alpha cross-reactive antigen	
23	U79100	Hs 63190	EST	
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23	U63037	Hs 63337	EST	
23	U67010	Hs 108703	EST	
23	AB05316	Hs 66093	EST	
23	U63037	Hs 63337	EST	
23	U67010	Hs 108703	EST	
23	U59405	Hs 63263	EST Moderately similar to the ALU SURFAMILY 5X WARNING ENTRY, 1p (H sapiens)	
23	U59405	Hs 63532	Membrane cofactor protein (CD46) transmembrane alpha cross-reactive antigen	
23	U79100	Hs 63190	EST	
23	A11987	Hs 108678	EST	
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23	U63037	Hs 63337	EST	
23	U67010	Hs 108703	EST	
23	AB05316	Hs 66093	EST	
23	U63037	Hs 63337	EST	
23	U67010	Hs 108703	EST	
23	U59405	Hs 63263	EST Moderately similar to the ALU SURFAMILY 5X WARNING ENTRY, 1p (H sapiens)	
23	U59405	Hs 63532	Membrane cofactor protein (CD46) transmembrane alpha cross-reactive antigen	
23	U79100	Hs 63190	EST	
23	A11987	Hs 108678	EST	
23	F04320	Hs 325120	Replication factor C 3.7.10 subunit	
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23	AB05313	Hs 74290	Home sapiens voltage dependent anion channel protein mRNA, complete cds	
23	U63037	Hs 63337	EST	
23	U67010	Hs 108703	EST	
23	AB05316	Hs 66093	EST	
23	U63037	Hs 63337	EST	
23	U67010	Hs 108703	EST	
23	U59405	Hs 63263	EST Moderately similar to the ALU SURFAMILY 5X WARNING ENTRY, 1p (H sapiens)	
23	U59405	Hs 63532	Membrane cofactor protein (CD46) transmembrane alpha cross-reactive antigen	
23	U79100	Hs 63190	EST	
23	A11987	Hs 108678	EST	
23	F04320	Hs 325120	Replication factor C 3.7.10 subunit	
23	A059496	Hs 7301	Home sapiens voltage dependent anion channel protein mRNA, complete cds	
23	AB05313	Hs 74290	Home sapiens voltage dependent anion channel protein mRNA, complete cds	
23	U63037	Hs 63337		

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FIGURE 4 (CONT.)

41031	22	N91248	Hs.102897 ESTs	
24711	22	Z23645	Hs.21470 ESTs	
4733	22	U38538	Hs.15788 Human unknown protein mRNA within the p53 intron 1 complex cds	
29733	22	U92336	Hs.42860 ESTs	
34336	22	U92336	Hs.42860 ESTs	
1889	22	A4262892	Hs.104473 ESTs	
4135	22	L20591	Hs.1370 Adrenin II (epididym III)	
20276	22	U26014	Hs.71722 IC12 PROTEASE PRECURSOR	
18236	22	N32919	Hs.27931 ESTs	
13250	22	AA205352	Hs.41145 ESTs	
34370	21	AA231829	Hs.104038 ESTs Weakly similar to HYPOTHETICAL 27.4 KD PROTEIN IN MER-OR7 INTERGENIC REGION (Saccharomyces cerevisiae)	
18654	21	AA231829	Hs.104038 ESTs Weakly similar to dyx14 chain cyclase (R. norvegicus)	
34352	21	AA231829	Hs.104038 ESTs Weakly similar to dyx14 chain cyclase (R. norvegicus)	
37415	21	AA231829	Hs.104038 ESTs Weakly similar to dyx14 chain cyclase (R. norvegicus)	
14562	21	AA231829	Hs.104038 ESTs Weakly similar to dyx14 chain cyclase (R. norvegicus)	
5173	21	U81354	Hs.10060 ESTs Weakly similar to HYPOTHETICAL 39.6 KD PROTEIN IN MTD1 NUP133 INTERGENIC REGION (Saccharomyces cerevisiae)	
19772	21	Hs.3839	Hs.33376 ESTs	
23391	21	N52966	Hs.13034 ESTs	
40145	21	Hs.1391	Hs.81182 Human mRNA for histamine N-methyltransferase complex cds	
41893	21	U72501	Hs.51251 ESTs	
5807	21	AA231829	Hs.104038 ESTs Weakly similar to dyx14 chain cyclase (R. norvegicus)	
38155	21	AA231829	Hs.104038 ESTs Weakly similar to dyx14 chain cyclase (R. norvegicus)	
924	21	HG1112-HT1112	Hs.105590 EST - HG1112-HT1112	
8384	21	AA242422	Hs.91728 Human T5-O autoantigen (TM-SC1) mRNA complex cds	
22185	21	AA272737	Hs.30705 Refinex polymerase 3 (K-lined recessive)	
24348	21	U68469	Hs.77899 Tropomyosin alpha chain (skeletal muscle)	
35340	21	AA398920	EST - RC_AA398920	
10888	21	AA112023	Hs.15313 ESTs Weakly similar to PRE-MIRNA SPLICING HELICASE BHR2 (S. cerevisiae)	
381	21	D28473	Hs.10770 Isomerase RNA synthetase	
27051	21	AA231829	Hs.104038 ESTs Weakly similar to dyx14 chain cyclase (R. norvegicus)	
11829	21	AA231829	Hs.104038 ESTs Weakly similar to dyx14 chain cyclase (R. norvegicus)	
5448	21	AA231829	Hs.104038 ESTs Weakly similar to dyx14 chain cyclase (R. norvegicus)	
35956	21	AA125333	Hs.69855 Neuroblastoma RAS viral (v-ras) oncogene homolog	
7525	21	AA149258	Hs.69851 ESTs	
35532	21	F99351	Hs.18492 ESTs Weakly similar to weakly similar to S. cerevisiae PTM1 precursor (C. elegans)	
28229	21	AA178479	Hs.71992 ESTs	
18423	21	AA232103	Hs.59112 ESTs	
33366	21	U68914	Hs.47293 ESTs	
20590	21	Hs.146	Hs.34227 ESTs	
12907	21	AA272577	Hs.25502 ESTs	
22958	21	U10268	Hs.116122 ESTs	
14350	21	AA231829	Hs.104038 ESTs Weakly similar to dyx14 chain cyclase (R. norvegicus)	
24629	21	AA488831	Hs.17121 ESTs sapiens mRNA for Cdk7-related kinase complex cds	
26529	21	AA113149	Hs.81350 Homo sapiens (H. sapiens) mRNA complex cds	
6981	21	AA272594	Hs.30481 ESTs	
16878	21	Y03971	Hs.2910 Phosphatidylinositol 3-kinase (PI3K) mRNA complex cds	
38040	21	AA205338	Hs.63314 ESTs	
4111	21	U28312	Hs.63550 Human heterochromatin protein HP1-Hs-gamma mRNA complex cds	

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FIGURE 4 (CONT.)

[illegible]

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FIGURE 5

Primary Key	fold downregulated of Tumor vs	Accession	Unigene CLUSTER	Unigene Descriptor
2348	>10	M15656	Hs.75592	Aldolase B fructose-bisphosphate
5463	>10	X90908	Hs.74126	H.sapiens mRNA for L-15P (L-BABP) protein
42133	>10	T73335	Hs.93184	APOLIPOPROTEIN A-I PRECURSOR
4544	>10	U48959	Hs.75950	H.sapiens mRNA for myosin light chain kinase
1583	>10	K02765	Hs.59512	COMPLEMENT C3 PRECURSOR
2426	>10	M18828	Hs.585	Apolipoprotein B (including Ag(x) antigen)
8859	>10	AB002351	Hs.10587	Human mRNA for KIAA0353 gene partial cds
24572	>10	Z38688	Hs.24192	ESTs
17810	>10	AA151402	Hs.46531	ESTs
7006	>10	Z70295	Hs.32966	H.sapiens mRNA for GCAP-III/uroguanylin precursor
1304	>10	U64310	Hs.65424	EST - HG4310-HT4580
5980	>10	X64559	Hs.121713	Tetranectin (plasminogen-binding protein)
41987	>10	T47089	Hs.3907	Cytodrome P450 subfamily XXI (steroid 21-hydroxylase congenital adrenal hyperplasia)
24461	>10	W94427	Hs.89552	ESTs Weakly similar to SODIUMPOTASSIUM-TRANSPORTING ATPASE GAMMA CHAIN [Mus
2372	>10	M15594	Hs.89552	Glutathione S-transferase A2
6001	>10	X65727	Hs.89552	Glutathione S-transferase A2
1750	>10	L10955	Hs.89485	Carbonic anhydrase IV
12467	>10	U77643	Hs.95655	Human sapiens K12 protein precursor mRNA complete cds
41148	>10	AA402656	Hs.28284	ESTs
31652	>10	R06984	Hs.50404	EST - RC_R06984_3
4605	>10	U51010	Hs.50404	Human chemokine (TECK) mRNA complete cds
28359	>10	AA609133	Hs.58115	ESTs
24066	>10	W32506	Hs.111676	ESTs Weakly similar to HEAT SHOCK 27 KD PROTEIN [H.sapiens]
33282	>10	W73194	Hs.80552	ESTs
12084	>10	AA284767	Hs.21910	ESTs
41473	>10	R48732	Hs.11006	ESTs
27108	>10	AA404397	Hs.58414	ESTs Highly similar to ENDOTHELIAL ACTIN-BINDING PROTEIN [Homo sapiens]
2848	>10	M58286	Hs.159	TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR
19537	>10	H00270	Hs.32583	ESTs
18784	>10	F09748	Hs.7974	ESTs
5773	>10	X54162	Hs.79386	64 KD AUTOANTIGEN D1

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FIGURE 5 (CONT.)

27387	>10	AA426330	Hs.78264	ESTs	
2886	>10	N59815	Hs.76682	Complement component 4A	
42630	>10	W72859	Hs.74869	ESTs Weakly similar to SYNAPTOBREVIN 2 [H.sapiens]	
827	>10	D87433	Hs.84753	Human mRNA for KIAA0246 gene partial cds	
550	>10	O78014	Hs.74566	Human mRNA for dihydropyrimidinase related protein-3 complete cds	
7026	>10	Z80345	Hs.127610	Acyl-Coenzyme A dehydrogenase C-2 to C-3 short chain	
16736	>10	AA045306	Hs.42895	ESTs	
4630	>10	U52101	Hs.9689	Human YMP mRNA complete cds	
4655	>10	U52869	Hs.80296	BRAIN SPECIFIC POLYPEPTIDE PEP-19	
42758	>10	Z41411	Hs.107040	ESTs	
35537	>10	AA402533	Hs.29283	ESTs	
40392	>10	H95587	Hs.106890	ESTs	
7354	>10	AA092348	Hs.7858	ESTs	
8034	>10	C01833	Hs.29759	ESTs Weakly similar to IIII ALU SUBFAMILY SX WARNING ENTRY IIII [H.sapiens]	
10535	>10	AA121534	Hs.6923	ESTs Highly similar to TUBULIN BETA-5 CHAIN [Gallus gallus]	
5520	>10	X06256	Hs.119218	Integrin alpha 5 (fibronectin receptor alpha polypeptide)	
2547	>10	M25609	Hs.10059	ATPase H+ transporting lysosomal (vacuolar proton pump) beta polypeptide 55/58kD isoform 1	
9003	>10	C00608	Hs.107882	ESTs	
41628	>10	R70212	Hs.79530	Immunoglobulin-associated alpha	
21934	>10	R44449	Hs.48778	ESTs	
11129	6	AA156873	Hs.15970	ESTs	
40387	7	H69460	Hs.106873	ESTs	

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FIGURE 6

Primary Key	Fold downregulated of Tumor	Accession	Unigene CLUSTER	Unigene Descriptor
2348	>10	M15656	Hs.75592	Aldolase B fructose-bisphosphate
6463	>10	X90908	Hs.74128	H.sapiens mRNA for I-15P (I-BABP) protein
42139	>10	T73335	Hs.83194	APOLIPOPROTEIN A-I PRECURSOR
4544	>10	U48959	Hs.75950	H.sapiens mRNA for myosin light chain kinase
1583	>10	K02765	Hs.58512	COMPLEMENT C3 PRECURSOR
2428	>10	M19828	Hs.595	Apelipoprotein B (including Ag(x) antigen)
8859	>10	AB002351	Hs.10587	Human mRNA for KIAA0353 gene partial cds
24572	>10	Z38688	Hs.24192	ESTs
17810	>10	AA151402	Hs.46531	ESTs
7006	>10	Z70295	Hs.32956	H.sapiens mRNA for GCAP-III/inguanilin precursor
1304	>10	HG4310	Hs.65424	EST - HG4310-HT4580
5960	>10	X64559	Hs.121713	Tetradecan (plasminogen-binding protein)
41887	>10	T47089	Hs.3807	Cytochrome P450 subfamily XXI (steroid 21-hydroxylase congenital adrenal hyperplasia)
24451	>10	W94427	Hs.89552	ESTs Weakly similar to SODIUMPOTASSIUM-TRANSPORTING ATPASE GAMMA CHAIN [Mus musculus]
2372	>10	M16594	Hs.89552	Glutathione S-transferase A2
6001	>10	X65727	Hs.89485	Glutathione S-transferase IV
1750	>10	L10555	Hs.95655	Carbonic anhydrase IV
15130	>10	U77643	Hs.28264	Homo sapiens K12 protein precursor mRNA complete cds
12467	>10	AA402856	Hs.50404	ESTs
41148	>10	R06984	Hs.143289	EST - RC_R06984_s
31652	>10	N73958	Hs.50404	Human chemokine (TECK) mRNA complete cds
23483	>10	T68873	Hs.143289	H.sapiens mRNA for metallothionein isoform 1R
4605	>10	U51010	EST - U51010	EST - U51010
28359	>10	AA509133	Hs.58115	ESTs
24066	>10	W32506	Hs.111676	ESTs Weakly similar to HEAT SHOCK 27 KD PROTEIN [H. sapiens]
33282	>10	W73194	Hs.80552	ESTs
12084	>10	AA284767	Hs.21910	ESTs
41473	>10	R48732	Hs.11006	ESTs
32568	>10	T29248	Hs.143113	Human pancreatic lipase related protein 2 (PLRP2) mRNA complete cds
6413	>10	X87159	Hs.37129	Sodium channel nonvoltage-gated 1 beta (Liddle syndrome)
20707	>10	NG4436	Hs.20813	ESTs
27108	>10	AA043397	Hs.58414	ESTs Highly similar to ENDOTHELIAL ACTIN-BINDING PROTEIN [Homo sapiens]
12477	>10	AA403032	Hs.21701	ESTs
42059	>10	T61654	Hs.93194	APOLIPOPROTEIN A-I PRECURSOR
25468	>10	AA078072	Hs.1477	Insulin-like growth factor binding protein 6
26910	>10	AA303081	Hs.78293	ESTs

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FIGURE 6 (CONT.)

16938	>10	AA059473	Hs.56783	ESTs	
41789	>10	T03735	Hs.26885	ESTs	Human NF-IL6-beta protein mRNA complete cds
7754	>10	AA234634	Hs.76722	ESTs	Endoglin (Osler-Rendu-Weber syndrome 1)
8122	>10	X72012	Hs.75962	ESTs	TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR
2848	>10	M58286	Hs.150	ESTs	
23013	>10	T18661	Hs.6725	ESTs	
19537	>10	H30270	Hs.32583	ESTs	
4584	>10	U50350	EST - U50350	ESTs	
37410	>10	AA453652	Hs.59344	ESTs	
27969	>10	AA464594	Hs.63382	ESTs	
35497	>10	AA400606	Hs.144344	EST	
37013	>10	AA443690	Hs.136268	ESTs	ESTs Highly similar to ZINC FINGER PROTEIN HF-12 (Homo sapiens)
39247	>10	AA621553	Hs.112998	ESTs	
13471	>10	AA452598	Hs.109590	ESTs	
42110	>10	T88878	Hs.76588	ESTs	Carboxylesterase 2 (liver)
10965	>10	AA128997	Hs.18953	ESTs	Homo sapiens cGMP-specific phosphodiesterase (PDE9A2) mRNA complete cds
4918	>10	U67733	Hs.3831	ESTs	Human cGMP-stimulated 3',5'-cyclic nucleotide phosphodiesterase PDE2A3 (PDE2A) mRNA complete cds
40737	>10	N54950	Hs.61454	ESTs	H.sapiens KIK mRNA for katehexokinase clone pKHK2a
30403	>10	N45300	Hs.110647	ESTs	Meis1 (mouse) homolog
11432	>10	AA233389	Hs.361	ESTs	
18784	>10	F09748	Hs.7974	ESTs	
40662	>10	N49281	EST - RC_N49281	ESTs	
5773	>10	X54162	Hs.79386	ESTs	84 KD AUTOANTIGEN D1
35041	>10	AA350586	Hs.30862	ESTs	
20868	>10	N70068	Hs.7243	ESTs	
39729	>10	H11489	Hs.105805	ESTs	
27387	>10	AA426330	Hs.78264	ESTs	
39756	>10	I115814	Hs.80485	ESTs	Human apM1 mRNA for GS3109 (novel adipose specific collagen-like factor) complete cds
4319	>10	U37283	Hs.56882	ESTs	Human microfilament-associated glycoprotein-2 MAGP-2 mRNA complete cds
2866	>10	M59815	Hs.76582	ESTs	Complement component 4A
30332	>10	N59075	Hs.44934	EST	
41344	>10	R40189	Hs.6985	ESTs	
28271	>10	AA521200	Hs.48778	ESTs	
5834	>10	X57129	Hs.7644	ESTs	HISTONE H1D
19048	>10	H05464	Hs.100251	ESTs	
14729	>10	J02854	Hs.9515	ESTs	Human 20-kDa myosin light chain (MLC-2) mRNA complete cds
19401	>10	H27010	Hs.107384	ESTs	
29992	>10	N26386	Hs.33084	ESTs	Solute carrier family 2 (facilitated glucose transporter) member 5
2041	>10	L36033	Hs.77423	ESTs	Stromal cell-derived factor 1
22865	>10	R59909	Hs.36186	ESTs	

FIGURE 6 (CONT.)

11624	>10	AA243654	Hs.17998	ESTs	
12512	>10	AA405199	Hs.20733	ESTs	
41443	>10	R45577	Hs.10683	ESTs	
5055	>10	U77180	Hs.50002	Human mRNA for EBI1 ligand chemokine complete cds	
6038	>10	X08945	Hs.748	Basic fibroblast growth factor (bFGF) receptor (shorter form)	
42530	>10	W72959	Hs.74689	ESTs Weakly similar to SYNAPTOBREVIN 2 [H.sapiens]	
827	>10	D87433	Hs.84753	Human mRNA for KIAA0246 gene partial cds	
650	>10	D78014	Hs.74566	Human mRNA for dihydropyrimidinase related protein-3 complete cds	
37350	>10	AA452606	Hs.99289	EST	
37488	>10	AA455178	Hs.99397	ESTs	
36646	>10	AA431797	Hs.98783	EST	
38599	>10	AA609907	EST - RC_AA609907		
38191	>10	AA487895	Hs.17311	ESTs	
9844	>10	N57464	Hs.74670	Human mRNA for KIAA0146 gene partial cds	
8139	>10	AA341723	Hs.107374	ESTs	
41522	>10	R53966	Hs.75092	N-CHIMAERIN	
38090	>10	AA482603	Hs.111301	Mabk metalloproteinase 2 (gelatinase A 72kD gelatinase 72kD type IV collagenase)	
41175	>10	R09241	EST - RC_R09241		
36947	>10	AA437388	Hs.115726	ESTs	
4175	>10	U29953	Hs.76110	Pigment epithelium-derived factor	
35421	>10	AA399686	Hs.97669	EST	
4358	>10	U39467	Hs.250	Xanthine dehydrogenase	
35463	>10	AA400272	Hs.97758	EST	
7026	>10	Z80345	Hs.127610	Acyl-Coenzyme A dehydrogenase C-2 to C-3 short chain	
34625	>10	AA282238	Hs.118463	Homo sapiens clone 24519 unknown mRNA partial cds	
20179	>10	N24879	Hs.9693	ESTs	
36805	>10	AA435901	Hs.55874	ESTs Weakly similar to p20 protein [R.norvegicus]	
24447	>10	W83121	Hs.23841	Human mRNA for KIAA0355 gene complete cds	
10247	>10	R74386	Hs.108924	ESTs	
3618	>10	U02388	Hs.101	Leukotriene B4 omega hydroxylase (cytochrome P450 subfamily IVF)	
1464	>10	J03474	Hs.3157	SERUM AMYLOID A PROTEIN PRECURSOR	
16842	>10	AA055163	Hs.57975	Homo sapiens mRNA for cardiac caldesmon complete cds	
16735	>10	AA045308	Hs.42598	ESTs	
22865	>10	R85880	Hs.33455	ESTs	
5248	>10	U86358	Hs.50404	Human chemokine (TECK) mRNA complete cds	
7510	>10	AA136353	Hs.38022	ESTs	
34683	>10	AA264920	Hs.13716	ESTs	
19885	>10	H86980	Hs.12112	ESTs Moderately similar to protein phosphatase 1 binding protein PTG [M.musculus]	
9559	>10	N75215	Hs.43148	ESTs	
38135	>10	AA468185	Hs.125176	ESTs	

FIGURE 6 (CONT.)

36702	>10	AA434108	Hs.101393	ESTs Moderately similar to DNAJ PROTEIN HOMOLOG 1 [Homo sapiens]
3357	>10	M99487	Hs.1915	PROSTATE-SPECIFIC MEMBRANE ANTIGEN
36783	>10	AA435805	Hs.112065	EST
4876	>10	U60661	Hs.2048	Protease serine 2 (lypsin 2)
41149	>10	R06986	Hs.76487	ESTs
15925	>10	Y13492	Hs.78483	Homo sapiens mRNA for smoothelin
12944	>10	AA428258	Hs.8769	ESTs
9317	>10	D87468	Hs.40888	Human mRNA for KIAA0278 gene partial cds
19331	>10	H17885	Hs.23213	ESTs
5032	>10	U74382	Hs.90357	Homo sapiens telomeric repeat binding factor (TRF1) mRNA complete cds
34239	>10	AA235009	Hs.32246	ESTs
32852	>10	W31906	Hs.118428	ESTs
6432	>10	X69096	Hs.94413	Transient receptor potential channel 1
37001	>10	AA443311	Hs.96998	ESTs
4830	>10	U52101	Hs.9999	Human YMP mRNA complete cds
19489	>10	H27852	Hs.28137	ESTs
23028	>10	T17215	Hs.5952	ESTs
35359	>10	AA399061	Hs.112961	ESTs Moderately similar to PANCREATITIS-ASSOCIATED PROTEIN 1 PRECURSOR [H.sapiens]
4655	>10	U52969	Hs.80296	BRAIN SPECIFIC POLYPEPTIDE PEP-19
26030	>10	AA235884	Hs.87469	ESTs
41340	>10	R40395	Hs.112125	Lectin-like cholesterol acyltransferase
14494	>10	AA609645	Hs.25632	ESTs Weakly similar to PNG gene [H.sapiens]
4453	>10	U43916	Hs.79368	Human epithelial membrane protein (CL-20) mRNA complete cds
42758	>10	Z41411	Hs.107040	ESTs
35637	>10	AA402933	Hs.25283	ESTs
40382	>10	H99587	Hs.108880	ESTs
19360	>10	H19204	Hs.130468	ESTs
5184	>10	U82169	Hs.87234	Human frizzled homolog (FZD3) mRNA complete cds
850	>10	D87468	Hs.40888	Human mRNA for KIAA0278 gene partial cds
1555	>10	K03207	Hs.103972	Salivary proline-rich protein
15574	>10	W38778	Hs.28218	ESTs
8985	>10	C00125	Hs.24332	ESTs Weakly similar to deoxyribose-phosphate aldolase [C.elegans]
33965	>10	AA182845	Hs.139088	Homo sapiens FIP2 alternatively translated mRNA complete cds
7949	>10	AA283620	Hs.34956	ESTs
11870	>10	AA252191	Hs.25199	Homo sapiens PAC clone DJ130H16 from 22q12.1-qter
7354	>10	AA092348	Hs.7858	ESTs
38151	>10	AA419011	Hs.98744	ESTs
42136	>10	T72481	Hs.73849	Apolipoprotein C-III
289	>10	D16480	Hs.75860	Hydroxyacyl-Coenzym A dehydrogenase3-kelbacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein) alpha subunit
41379	>10	R42233	Hs.106487	Homo sapiens mRNA for KIAA0873 protein partial cds

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FIGURE 6 (CONT.)

34764	>10	AA287870	Hs.890	Lymphotoxin-beta
24515	>10	Z38289	Hs.12701	ESTs
18652	>10	F03111	Hs.22505	ESTs
37815	>10	AA469952	Hs.97899	ESTs
9034	>10	C01833	Hs.29759	ESTs Weakly similar to III ALU SUBFAMILY SX WARNING ENTRY III [H.sapiens]
34805	>10	AA291522	Hs.97250	EST
12248	>10	AA348198	Hs.14829	Homo sapiens mRNA for GABA-BR1a (GCB1a) receptor
42153	>10	T77729	Hs.89890	Pyruvate carboxylase
27110	>10	AA404494	Hs.84112	CTP synthetase
28831	>10	D59722	Hs.92824	ESTs
6333	>10	X82494	Hs.2653	Fibulin 2
10935	>10	AA121534	Hs.6923	ESTs Highly similar to TUBULIN BETA-5 CHAIN [Gallus gallus]
27257	>10	AA418001	Hs.46148	ESTs Weakly similar to mitogen-activated kinase kinase 5 [H.sapiens]
3631	>10	U03090	Hs.290	Homo sapiens Ca2+-dependent phospholipase A2 mRNA complete cds
4752	>10	U96322	Hs.3847	Glycoprotein Ib (platelet) beta polypeptide
3786	>10	U09579	Hs.74984	CYCLIN-DEPENDENT KINASE INHIBITOR 1
4310	>10	U37055	Hs.76034	Macrophage stimulating 1 (hepatocyte growth factor-like)
26923	>10	AA342302	Hs.55036	ESTs
5520	>10	X06256	Hs.119218	Integrin alpha 5 (fibronectin receptor alpha polypeptide)
16720	>10	AA044732	Hs.77208	ESTs
25336	>10	AA053405	Hs.101404	ESTs
2547	>10	M25809	Hs.1009	ATPase H+ transporting lysosomal (vacuolar proton pump) beta polypeptide 56/58KD isoform 1
9786	>10	M63509	Hs.73974	Glutathione S-transferase M2 (muscle)
5206	>10	U82979	Hs.67846	Human clone HM18 monocytic inhibitory receptor precursor mRNA complete cds
9377	>10	H12674	Hs.9396	ESTs
41960	>10	T33511	Hs.4844	ESTs
21911	>10	R43980	Hs.26320	ESTs
16225	>10	AA011305	Hs.10029	Calhepsin C
16071	>10	AA001426	Hs.40863	ESTs
29335	>10	H88239	Hs.39122	ESTs
34966	>10	AA344866	Hs.1285	Complement component 8 gamma polypeptide
21076	>10	N99976	Hs.8016	ESTs
4402	>10	U41518	Hs.74602	AQUAPORIN-CHIP
20423	>10	N49308	Hs.104938	ESTs
16575	>10	AA031948	Hs.57548	ESTs
28284	>10	AA521080	Hs.46765	ESTs
9003	>10	C00808	Hs.107882	ESTs
5632	>10	X15357	EST - X15357	
20852	>10	N69540	Hs.17713	ESTs
34585	>10	AA281002	Hs.40735	ESTs

FIGURE 6 (CONT.)

33690	>10	Z38607	Hs.62248	ESTs	Human GOS3 mRNA complete cds
8904	>10	AF002256	Hs.86180	ESTs	Human GOS3 mRNA complete cds
3307	>10	M85808	Hs.89578	ESTs	Human GOS3 mRNA complete cds
39200	>10	AA621246	Hs.112956	EST	Human GOS3 mRNA complete cds
24712	>10	Z39652	Hs.27457	ESTs	Human GOS3 mRNA complete cds
2199	>10	L49169	Hs.75678	ESTs	Human GOS3 mRNA complete cds
38942	>10	AA609546	Hs.94970	ESTs	Human GOS3 mRNA complete cds
41628	>10	R70212	Hs.79630	ESTs	Human GOS3 mRNA complete cds
6834	>10	Z18954	Hs.29960	ESTs	Human GOS3 mRNA complete cds
40562	>10	N33212	Hs.107197	ESTs	Human GOS3 mRNA complete cds
37333	>10	AA452156	Hs.75122	ESTs	Human GOS3 mRNA complete cds
3992	>10	U19713	Hs.76354	EST	Human GOS3 mRNA complete cds
38734	>10	AA608792	Hs.112591	EST	Human GOS3 mRNA complete cds
37836	>10	AA470135	Hs.112238	ESTs	Human GOS3 mRNA complete cds
10000	>10	N79874	Hs.7915	ESTs	Human GOS3 mRNA complete cds
30658	>10	N51105	Hs.111223	ESTs	Human GOS3 mRNA complete cds
17629	>10	AA431919	Hs.69009	ESTs	Human GOS3 mRNA complete cds
38260	>10	AA423970	Hs.96378	ESTs	Human GOS3 mRNA complete cds
24122	>10	W46947	Hs.41186	ESTs	Human GOS3 mRNA complete cds
1056	>10	HG2705-	Hs.41186	ESTs	Human GOS3 mRNA complete cds
12380	>10	AA398633	Hs.24872	ESTs	Human GOS3 mRNA complete cds
26025	>10	AA235874	Hs.86888	EST	Human GOS3 mRNA complete cds
41104	>10	R01398	Hs.73166	ESTs	Human GOS3 mRNA complete cds
33586	>10	W83015	Hs.111841	ESTs	Human GOS3 mRNA complete cds
26379	>10	AA058893	Hs.72447	ESTs	Human GOS3 mRNA complete cds
17607	>10	AA180530	Hs.95851	ESTs	Human GOS3 mRNA complete cds
36838	>10	AA436163	Hs.83468	ESTs	Human GOS3 mRNA complete cds
19524	>10	H29566	Hs.48778	ESTs	Human GOS3 mRNA complete cds
21934	>10	R44449	Hs.65264	ESTs	Human GOS3 mRNA complete cds
32456	>10	T15829	Hs.111552	ESTs	Human GOS3 mRNA complete cds
15440	>10	W27301	Hs.87428	ESTs	Human GOS3 mRNA complete cds
2807	>10	M55210	Hs.128630	ESTs	Human GOS3 mRNA complete cds
34193	>10	AA232251	Hs.128630	ESTs	Human GOS3 mRNA complete cds
14584	>10	AA621414	Hs.110903	EST	Human GOS3 mRNA complete cds
38752	>10	AA608852	Hs.112503	EST	Human GOS3 mRNA complete cds
5294	>10	U80085	Hs.79351	EST	Human GOS3 mRNA complete cds
84	>10	AF001359	Hs.82071	EST	Human GOS3 mRNA complete cds
4856	>10	U65093	Hs.21107	ESTs	Human GOS3 mRNA complete cds
13974	>10	AA479299	Hs.108508	ESTs	Human GOS3 mRNA complete cds
26151	>10	AA250836	Hs.108508	ESTs	Human GOS3 mRNA complete cds

FIGURE 6 (CONT.)

5938	>10	X62535	Hs.74044	Diacylglycerol kinase alpha (80KD)
17717	>10	AA138541	Hs.71647	EST
12404	>10	AA400292	Hs.23786	ESTs
2407	>10	M18737	Hs.90708	GRANZYME A PRECURSOR
26620	10	AA280413	Hs.89843	Spleen focus forming virus (SFFV) proviral integration oncogene sp1
37675	10	AA460377	Hs.99816	ESTs
41827	10	T15445	Hs.99491	H.sapiens mRNA for F25R3.3 kinase like protein from C.elegans
82	10	AF000959	Hs.110903	Homo sapiens transmembrane protein mRNA complete cds
203	10	D12820	Hs.106242	CYTCHROME P450 IVF3
24159	10	W57862	Hs.21289	ESTs
5302	10	U90543	Hs.75041	Human butyrophilin (BTFL1) mRNA complete cds
2219	10	L75670	Hs.105610	Homo sapiens rcal7 mRNA complete cds
24392	10	W88588	Hs.58569	Homo sapiens glycogenin-2 gamma (glycogenin-2) mRNA complete cds
36159	10	AA419279	Hs.82813	Colony-stimulating factor 1 (M-CSF)
28251	10	AA504512	Hs.76852	ESTs Weakly similar to ZK792.1 [C.elegans]
37592	10	AA458668	Hs.95898	ESTs
39519	9	F10640	Hs.12354	ESTs
8240	9	AA397841	Hs.108879	ESTs
10887	9	AA101632	Hs.22971	ESTs
37500	9	AA455474	Hs.100530	ESTs
42550	9	W92272	Hs.25601	Homo sapiens zinc-finger helixase (hZFh) mRNA complete cds
9011	9	C01394	Hs.108823	Homo sapiens clone 24818 mRNA sequence
3490	9	S77763	Hs.75643	Homo sapiens NF-E2 protein (NF-E2) mRNA complete cds
36691	9	AA432381	Hs.67357	ESTs Moderately similar to NITRIC OXIDE SYNTHASE INDUCIBLE [H.sapiens]
3478	9	S76992	Hs.104005	Vav 2 oncogene
42034	9	T56281	Hs.110440	Human metallothionein (MT)-I-F gene
11945	9	AA259064	Hs.10839	ESTs Weakly similar to unknown [S.cerevisiae]
19317	9	H17476	Hs.11615	ESTs Weakly similar to dual specificity phosphatase [H.sapiens]
42395	8	W42733	Hs.108670	ESTs
11425	8	AA233257	Hs.25511	Homo sapiens mRNA for Hic-5 partial cds
15310	8	W19098	Hs.7921	ESTs
36801	8	AA431337	Hs.98017	ESTs
13499	8	AA453458	Hs.7301	ESTs
37514	8	AA455914	Hs.1019	Parathyroid hormone receptor 1
5998	8	X65844	Hs.75083	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 ENHANCER-BINDING PROTEIN 2
33589	8	W93074	Hs.59342	ESTs
5801	8	X55448	Hs.3118	H.sapiens mRNA for 2.19 gene
11129	8	AA156873	Hs.15970	ESTs
31987	8	N94551	Hs.55060	ESTs
40438	8	N21684	Hs.80500	Human mRNA for KIAA0061 gene partial cds

FIGURE 6 (CONT.)

34471	8	AA258843	Hs.111376	ESTs	
25530	8	AA098834	Hs.83428	Nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105)	
39471	7	D60265	Hs.107894	ESTs	
25100	7	AA019428	Hs.103343	EST	
15915	7	Y08858	Hs.82577	Human DNA sequence from clone 323P24 on chromosome Xp11.21-11.23 Contains SPIN (spindlin homolog (PROTEIN DXF34) hypothetical protein E	
19097	7	H08171	Hs.30842	ESTs	
35353	7	AA398862	Hs.97699	ESTs	
36822	7	AA435978	Hs.98852	EST	
35530	7	AA400893	Hs.41717	Human 3'5' cyclic nucleotide phosphodiesterase (HSPDE1A3A) mRNA complete cds	
3869	7	U14417	Hs.106185	Human Rai guanine nucleotide dissociation stimulator mRNA partial cds	
1979	7	L29339	Hs.1064	Solute carrier family 5 (sodium/glucose cotransporter) member 1	
26178	7	AA251153	Hs.27910	Homo sapiens centromere Nek2-associated protein 1 (C-NAP1) mRNA complete cds	
36428	7	AA427605	Hs.98551	Human cardiac myosin binding protein-C (MyBP-C) gene complete cds	
26333	7	AA256075	Hs.82280	Homo sapiens regulator of G protein signaling 10 mRNA complete cds	
40387	7	H99460	Hs.108873	ESTs	
27236	7	AA417037	Hs.67805	ESTs	
20083	7	H98979	Hs.28029	ESTs Highly similar to EPIDERMAL GROWTH FACTOR PRECURSOR [Mus musculus]	
21561	7	R33245	Hs.23076	ESTs	
21223	7	R08175	Hs.110130	Homo sapiens chromosome 19 cosmid F22329	
13405	7	AA450118	Hs.25722	ESTs Weakly similar to KRUPPEL-RELATED ZINC FINGER PROTEIN 1 [Homo sapiens]	
34845	7	AA293420	Hs.95464	ESTs Moderately similar to transcription enhancer factor TEF1 [H.sapiens]	
15059	7	U53831	Hs.85280	Human interferon regulatory factor 7 (humirf7) mRNA complete cds	
1945	7	L25878	Hs.89849	Epoxide hydrolase 1 microsomal (xenobiotic)	
42848	7	W92150	Hs.79310	Human GAP SH3 binding protein mRNA complete cds	
20041	7	H97012	Hs.11050	ESTs Weakly similar to L8004.7 gene product [S.cerevisiae]	
7053	6	Z84721	Hs.75702	Hemoglobin alpha 1	
23843	6	T92561	Hs.110422	ESTs	
25815	6	AA149889	Hs.96200	ESTs Weakly similar to A-kinase anchor protein 95 AKAP95 [R.norvegicus]	
8473	6	AA437346	Hs.2967	SHB adaptor protein (a Src homology 2 protein)	
34618	6	AA282143	Hs.58094	H.sapiens mRNA for melanoma growth regulatory protein MIA	
11074	6	AA148983	Hs.29068	ESTs	
17533	6	AA127098	Hs.71057	EST	
28973	6	F04014	Hs.65596	ESTs	
17042	6	AA070397		EST - RC_AA070397	
15248	6	W01094	Hs.84628	ESTs	
2247	6	M10321	Hs.110802	VON WILLEBRAND FACTOR PRECURSOR	
30810	6	N53419	Hs.47646	ESTs	
13348	6	AA449267	Hs.17914	ESTs Weakly similar to HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR BETA-SUBUNIT [M.musculus]	
1789	6	L13258	Hs.936	Solute carrier family 17 (sodium phosphate) member 2	
16827	5	AA038779	Hs.61826	Homo sapiens clone 23928 mRNA sequence	

FIGURE 6 (CONT.)

27103	5	AA040282	Hs.63481	ESTs Weakly similar to kynurenine/alpha-aminoacidate aminotransferase [R.norvegicus]
12631	5	AA412293	Hs.21258	ESTs
11599	5	AA242829	Hs.7508	ESTs
9010	5	C01360	Hs.67384	Homo sapiens clone 23904 mRNA sequence
4660	5	U53225	Hs.75283	Scoring nexin 1
5244	5	U85992	Hs.87197	Human clone IMAGE:35527 unknown protein mRNA partial cds
7953	5	AA284403	Hs.74750	Homo sapiens mRNA for KIA00554 protein partial cds
27617	5	AA448114	Hs.55409	ESTs
39480	5	D60419	Hs.81915	STATMIN
37528	5	AA456112	Hs.99410	ESTs
11858	5	AA262308	Hs.106385	ESTs
37294	5	AA450127	Hs.110571	ESTs Highly similar to MYELOID DIFFERENTIATION PRIMARY RESPONSE PROTEIN MYD118 [Mus musculus]
23201	5	T40552	Hs.8278	ESTs
26767	5	D45608	Hs.83792	Surfactant pulmonary-associated protein D
3151	4	M83852	Hs.53155	Properdin P factor complement
29196	4	H24456	Hs.85053	Homo sapiens clone 24440 mRNA sequence
12863	4	AA425782	Hs.27973	ESTs
42486	4	W68410	Hs.106857	Calbindin 2 (28KD calretinin)
23571	4	T80628	Hs.108169	ESTs
27894	4	AA395271	Hs.19610	ESTs
28935	4	AA460319	Hs.48469	ESTs
4238	4	AFEX-		AFEX-HUMGAPDH33197_M
41844	4	U33053	Hs.2499	Human lipid-activated protein kinase PRK1 mRNA complete cds
20111	4	T15833	Hs.100227	EST
8316	4	N21380	Hs.25497	Hsapiens mRNA for ROX protein
39794	4	AA410529	Hs.30732	ESTs
1517	4	H21819	Hs.14896	Homo sapiens clone 24590 mRNA sequence
9164	4	J04501	Hs.772	Glycogen synthase 1 (muscle)
35027	4	D38081	Hs.89887	Thromboxane A2 receptor
14158	4	AA349986	Hs.99537	ESTs
41950	4	AA480182	Hs.118598	ESTs
34360	4	T33137	Hs.7967	ESTs
6547	4	AA251547	Hs.104358	EST
20863	4	X95508	Hs.9588	Human mRNA for KIA00385 gene complete cds
12734	4	N93089	Hs.19167	ESTs
39497	4	AA419200	Hs.5737	ESTs
1600	4	D80154	Hs.56340	ESTs
27148	4	K03474		EST - K03474
10763	4	AA406231	Hs.100113	Human mRNA for KIA00381 gene partial cds
	4	AA057620	Hs.30807	ESTs

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FIGURE 6 (CONT.)

17007	4	AA069696	Hs.67317	ESTs	
13522	4	AA454115	Hs.5000	ESTs	
18444	4	AA232646	Hs.58051	ESTs	
27665	3	AA447759	Hs.134724	ESTs	
21382	3	R16806	Hs.60615	PROTEIN KINASE C THETA TYPE	
2052	3	L36818	Hs.75339	Inositol polyphosphate phosphatase-like protein 1 (51C protein)	
9039	3	C02049	Hs.106291	ESTs	
34888	3	AA303078	Hs.94479	Human GT334 protein (GT334) gene mRNA complete cds	
11047	3	AA142848	Hs.22650	ESTs	
19451	3	H23747	Hs.31697	ESTs	
2822	3	M55621	Hs.117946	N-acetylglucosaminyltransferase I	
13928	3	AA479441	Hs.11590	ESTs	
12064	3	AA283948	Hs.11367	ESTs Weakly similar to KIAA0009 [H.sapiens]	
3836	3	U12707	Hs.2157	Wiskott-Aldrich syndrome (eczema-thrombocytopenia)	
4528	3	U48251	Hs.75871	Homo sapiens protein kinase C-binding protein RACK7 mRNA partial cds	
42064	3	T63364	Hs.9225	ESTs Highly similar to FIBRINOGEN-LIKE PROTEIN A PRECURSOR [Parastichopus parvimensis]	
4596	3	U50743	Hs.19520	Sodium/potassium ATPase gamma subunit	
4914	3	U67611	EST - U67611		
20168	3	N24106	Hs.2799	Cartilage linking protein 1	
24281	3	W79773	Hs.18511	ESTs	
19634	3	H44866	Hs.31597	ESTs	
10989	3	AA132356	Hs.8023	Homo sapiens mRNA for SPOP	
6587	3	X97748	EST - X97748		
14066	3	AA487558	Hs.8135	ESTs	
13350	3	AA448297	Hs.8944	ESTs Weakly similar to type 1 procollagen C-proteinase enhancer protein precursor [H.sapiens]	
33930	3	AA169539	Hs.95870	ESTs	
34215	3	AA233655	Hs.104252	UTROPHIN	
22509	3	R71393	Hs.29190	ESTs	
20065	3	H98857	Hs.27291	ESTs	
31091	3	N63078	Hs.138746	EST	
2493	3	M22919	Hs.77385	MYOSIN LIGHT CHAIN ALKALI SMOOTH-MUSCLE ISOFORM	
28913	3	F01560	Hs.22583	ESTs Highly similar to co-repressor protein [M.musculus]	
14323	3	AA598575	Hs.12851	ESTs	
34914	3	AA338729	Hs.133056	ESTs	
14236	3	AA496891	Hs.5011	ESTs Weakly similar to The ha1237 gene product is related to S.pombe rad21 gene product, [H.sapiens]	
24594	3	Z38804	Hs.22555	ESTs Highly similar to OP10D BINDING PROTEIN/CELL ADHESION MOLECULE PRECURSOR [Roa taurus]	
22589	3	R79580	Hs.29874	ESTs	
22156	3	R52145	Hs.25894	ESTs	
16404	3	AA021284	Hs.60354	ESTs Moderately similar to sodium-calcium exchanger form 3 [R.norvegicus]	
29310	3	H68842	Hs.88729	ESTs	

FIGURE 6 (CONT.)

8758	3	M26393	Hs.127810	Acyl-Coenzyme A dehydrogenase C-2 to C-3 short chain
9808	2	M79462	Hs.89033	Probable transcription factor PVL (alternative products)
19289	2	H16568	Hs.23748	ESTs
34031	2	AA192614	Hs.83577	Human LIM protein MLP mRNA complete cds
33299	2	W73700	Hs.73803	IMMUNOGLOBULIN-RELATED 14.1 PROTEIN PRECURSOR
3276	2	M93718	Hs.76983	Nitric oxide synthase 3 (endothelial cell)
31704	2	N75055	Hs.14532	ESTs
10310	2	R87373	Hs.75429	ESTs
22388	2	R63695	Hs.1432	Protein kinase C substrate 80K-H
20938	2	N73988	Hs.37477	ESTs Weakly similar to No definition line found [C.elegans]
5935	2	X62466	Hs.108338	CDW52 antigen (CAMPATH-1 antigen)
41485	2	R49889	Hs.5280	ESTs Weakly similar to C0608.3 [C.elegans]
25403	2	AA068316	EST - RC_AA068316	EST - RC_AA068316
27965	2	AA464267	Hs.24912	Homo sapiens bicucullat-D (BICO) mRNA complete cds
40632	2	N45221	EST - RC_N45221	EST - RC_N45221
15527	2	W28798	Hs.63260	Phosphodiesterase 6A cGMP-specific rod alpha
31672	2	N74335	Hs.91681	ESTs
964	2	HG1804	EST - HG1804-JHT1829	EST - HG1804-JHT1829
12439	2	AA401452	Hs.32060	ESTs
24223	2	W70158	Hs.29696	ESTs
21052	2	N93764	Hs.10175	ESTs Weakly similar to hypothetical protein [H.sapiens]
34140	2	AA215637	Hs.104186	ESTs
5130	2	U79288	Hs.85053	Homo sapiens clone 24440 mRNA sequence
30041	2	N27628	Hs.132744	Homo sapiens clone 24525 mRNA sequence
19202	2	H11509	Hs.22482	ESTs
41350	2	R40442	Hs.75852	Glutathione S-transferase M5
914	2	HG1019	EST - HG1019-HT1019	EST - HG1019-HT1019
31958	2	N93495	Hs.54960	ESTs
12014	2	AA281769	Hs.7214	Human HpaST (HPAST) mRNA complete cds
39777	2	H18412	Hs.75253	Human clone ID 193225 NAD (H)-specific isocitrate dehydrogenase gamma subunit mRNA alternatively spliced partial cds
19147	2	H09751	Hs.117619	ESTs
11199	2	AA176446	Hs.10024	ESTs
6477	2	X91504	Hs.64904	Transcription factor COUP 2 (a.k.a. ARP1)
16336	2	AA018601	Hs.75849	EXTRACELLULAR SIGNAL-REGULATED KINASE 3
24058	2	W23709	Hs.109047	ESTs
26180	2	AA251230	Hs.112272	ESTs
37177	2	AA447988	Hs.7765	ESTs
41984	2	T47601	Hs.138805	ESTs
36532	2	AA429889	Hs.68882	Acrosin
1450	2	J03071	Hs.115352	Growth hormone 1

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FIGURE 6 (CONT.)

24819	2	Z40923	Hs.24812	ESTs	
6532	2	X95325	Hs.89491	DNA-BINDING PROTEIN A	
27085	2	AA402495	Hs.77978	ESTs	
20487	2	N52322	Hs.19978	ESTs	
724	2	D83703	Hs.30729	Peroxisomal biogenesis factor 6	
4132	2	U27655	Hs.82284	Human RGP3 mRNA complete cds	
13375	2	AA449716	Hs.5723	ESTs	
13988	2	AA480045	Hs.7934	ESTs	
22306	2	R59906	Hs.100530	ESTs	
23167	2	T33164	Hs.12840	Homo sapiens germline mRNA sequence	
11320	2	AA213667	Hs.22222	ESTs	
24608	2	Z38888	Hs.25048	ESTs	
13163	2	AA437225	Hs.22410	ESTs	
1139	2	HG3227-	EST - HG3227-HT3404		
35572	2	AA401489	EST - RC_AA401489		
6964	2	Z49105	Hs.137591	H.sapiens HD21 mRNA	
30953	2	N59373	Hs.26812	ESTs	
16164	2	AA007509	Hs.75395	Human mRNA for TPRD complete cds	
2174	2	L42811	Hs.111758	KERATIN TYPE II CYTOSKELETAL 8D	
38958	2	AA609707	Hs.112751	ESTs	
37919	2	AA478162	Hs.104865	ESTs	
28905	2	D81123	Hs.57475	ESTs	
3745	2	U09117	Hs.80776	Human phospholipase c delta 1 mRNA complete cds	
19545	2	H37834	Hs.32699	ESTs	
8416	2	AA428531	EST - AA428531		
17569	2	AA128926	EST - RC_AA128926		
19354	2	H18829	Hs.121515	ESTs	
7598	2	AA174195	Hs.3354	Homo sapiens ezrin-radixin-moesin binding phosphoprotein-50 mRNA complete cds	
25385	2	AA059099	Hs.109727	ESTs	
14176	2	AA480620	Hs.11809	ESTs	
29487	2	H85120	Hs.80881	N-ACETYLACTOSAMINE SYNTHASE	
10197	2	R64199	Hs.50785	Homo sapiens vesicle trafficking protein sec22b mRNA complete cds	
19488	2	H27675	Hs.25804	ESTs	
10568	2	AA029703	Hs.38574	ESTs	
30799	2	N53143	Hs.64001	ESTs	
9638	2	L07592	Hs.106415	Human peroxisome proliferator activator receptor mRNA complete cds	
27195	2	AA411473	Hs.65311	ESTs	
17438	2	AA115508	Hs.2780	Jun D proto-oncogene	
24532	2	AFEX-	AFEX-HSAC07X00351.M		
10944	2	AA125868	Hs.34769	ESTs Weakly similar to F35G12.9 [C.elegans]	

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FIGURE 6 (CONT.)

42324	2	T98199	Hs.142702	ESTs	
34756	2	AA287665	Hs.8245	ESTs	
12743	2	AA421050	Hs.24545	ESTs	
13676	2	AA459389	Hs.26350	Homo sapiens mRNA for tyrosyl sulfotransferase-2	
13009	2	AA430474	Hs.16468	ESTs	
7403	2	AA094921	Hs.79788	ESTs	
35689	2	AA404707	Hs.54865	ESTs	
17701	2	AA135941	Hs.71626	ESTs	
18713	2	F04686	Hs.21782	ESTs	
8314	2	AA410355	Hs.103081	ESTs Highly similar to RIBOSOMAL PROTEIN S6 KINASE [Homo sapiens]	
7990	2	AA291788	Hs.32822	ESTs Weakly similar to HYPOTHETICAL PROTEIN KIAA0768 [H.sapiens]	
42791	2	AFX-		AFX-HUMGAPDHM33197_M	
6893	1	Z30543	Hs.123123	H.sapiens mRNA for chloride channel (putative) 2139bp	
35607	1	AA402287	Hs.133475	ESTs Weakly similar to zinc finger protein [H.sapiens]	
9468	1	H48074	Hs.31562	ESTs	
29469	1	H82929		EST - RC_H82929	
18692	1	F04444	Hs.8217	ESTs	
35205	1	AA398181	Hs.97602	ESTs	
22184	1	R53520	Hs.102755	ESTs	
28815	1	D59287	Hs.56782	ESTs	
17813	1	AA151480	Hs.91202	ESTs	
24655	1	Z39191	Hs.27282	ESTs Weakly similar to Lph17p [S.cerevisiae]	
15611	1	W51743	Hs.35096	ESTs	
15700	1	W73859	Hs.78061	Homo sapiens mesoderm-specific basic-helix-loop-helix protein (POD1) mRNA complete cds	
38770	1	AA435753		EST - RC_AA435753	
32400	1	R97178	Hs.110783	ESTs	
10802	1	AA069425	Hs.20573	ESTs	
17593	1	AA129858		EST - RC_AA129858	
20266	1	N32118	Hs.107305	ESTs Highly similar to THREONYL-TRNA SYNTHETASE CYTOPLASMIC [Homo sapiens]	
14447	1	AA608045	Hs.11759	ESTs	
12892	1	AA426521	Hs.18528	Homo sapiens mRNA for NA14 protein	
19738	1	H53059	Hs.15548	ESTs	
14471	1	AA609346	Hs.20102	ESTs	
5786	1	X55018	Hs.98975	Cholinergic receptor nicotinic delta polypeptide	
18441	1	AA232508	Hs.77480	ESTs	
10164	1	R54743	Hs.19400	ESTs Weakly similar to MITOTIC MAO2 PROTEIN [S.cerevisiae]	
8830	1	AB002319	Hs.8863	Human mRNA for KIAA0321 gene partial cds	
8682	1	AA477891	Hs.104476	ESTs	
35620	1	AA402493	Hs.10552	ESTs Highly similar to c-Jun leucine zipper interactive [M.musculus]	
35401	1	AA399593	Hs.97682	EST	

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FIGURE 6 (CONT.)

10801	1	AA112307	Hs.25224	ESTs	
18548	1	H37501	Hs.32705	ESTs	
30282	1	H39578	Hs.82364	ESTs	
39087	1	AA620907	Hs.111591	ESTs	
37896	1	AA477463	Hs.77039	Ribosomal protein S28	
41552	1	R59352	Hs.101253	Human mRNA for KIAA0296 gene complete cds	
11467	1	AA234089	Hs.14593	ESTs	
8215	1	AA389873	Hs.84344	ESTs Weakly similar to No definition line found [C.elegans]	
15505	1	W28366	Hs.7252	Homo sapiens clone 24800 mRNA sequence	
9834	1	M62259	Hs.22554	Homo sapiens clone 24800 mRNA sequence	
9159	1	D31483	Hs.90062	Homo sapiens clone 23565 unknown mRNA partial cds	
42218	1	T86444	Hs.110095	ESTs	
15526	1	W28790	Hs.8124	ESTs	
17780	1	AA150182	Hs.42262	ESTs Weakly similar to HYPOTHETICAL 88.1 KD PROTEIN K02D10.1 IN CHROMOSOME III [C.elegans]	
9777	1	M57888	Hs.95946	GRANZYME H PRECURSOR	
15373	1	W26376	Hs.74563	THY-1 MEMBRANE GLYCOPROTEIN PRECURSOR	
12076	1	AA284382	Hs.5448	ESTs Weakly similar to No definition line found [C.elegans]	
15391	1	W26651	Hs.15961	ESTs	
12905	1	AA427537	Hs.32419	ESTs	
39820	1	H24085	Hs.25443	ESTs	
13109	1	AA435638	Hs.7985	ESTs	
24249	1	W73069	Hs.12600	ESTs	
16514	1	AA027946	Hs.46608	ESTs	
16767	1	AA046650	Hs.40342	ESTs	
15331	1	W26498	Hs.107725	ESTs Weakly similar to LIS-1 protein [H.sapiens]	
11690	1	AA252762	Hs.31235	ESTs	
22999	1	T16510	Hs.6624	ESTs	
24480	1	Z38153	Hs.26921	ESTs	
24368	1	W87280	Hs.124800	ESTs	
22565	1	R77631	Hs.29126	ESTs	
15356	1	W26105	Hs.8981	ESTs	
22772	1	W61319	Hs.37482	ESTs Highly similar to COATOMER ZETA SUBUNIT [Bos taurus]	
16434	1	R58922	Hs.26590	ESTs	
22692	1	AA024484	Hs.81199	ESTs	
38830	1	R88711	Hs.34183	ESTs	
42547	1	AA609189	Hs.116415	ESTs	
34885	1	W73946	EST - RC_W73946		
18445	1	AA302831	Hs.57732	Homo sapiens p38beta2 MAP kinase mRNA complete cds	
18070	1	AA232848	Hs.87068	ESTs	
	1	AA180352	Hs.72733	ESTs	

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FIGURE 6 (CONT.)

23923 1 T98407 Hs.17812 ESTs

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FIGURE 7

Primary Key	fold downregulated of Tumor vs	Accession	Unigene CLUSTER	Unigene Descriptor
2348	>10	M15656	Hs.75592	Aldolase B fructose-bisphosphate
6463	>10	X90908	Hs.74126	Hs.splens mRNA for I-15P (I-BASP) protein
42139	>10	T73335	Hs.93194	APOLIPOPROTEIN A-I PRECURSOR
4544	>10	U48959	Hs.75950	Hs.splens mRNA for myosin light chain kinase
1583	>10	K02785	Hs.58512	COMPLEMENT C3 PRECURSOR
2426	>10	M18828	Hs.585	Apolipoprotein B (including Ag(x) antigen)
8659	>10	AB002351	Hs.10587	Human mRNA for KIAA0353 gene partial cds
24572	>10	Z36688	Hs.24192	ESTs
17810	>10	AA151402	Hs.46531	ESTs
7006	>10	Z70295	Hs.32968	Hs.splens mRNA for GCAP-II/uroguanylin precursor
1304	>10	HG4310-	EST - HG4310-HT4580	
5980	>10	X64559	Hs.65424	Tetranectin (plasminogen-binding protein)
41887	>10	T47089	Hs.121713	Cytochrome P450 subfamily XXI (steroid 21-hydroxylase congenital adrenal hyperplasia)
24461	>10	W94427	Hs.3807	ESTs Weakly similar to SODIUM/POTASSIUM-TRANSPORTING ATPASE GAMMA CHAIN [Mus musculus]
2372	>10	M16584	Hs.89552	Glutathione S-transferase A2
6001	>10	X65727	Hs.89552	Glutathione S-transferase A2
1750	>10	L10955	Hs.89485	Carbonic anhydrase IV
15130	>10	U77643	Hs.85655	Homo sapiens K12 protein precursor mRNA complete cds
12467	>10	AA026556	Hs.26264	ESTs
41148	>10	R06984	EST - RC_R06984_3	
31652	>10	N73958	Hs.50404	Human chemokine (TECK) mRNA complete cds
23483	>10	T68873	Hs.143289	Hs.splens mRNA for metallothionein isoform 1R
4605	>10	U51010	EST - U51010	
28359	>10	AA608133	Hs.58115	ESTs
24066	>10	W32506	Hs.111676	ESTs Weakly similar to HEAT SHOCK 27 KD PROTEIN [H.sapiens]
33282	>10	W73194	Hs.80552	ESTs
12084	>10	AA284767	Hs.21910	ESTs
41473	>10	R48732	Hs.11006	ESTs
32568	>10	T29248	Hs.143113	Human pancreatic lipase related protein 2 (PLRP2) mRNA complete cds
6413	>10	X87159	Hs.37129	Sodium channel nonvoltage-gated 1 beta (Liddle syndrome)
20707	>10	N84436	Hs.20813	ESTs
27108	>10	AA04397	Hs.58414	ESTs Highly similar to ENDOTHELIAL ACTIN-BINDING PROTEIN [Homo sapiens]
12477	>10	AA03032	Hs.21701	ESTs
42059	>10	T61654	Hs.03104	APOLIPOPROTEIN A-I PRECURSOR
25488	>10	AA079072	Hs.1477	Insulin-like growth factor binding protein 6
26910	>10	AA303081	Hs.78293	ESTs

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FIGURE 7 (CONT.)

16938	>10	AA058473	Hs.68783	ESTs	
41788	>10	T03735	Hs.25885	ESTs	
7754	>10	AA234634	Hs.76722	Human NF-IL6-beta protein mRNA complete cds	
6122	>10	X72012	Hs.75962	Endoglin (Osler-Rendu-Weber syndrome 1)	
2048	>10	M58286	Hs.159	TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR	
23013	>10	T16661	Hs.6725	ESTs	
19537	>10	H30270	Hs.32583	ESTs	
4584	>10	U50360	EST - U50360		
37410	>10	AA453652	Hs.93344	ESTs	
27669	>10	AA464594	Hs.63382	ESTs	
35497	>10	AA400608	Hs.144344	EST	
37013	>10	AA443690	Hs.138268	ESTs Highly similar to ZINC FINGER PROTEIN HF.12 [Homo sapiens]	
39247	>10	AA621553	Hs.112998	ESTs	
13471	>10	AA452598	Hs.105990	ESTs	
42110	>10	T68878	Hs.76688	Carboxylesterase 2 (liver)	
10955	>10	AA128997	Hs.18953	Homo sapiens cGMP-specific phosphodiesterase (PDE9A2) mRNA complete cds	
4918	>10	U67733	Hs.3831	Human cGMP-stimulated 3',5'-cyclic nucleotide phosphodiesterase PDE2A3 (PDE2A) mRNA complete cds	
40737	>10	N54950	Hs.81454	H. sapiens KHK mRNA for ketohexokinase clone pl KHK3a	
30403	>10	N45300	Hs.110647	Meis1 (mouse) homolog	
11432	>10	AA233369	Hs.361	ESTs	
18784	>10	F03748	Hs.7974	ESTs	
40662	>10	N49281	EST - RC_N49281		
35041	>10	X54162	Hs.79396	64 KD AUTOANTIGEN D1	
20868	>10	AA350586	Hs.30862	ESTs	
39729	>10	N70068	Hs.7243	ESTs	
27387	>10	H11489	Hs.105805	ESTs	
39758	>10	AA426330	Hs.78284	ESTs	
4319	>10	H15814	Hs.80485	Human apM1 mRNA for GS3109 (novel adipose specific collagen-like factor) complete cds	
2866	>10	U37283	Hs.58882	Human microfibril-associated glycoprotein-2 MAGP-2 mRNA complete cds	
30332	>10	M59815	Hs.76682	Complement component 4A	
41344	>10	N39075	Hs.44934	EST	
28271	>10	R40189	Hs.5985	ESTs	
5034	>10	AA521200	Hs.48778	ESTs	
10048	>10	X57129	Hs.7644	HISTONE H1D	
1429	>10	H05464	Hs.100251	ESTs	
19491	>10	J02854	Hs.9515	Human 20-kDa myosin light chain (MLC-2) mRNA complete cds	
29992	>10	H27910	Hs.107384	ESTs	
2041	>10	N26386	Hs.33084	Solute carrier family 2 (facilitated glucose transporter) member 5	
27865	>10	L36033	Hs.77423	Stromal cell-derived factor 1	
	>10	R09809	Hs.36186	ESTs	

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FIGURE 7 (CONT.)

11624	>10	AA243654	Hs.17898	ESTs
12512	>10	AA405199	Hs.20733	ESTs
41443	>10	R45577	Hs.10583	ESTs
5055	>10	U77180	Hs.50002	Human mRNA for EB11-ligand chemokine complete cds
6038	>10	X68945	Hs.748	Basic fibroblast growth factor (bFGF) receptor (shorter form)
42530	>10	W72859	Hs.74669	ESTs Weakly similar to SYNAPTOBREVIN 2 [H.sapiens]
827	>10	D87433	Hs.84753	Human mRNA for KIAA0246 gene partial cds
650	>10	D78014	Hs.74566	Human mRNA for dihydropyrimidinase related protein-3 complete cds
37350	>10	AA452606	Hs.99289	EST
37488	>10	AA455178	Hs.99397	ESTs
38646	>10	AA431797	Hs.98763	EST
38996	>10	AA609907		EST - RC_AA609907
38191	>10	AA487895	Hs.17311	ESTs
9944	>10	N57464	Hs.74670	Human mRNA for KIAA0148 gene partial cds
8138	>10	AA341723	Hs.107374	ESTs
41522	>10	R53966	Hs.75092	N-CHIMAERIN
38090	>10	AA482603	Hs.111301	Matrix metalloproteinase 2 (gelatinase A 72kD gelatinase 72kD type IV collagenase)
41175	>10	R09241		EST - RC_R09241
36947	>10	AA437388	Hs.115728	ESTs
4175	>10	U29953	Hs.76110	Pigment epithelium-derived factor
35421	>10	AA389686	Hs.97659	EST
4358	>10	U39487	Hs.250	Xanthine dehydrogenase
35463	>10	AA400272	Hs.97758	EST
7028	>10	Z80345	Hs.127610	Acyl-Coenzyme A dehydrogenase C-2 to C-3 short chain
34625	>10	AA282236	Hs.118483	Homo sapiens clone 24518 unknown mRNA partial cds
20179	>10	N24879	Hs.9683	ESTs
36805	>10	AA435901	Hs.56874	ESTs Weakly similar to p20 protein [R.norvegicus]
24447	>10	W93121	Hs.23841	Human mRNA for KIAA0355 gene complete cds
10247	>10	R74386	Hs.108924	ESTs
3618	>10	U02388	Hs.101	Leukotriene B4 omega hydroxylase (cytochrome P450 subfamily IVF)
18730	>10	F08876	Hs.8008	ESTs
22529	>10	R73075	Hs.28327	EST
37520	>10	AA455960	Hs.99405	ESTs
41122	>10	R05483	Hs.138500	ESTs
4417	>10	U42031	Hs.7557	Human 54 kDa progesterone receptor-associated immunophilin FKBP54 mRNA partial cds
9742	>10	M14777	Hs.89552	Glutathione S-transferase A2
36194	>10	AA421142	Hs.104672	ESTs
4445	>10	U43653	Hs.3261	Leptin (murine obesity homolog)
19749	>10	H53728	Hs.36608	ESTs
19763	>10	H56965	Hs.34564	ESTs

FIGURE 7 (CONT.)

12713	>10	AA418398	Hs.17778	ESTs	SERUM AMYLOID A PROTEIN PRECURSOR
1464	>10	J03474	Hs.3157	ESTs	Homo sapiens mRNA for cardiac caldesmon complete cds
16842	>10	AA055163	Hs.57875	ESTs	
34229	>10	AA234383	Hs.3578	ESTs	
35563	>10	AA401404	Hs.112087	ESTs	
16736	>10	AA045306	Hs.42996	ESTs	
33607	>10	W93487	Hs.59488	ESTs	
16146	>10	AA005236	Hs.60162	ESTs	
22668	>10	R85890	Hs.33455	ESTs	
22562	>10	R77493	Hs.28653	EST	
22985	>10	T16211	Hs.6326	EST	Homo sapiens clone 23789 and 23825 mRNA sequence
5248	>10	U86358	Hs.50404	ESTs	Human clemokine (TECK) mRNA complete cds
27608	>10	AA443800	Hs.43125	ESTs	
7510	>10	AA135353	Hs.38022	ESTs	
34683	>10	AA284920	Hs.13718	ESTs	
27633	>10	AA446659	Hs.2563	ESTs	Tachykinin 2 (substance K neurokinin A neurokinin 2 neurokinin L neurokinin alpha neuropeptide K neuropeptide gamma)
32485	>10	T16335	Hs.65325	EST	
30791	>10	AA609018	Hs.112629	ESTs	
32020	>10	N95796	Hs.55181	ESTs	
18686	>10	H89980	Hs.12112	ESTs	Moderately similar to protein phosphatase 1 binding protein PTC [M.musculus]
30748	>10	N52254	Hs.47438	ESTs	
8903	>10	AF002246	Hs.21226	ESTs	Homo sapiens neural cell adhesion molecule (CALL) mRNA complete cds
9959	>10	N75215	Hs.43148	ESTs	
38138	>10	AA486185	Hs.125176	ESTs	
19845	>10	H59887	Hs.35187	ESTs	
1127	>10	HG3117-	HG3117-HT3293	EST	
23837	>10	T85315	Hs.15903	ESTs	
16599	>10	AA043349	Hs.62630	ESTs	
36702	>10	AA434108	Hs.101393	ESTs	Moderately similar to DNAJ PROTEIN HOMOLOG 1 [Homo sapiens]
28930	>10	F02702	Hs.141503	ESTs	Small inducible cytokine A5 (RANTES)
9228	>10	D62584	Hs.109439	ESTs	Highly similar to OSTEOINDUCTIVE FACTOR PRECURSOR [Des launus]
3357	>10	M99487	Hs.1915	ESTs	PROSTATE-SPECIFIC MEMBRANE ANTIGEN
36783	>10	AA435805	Hs.112065	EST	
4876	>10	U66081	Hs.2048	ESTs	Protease serpin 2 (trypsin 2)
41149	>10	R06986	Hs.78487	ESTs	
22200	>10	R54179	Hs.26100	ESTs	
15925	>10	Y13492	Hs.78483	ESTs	Homo sapiens mRNA for smoothelin
10911	>10	AA113387	Hs.24305	ESTs	
3336	>10	M97675	Hs.1944	ESTs	Human protein tyrosine kinase L-Ror1 (Ror1) mRNA complete cds
31889	>10	N91897	Hs.50652	ESTs	

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FIGURE 7 (CONT.)

10406	>10	AA007629	Hs.25478	ESTs	Integrin beta 2 (antigen CD18 (p85) lymphocyte function-associated antigen 1 macrophage antigen 1 (mac-1) beta subunit)
17737	>10	AA142875	Hs.71719	ESTs	
38939	>10	AA609632	Hs.112737	EST	
16206	>10	AA010611	Hs.80418	EST	
32810	>10	W15376	Hs.122656	ESTs	
18210	>10	AA196306	Hs.86045	ESTs	
24054	>10	W15580	Hs.15342	ESTs	
23047	>10	T23457	Hs.7120	ESTs	
12944	>10	AA428258	Hs.8769	ESTs	
34172	>10	AA227469	Hs.139171	EST	Human mRNA for KIAA0278 gene partial cds
9317	>10	D87488	Hs.40888	ESTs	
19331	>10	H17865	Hs.23213	ESTs	
21035	>10	N92824	Hs.14898	ESTs	
34208	>10	AA233380	Hs.104249	EST	
5974	>10	X64072	Hs.83968	ESTs	
5032	>10	U74382	Hs.90357	ESTs	
41941	>10	T32561	Hs.5476	ESTs	
34239	>10	AA235009	Hs.32246	ESTs	
32852	>10	W31906	Hs.116428	ESTs	
7662	>10	AA203527	Hs.18747	ESTs	Homo sapiens ribonuclease P protein subunit p20 (RPP20) mRNA complete cds
6432	>10	X89066	Hs.94413	ESTs	
37001	>10	AA443311	Hs.98998	ESTs	Transient receptor potential channel 1
4630	>10	U52101	Hs.9899	ESTs	Human YMP mRNA complete cds
19489	>10	H27852	Hs.28137	ESTs	
28483	>10	C14270	Hs.66357	ESTs	
19801	>10	H57357	Hs.18767	ESTs	Weakly similar to unknown protein [H.sapiens]
24672	>10	Z39300	Hs.124952	ESTs	
31153	>10	N63989	EST	EST - RC_N63988	
40250	>10	H82451	Hs.110	ESTs	Solute carrier family 3 (cystine dibasic and neutral amino acid transporters activator of cystine dibasic and neutral amino acid transport) member 1
23028	>10	T17215	Hs.6952	ESTs	
28072	>10	AA480886	Hs.55693	ESTs	
11868	>10	AA262556	Hs.28802	ESTs	Weakly similar to centaurin alpha [R.norvegicus]
35359	>10	AA399061	Hs.112961	ESTs	Moderately similar to PANCREATITIS-ASSOCIATED PROTEIN 1 PRECURSOR [H.sapiens]
4285	>10	I155130	Hs.50130	ESTs	Human NECDIN related protein mRNA complete cds
4655	>10	U52989	Hs.80296	ESTs	BRAIN SPECIFIC POLYPEPTIDE PEP-19
26030	>10	AA235984	Hs.87469	ESTs	
2042	>10	L36051	Hs.1168	ESTs	Thrombopoietin (myeloproliferative leukemia virus oncogene ligand megakaryocyte growth and development factor)
25282	>10	AA045501	Hs.30250	ESTs	Homo sapiens short form transcription factor C-MAF (c-maf) mRNA complete cds
34821	>10	AA291983	Hs.144599	ESTs	
42405	>10	W44652	Hs.109888	ESTs	

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FIGURE 7 (CONT.)

41348	>10	R40395	Hs.112125	Lectin-cholesterol acyltransferase
14494	>10	AA609645	Hs.25632	ESTs Weakly similar to PNG gene [H.sapiens]
4453	>10	U43916	Hs.79368	Human epithelial membrane protein (CL-20) mRNA complete cds
42758	>10	Z41411	ESTs	
2098	>10	L39009	EST - L39009	
35637	>10	AA402933	Hs.29283	ESTs
16549	>10	AA029697	Hs.94854	ESTs
1220	>10	HG3733-	EST - HG3733-HT4003	
39534	>10	H52185	Hs.124994	ESTs
7735	>10	AA232121	Hs.109631	Human tyrosyl-IRNA synthetase mRNA complete cds
40392	>10	H98587	Hs.108980	ESTs
37170	>10	AA447779	Hs.99145	EST
18361	>10	AA223502	Hs.86899	ESTs
19366	>10	H19204	Hs.133466	ESTs
38429	>10	AA498965	Hs.108694	Glycophorin A
38021	>10	AA481059	Hs.105152	ESTs
5184	>10	U92109	Hs.87234	Human frizzled homolog (FZD3) mRNA complete cds
27863	>10	AA458923	Hs.70202	ESTs Weakly similar to F23B2.4 [C.elegans]
37476	>10	AA455051	Hs.99386	EST
859	>10	D87468	Hs.40888	Human mRNA for KIAA0278 gene partial cds
27185	>10	AA410895	Hs.62348	ESTs
41010	>10	N80686	Hs.21639	Human APEG-1 mRNA complete cds
38241	>10	AA488076	Hs.105101	ESTs
22701	>10	R89477	Hs.34299	ESTs
12152	>10	AA291271	Hs.10896	ESTs Weakly similar to uroporphyrinogen III synthase UROIII [H.sapiens]
36913	>10	AA609531	Hs.112050	ESTs
34034	>10	AA192871	Hs.83760	Troponin I (skeletal fast)
37644	>10	AA459857	Hs.89503	EST
4173	>10	U29725	Hs.3080	Human BMK1 alpha kinase mRNA complete cds
16178	>10	AA008839	Hs.1632	CD27L RECEPTOR PRECURSOR
20527	>10	N54161	Hs.124044	ESTs
41918	>10	T25873	Hs.102243	ESTs
1525	>10	J04621	Hs.1501	Syndecan 2 (heparan sulfate proteoglycan 1 cell surface-associated fibroglycan)
19160	>10	H10208	Hs.30972	EST
18860	>10	AA059633	Hs.58152	ESTs Weakly similar to Natsu [M.musculus]
36927	>10	AA437259	Hs.104944	EST
1595	>10	K03207	Hs.103972	Salivary proline-rich protein
15574	>10	W38778	Hs.26216	ESTs
8985	>10	C00125	Hs.24332	ESTs Weakly similar to similar to deoxyribose-phosphate aldolase [C.elegans]
33995	>10	AA182845	Hs.139088	Homo sapiens FIP2 alternatively translated mRNA complete cds

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FIGURE 7 (CONT.)

7949	>10	AA283620	Hs.34956	ESTs	
16607	>10	AA034918	Hs.85079	ESTs	
11670	>10	AA252191	Hs.25199	Homo sapiens PAC clone DU130H16 from 22q12.1-qter	
7354	>10	AA092348	Hs.7858	ESTs	
4277	>10	U34879	Hs.85279	ESTRADIOL 17 BETA-DEHYDROGENASE 1	
23214	>10	T40855	Hs.11807	Human protein tyrosine phosphatase PTPCAAX1 (pTTPCAAX1) mRNA complete cds	
22209	>10	R54594	Hs.25209	ESTs	
38151	>10	AA419011	Hs.96744	ESTs	
23372	>10	T59537	EST - RC_T59537		
42136	>10	T72491	Hs.73849	Apolipoprotein C-III	
289	>10	D16480	Hs.75860	Hydroxyacyl-Coenzyme A dehydrogenase/3-ketacyl-Coenzyme A thiolase/Coenzyme A hydratase (thiolase subunit)	
15974	>10	Z36531	Hs.2659	H.sapiens mRNA for fibrinogen-like protein (pT49 protein)	
41379	>10	R42233	Hs.105487	Homo sapiens mRNA for KIAA0873 protein partial cds	
34764	>10	AA287870	Hs.590	Lymphotxin-beta	
24027	>10	W01875	Hs.5734	Homo sapiens mRNA for KIAA0879 protein partial cds	
36197	>10	AA421158	Hs.97514	ESTs	
37211	>10	AA448334	EST - RC_AA448334		
27684	>10	AA448625	Hs.57929	ESTs	
31790	>10	N80278	Hs.50891	ESTs	
24515	>10	Z36289	Hs.12701	ESTs	
18652	>10	F03111	Hs.22505	ESTs	
16535	>10	AA037433	Hs.46887	ESTs	
37815	>10	AA469952	Hs.97899	ESTs	
6364	>10	X63957	Hs.495	Prostaglandin E receptor 3 (subtype EP3) (alternative products)	
9034	>10	C01833	Hs.29759	ESTs Weakly similar to III ALU SUBFAMILY SX WARNING ENTRY IIII [H.sapiens]	
16489	>10	AA025728	Hs.61307	ESTs	
27034	>10	AA400102	Hs.49051	ESTs	
42746	>10	Z40546	Hs.124953	ESTs	
35368	>10	AA399269	Hs.15250	Homo sapiens DBI-related protein mRNA complete cds	
34805	>10	AA291522	Hs.97250	EST	
19983	>10	H89355	Hs.6598	ESTs	
31126	>10	N63444	Hs.47568	ESTs	
22516	>10	R81940	Hs.124964	ESTs	
12246	>10	AA348198	Hs.14829	Homo sapiens mRNA for GABA-BR1a (GGB1a) receptor	
8777	>10	AA495865	Hs.7874	ESTs	
13488	>10	AA453034	Hs.21041	ESTs Highly similar to FIBROPELIN C PRECURSOR (Strongylocentrotus purpuratus)	
25572	>10	AA085721	Hs.95511	ESTs	
29073	>10	F12567	EST - RC_F12567		
5541	>10	X017203	Hs.89751	CD20 RECEPTOR	
41688	>10	R82942	Hs.107755	ESTs Weakly similar to GLYCEROPHOSPHORYL DIESTER PHOSPHODIESTERASE [E.coli]	

FIGURE 7 (CONT.)

32343	>10	R09665	Hs.125052	ESTs	
36335	>10	AA490916	Hs.112157	ESTs	
41729	>10	R02458	Hs.89554	Hemoglobin gamma-G	
36707	>10	AA434246	Hs.98802	EST	
28491	>10	C14784	Hs.12382	ESTs	
41702	>10	R06970	Hs.123363	ESTs	
32246	>10	R52163	Hs.144526	ESTs	
17314	>10	AA096487	Hs.107365	ESTs Highly similar to THREONYL-TRNA SYNTHETASE CYTOPLASMIC [Homo sapiens]	
30325	>10	N38967	Hs.44504	EST	
19823	>10	H58692	Hs.9520	ESTs Highly similar to FORMYL-TETRAHYDROFOLATE DEHYDROGENASE [Rattus norvegicus]	
42153	>10	T77729	Hs.89890	Pyruvate carboxylase	
19321	>10	H17511	Hs.24963	ESTs	
27110	>10	AA040494	Hs.84112	GTP synthetase	
26931	>10	D59722	Hs.92924	ESTs	
6333	>10	X82404	Hs.2653	Fibulin 2	
37679	>10	AA460661	Hs.99562	ESTs	
40828	>10	N64344	Hs.78362	Human clone 23839 mRNA sequence	
19132	>10	H09343	Hs.27261	ESTs	
19353	>10	H18706	Hs.31604	ESTs	
10935	>10	AA121534	Hs.6923	ESTs Highly similar to TUBULIN BETA-5 CHAIN [Gallus gallus]	
11621	>10	AA243574	Hs.14691	ESTs	
36538	>10	AA521370	Hs.104423	ESTs	
10095	>10	R22139	Hs.30343	ESTs	
30014	>10	N26740	Hs.42771	ESTs	
4464	>10	U44429	Hs.16511	Human D53 (hD53) mRNA partial cds	
3650	>10	U03877	Hs.78224	Human extracellular protein (S1-5) mRNA complete cds	
36377	>10	AA426056	Hs.99450	ESTs	
20437	>10	N50550	Hs.24587	Homo sapiens mRNA for E1a1 complete cds	
1576	>10	K02100	Hs.117050	ORNITHINE CARBAMOYLTRANSFERASE PRECURSOR	
42078	>10	T64891	Hs.144323	ESTs	
27257	>10	AA418001	Hs.45146	ESTs Weakly similar to mitogen-activated kinase kinase kinase 5 [H.sapiens]	
30592	>10	N49848	Hs.46974	EST	
3631	>10	U03090	Hs.290	Homo sapiens Ca2+-dependent phospholipase A2 mRNA complete cds	
19026	>10	H04768	Hs.30484	ESTs	
4752	>10	U59632	Hs.3947	Glycoprotein Ib (platelet) beta polypeptide	
3769	>10	U09579	Hs.74884	CYCLIN-DEPENDENT KINASE INHIBITOR 1	
1437	>10	J02923	Hs.76506	Lymphocyte cytosolic protein 1 (L-plasin)	
33905	>10	AFFX-		AFFX-TrpX-5	
4310	>10	U37055	Hs.76034	Macrophage stimulating 1 (hepatocyte growth factor-like)	
26923	>10	AA342302	Hs.55036	ESTs	

FIGURE 7 (CONT.)

5520	>10	X06258	Hs.119218	Integrin alpha 5 (fibronectin receptor alpha polypeptide)
37571	>10	AA457409	Hs.93458	EST
38800	>10	AA609052	Hs.112636	EST
27952	>10	AA463700	Hs.47042	Homo sapiens CD39L3 (CD39L3) mRNA complete cds
27621	>10	AA446242	Hs.55589	ESTs
38784	>10	AA609968	Hs.2051	Testis specific protein Y-linked
281	>10	D16532	Hs.73729	Very low density lipoprotein receptor
18014	>10	AA173168	Hs.57672	ESTs Weakly similar to myosin heavy chain [C.elegans]
16720	>10	AA044732	Hs.77208	ESTs
25336	>10	AA053405	Hs.101404	ESTs
2547	>10	M25809	Hs.1009	ATPase H+ transposing lysosomal (vacuolar proton pump) beta polypeptide 58/58kD isoform 1
39953	>10	H56010	Hs.108144	ESTs Weakly similar to III ALU SUBFAMILY J WARNING ENTRY III [H.sapiens]
13777	>10	AA463504	Hs.6052	ESTs
13419	>10	AA450336	Hs.22268	ESTs
1403	>10	J00123	Hs.93557	PROENKEPHALIN A PRECURSOR
42373	>10	W35352	Hs.103012	ESTs
21520	>10	R28267	Hs.24258	ESTs
9706	>10	M63509	Hs.73974	Glutathione S-transferase M2 (muscle)
35950	>10	AA404271	Hs.22631	Human glutamate receptor (GLUR5) mRNA complete cds
42501	>10	W69586	Hs.103156	ESTs
33912	>10	Z41239	Hs.106960	ESTs
42473	>10	W63731	Hs.122531	ESTs
25195	>10	AA033790	Hs.75736	Apolipoprotein D
28607	>10	C21481	Hs.84630	ESTs Moderately similar to III ALU SUBFAMILY SQ WARNING ENTRY III [H.sapiens]
3712	>10	U07620	Hs.89661	Human MAP kinase mRNA complete cds
6214	>10	X77307	Hs.2507	5-HYDROXYTRYPTAMINE 2B RECEPTOR
23575	>10	T80833	Hs.14794	ESTs
31775	>10	N79765	Hs.50947	ESTs
5206	>10	U82979	Hs.67846	Human clone HM18 monocytic inhibitory receptor precursor mRNA complete cds
22769	>10	R94521	Hs.124693	ESTs
9377	>10	H12674	Hs.5398	ESTs
29288	>10	H81046	Hs.70405	EST Moderately similar to III ALU SUBFAMILY J WARNING ENTRY III [H.sapiens]
11061	>10	AA147537	Hs.4811	ESTs
41960	>10	T33511	Hs.4844	ESTs
20416	>10	H77734	Hs.35702	Homo sapiens roundsbout 1 (robot) mRNA complete cds
38248	>10	AA489218	Hs.105229	ESTs
37256	>10	AA449424	Hs.98428	ESTs
21911	>10	R43960	Hs.26320	ESTs
23184	>10	T34622	Hs.8108	ESTs Weakly similar to HYPOTHETICAL_35.8 KD PROTEIN IN PRP16-SRP40 INTERGENIC REGION [S.coronariae]
18225	>10	AA011305	Hs.10029	Cathepsin C

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FIGURE 7 (CONT.)

27766	>10	AA453656	Hs.89417	ESTs	
16071	>10	AA001426	Hs.40863	ESTs	
17343	>10	AA100152	Hs.5921	ESTs	
10643	>10	AA040154	Hs.32478	ESTs	
26335	>10	F68239	Hs.39122	ESTs	
34868	>10	AA344888	Hs.1285	Complement component 8 gamma polypeptide	
26303	>10	AA255483	Hs.88042	EST	
1030	>10	HG2416-		EST - HG2416-HT2512	
26370	>10	AA609559	Hs.38550	ESTs Moderately similar to alpha subunit [H.sapiens]	
29303	>10	H65881	Hs.38427	ESTs	
21078	>10	N99976	Hs.8018	ESTs	
27100	>10	AA040231		EST - RC_AA040231	
11329	>10	AA216589	Hs.28462	ESTs	
4402	>10	UA1518	Hs.74602	AQUAPORIN-CHIP	
11050	>10	AA142919	Hs.5555	ESTs	
22844	>10	R98947		EST - RC_R98947	
31581	>10	N71371	Hs.39938	ESTs	
7253	>10	AA074407	Hs.139119	ESTs	
20423	>10	N49308	Hs.104938	ESTs	
39264	>10	AA621750		EST - RC_AA621750	
36415	>10	AA426598	Hs.24897	Homo sapiens chromosome 21q22.1 anonymous mRNA sequence	
18575	>10	AA031948	Hs.57548	ESTs	
37505	>10	AA455659	Hs.103233	ESTs	
26264	>10	AA521080	Hs.46765	ESTs	
23886	>10	T95325	Hs.16545	ESTs	
11781	>10	AA256485	Hs.33413	ESTs	
25603	>10	AA114250	Hs.48924	Homo sapiens mRNA for KIAA0512 protein complete cds	
9003	>10	C00808	Hs.107882	ESTs	
5632	>10	X15357		EST - X15357	
7680	>10	AA208946	Hs.8059	ESTs	
22783	>10	R95689	Hs.35437	ESTs	
20852	>10	N69540	Hs.17713	ESTs	
16795	>10	AA047896	Hs.49169	ESTs	
37558	>10	AA456975	Hs.75736	Apolipoprotein D	
35957	>10	AA412537	Hs.98149	EST	
42129	>10	T71561	Hs.84824	ESTs	
34585	>10	AA281002	Hs.40735	ESTs	
33690	>10	Z38607	Hs.62248	ESTs	
8904	>10	AF002256	Hs.86180	Homo sapiens killer cell receptor (KIR103) mRNA allele ASD1 complete cds	
2689	>10	M32373	Hs.1256	Arylsulfatase B	

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FIGURE 7 (CONT.)

40909	>10	N69084	Hs.49608	ESTs	
22377	>10	R63090	Hs.28391	ESTs	
21208	>10	R07851	Hs.20023	EST	
27304	>10	AA421783	Hs.56808	Homo sapiens mRNA for zinc finger protein FPM315 complete cds	
3307	>10	M95809	Hs.89578	BASIC TRANSCRIPTION FACTOR 82 KD SUBUNIT	
25370	>10	AA057556	Hs.28478	ESTs	
41423	>10	R44717	Hs.22917	ESTs	
2570	>10	M27160	Hs.2053	Tyrosinase (oculocutaneous albinism IA)	
14557	>10	AA620965	Hs.108300	ESTs Highly similar to ADENYLOSUCCINATE SYNTHETASE MUSCLE ISOZYME [Mus musculus]	
7023	>10	Z78291	Hs.48607	EST - Z78291	
31051	>10	N62696	Hs.112956	EST	
39200	>10	AA621246	Hs.27457	ESTs	
24712	>10	Z39652	Hs.9444	ESTs Moderately similar to IIII ALU CLASS A WARNING ENTRY IIII [H.sapiens]	
23296	>10	T52497	Hs.134846	ESTs	
12826	>10	AA424808	Hs.75678	Human GOS3 mRNA complete cds	
2198	>10	L49169	Hs.43498	ESTs	
27228	>10	AA416767	Hs.8175	ESTs	
7135	>10	AA028976	Hs.8175	EST - RC_AA074955	
17102	>10	AA074955	Hs.94870	Human mRNA for KIAA0306 gene partial cds	
38942	>10	AA609646	Hs.38336	ESTs	
29288	>10	H64973	Hs.54434	Interferon regulatory factor 5	
34336	>10	AA250843	Hs.47681	ESTs	
30816	>10	N53568	Hs.65093	ESTs	
16739	>10	AA045461	Hs.113025	ESTs	
42317	>10	T97599	Hs.113025	EST - L77563	
2228	>10	L77563	Hs.47927	ESTs	
30862	>10	N55171	Hs.97951	ESTs	
35954	>10	AA412526	Hs.98467	ESTs	
36403	>10	AA426383	Hs.98467	ESTs	
36949	>10	AA441812	Hs.98959	ESTs	
41628	>10	R70212	Hs.79630	Immunoglobulin-associated alpha	
39175	>10	AA621078	Hs.111966	ESTs	
37657	>10	AA460147	Hs.98397	ESTs Weakly similar to precursor of major fibrous sheath protein [M.musculus]	
36270	>10	AA424242	Hs.2060	S100 calcium-binding protein A5 (formerly S100D)	
6634	>10	Z18954	Hs.107197	ESTs	
40562	>10	N33212	Hs.22636	ESTs	
13770	>10	AA463272	Hs.78362	Human clone 23839 mRNA sequence	
5101	>10	U79249	Hs.78362	Human transducin-like enhancer protein (TLE3) mRNA complete cds	
3355	>10	M99438	Hs.31305	Human transducin-like enhancer protein (TLE3) mRNA complete cds	
8476	>10	AA442119	Hs.29790	ESTs	

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FIGURE 7 (CONT.)

34231	>10	AA234527	Hs.75772	Glucocorticoid receptor
42046	>10	T59148	Hs.50966	Carbamoyl-phosphate synthetase 1 mitochondrial
23913	>10	T96123	Hs.17749	ESTs
37333	>10	AA452150	Hs.75122	TRANSFORMING PROTEIN RHOB
27946	>10	AA463434	Hs.42858	ESTs
34407	>10	AA255523	Hs.42858	EST - RC_AA255523
16542	>10	AA029428	Hs.61555	ESTs
6248	>10	X78712	Hs.98008	Glycerol kinase 2 (testis specific)
8227	>10	AA393686	Hs.75709	Mannose-6-phosphate receptor (callon dependent)
3507	>10	S78774	Hs.75709	EST - S78774
40907	>10	N68830	Hs.25717	ESTs
33340	>10	W78688	Hs.58550	ESTs
19079	>10	H06371	Hs.20945	ESTs
3992	>10	U19713	Hs.76364	Atograft Inflammatory factor 1
36059	>10	AA417063	Hs.99189	ESTs
37634	>10	AA459582	Hs.99489	EST
41881	>10	R62313	Hs.126270	ESTs Weakly similar to RIT60 [R.norvegicus]
38734	>10	AA608792	Hs.112591	EST
37636	>10	AA470135	Hs.112238	ESTs
21303	>10	R11157	Hs.12610	ESTs
20125	>10	N22006	Hs.6202	ESTs
35516	>10	AA400795	Hs.97450	ESTs
26771	>10	AA284067	Hs.89287	EST
33558	>10	W90735	Hs.59332	EST
2830	>10	M57399	Hs.44	Pleiotrophin (heparin binding growth factor 8 neurite growth-promoting factor 1)
42625	>10	W89426	Hs.110128	ESTs
26152	>10	AA250845	Hs.87762	ESTs
31988	>10	N94581	Hs.55062	ESTs
17783	>10	AA148213	Hs.71873	ESTs Highly similar to 65 KD YES-ASSOCIATED PROTEIN [Gallus gallus]
21959	>10	R44949	Hs.22908	ESTs
10090	>10	N79674	Hs.7915	ESTs
30658	>10	N51105	Hs.111223	ESTs
17629	>10	AA131919	Hs.89009	ESTs
36260	>10	AA423970	Hs.98378	ESTs
285	>10	D16227	Hs.3618	Hippocalcin-like 1
26123	>10	AA243508	Hs.20887	ESTs
34535	>10	AA278391	Hs.104425	EST
29100	>10	H01428	Hs.92350	ESTs
24122	>10	W46947	Hs.4188	ESTs
19894	>10	H65942	Hs.36030	ESTs

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FIGURE 7 (CONT.)

22987	>10	T16258	Hs.25420	ESTs	
5985	>10	X64728	Hs.34514	H.sapiens CHML mRNA	
42461	>10	W62008	Hs.89717	Human preprocarboxypeptidase A2 (proCPA2) mRNA complete cds	
5422	>10	X00588	Hs.77432	Epidermal growth factor receptor	
16603	>10	AA034366	Hs.144627	ESTs	
33389	>10	W81607	Hs.58663	EST	
6931	>10	Z46788	Hs.3232	H.sapiens mRNA for cyclin II	
19324	>10	H17618	Hs.28180	ESTs	
32166	>10	R41836	Hs.9657	ESTs	
39987	>10	H58415	Hs.102160	EST	
17958	>10	AA168917	Hs.72639	ESTs	
39569	>10	AA598437	Hs.29385	ESTs Highly similar to MITOCHONDRIAL RESPIRATORY CHAIN COMPLEXES ASSEMBLY PROTEIN RCA1 [Saccharomyces cerevisiae]	
1006	>10	HG2280-	EST - HG2260-HT2349		
23552	>10	T79838	Hs.105818	ESTs	
38228	>10	AA488997	Hs.137530	ESTs	
1066	>10	HG2705-	EST - HG2705-HT2801		
23815	>10	T91283	EST - RC_T91283		
4689	>10	U57099	Human APEC-1 mRNA complete cds		
31306	>10	N66796	Hs.144212	ESTs	
12389	>10	AA399633	Hs.24872	ESTs	
34539	>10	AA279662	Hs.142452	ESTs Moderately similar to snRNP protein B [H.sapiens]	
20358	>10	N35584	Hs.17404	ESTs	
26070	>10	AA238868	Hs.87564	ESTs	
38210	>10	AA488659	Hs.105686	ESTs	
26025	>10	AA235574	PUTATIVE DNA BINDING PROTEIN A20		
4978	>10	U71207	Hs.29279	Homo sapiens clone 24534 eyes absent homolog (Eab1) mRNA partial cds	
4935	>10	U68162	Hs.84171	THROMBOPOIETIN RECEPTOR PRECURSOR	
3501	>10	S78467	EST - S78467		
14281	>10	AA505136	Hs.12420	ESTs	
31859	>10	N90688	Hs.54643	EST	
41104	>10	R01398	EST - RC_R01398		
5293	>10	U89695	Human DNA binding protein FKHL15 (FKHL15) mRNA complete cds		
3543	>10	S81957	EST - S81957		
27615	>10	AA443958	Hs.90960	ESTs	
7152	>10	AA038753	Hs.78484	Homo sapiens mRNA for KIAA0525 protein partial cds	
16197	>10	AA010328	Hs.39379	ESTs	
20178	>10	N24772	Hs.30213	Homo sapiens putative transmembrane protein (CLN5) mRNA complete cds	
33566	>10	W83015	Hs.73166	Treacher Collins syndrome susceptibility protein	
27265	>10	AA418392	Hs.46784	ESTs	
12453	>10	AA402000	Hs.20415	ESTs Weakly similar to GS3786 [H.sapiens]	

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FIGURE 7 (CONT.)

36302	>10	AA424652	Hs.124955	ESTs	
23192	>10	T40448	Hs.8204	ESTs	
17423	>10	AA114071	Hs.26270	ESTs	
23464	>10	T67026	Hs.13019	ESTs	
42762	>10	Z41697	Hs.106296	ESTs	
32628	>10	T56470	Hs.119190	Chromogranin A (parathyroid secretory protein 1)	
12605	>10	AA424331	Hs.28940	ESTs	
25379	>10	AA058803	Hs.111841	Human adenyl cyclase-associated protein homolog CAP2 (CAP2) mRNA complete cds	
39318	>10	C20817	Hs.108945	Homo sapiens mRNA for KIAA0515 protein partial cds	
29699	>10	H97938	Hs.75772	Glucocorticoid receptor	
17507	>10	AA160530	Hs.72447	ESTs	
35810	>10	AA411011	Hs.8038	ESTs	
36838	>10	AA436163	Hs.95851	Homo sapiens Pig12 (Pig12) mRNA complete cds	
29611	>10	H94043	Hs.41949	ESTs	
19650	>10	H46167	Hs.31542	ESTs	
33221	>10	W70305	Hs.64659	ESTs	
18940	>10	F10265	Hs.13287	ESTs	
2580	>10	M27533	EST - M27533	ESTs	
7274	>10	AA082171	Hs.8261	ESTs	
19524	>10	H28568	Hs.83466	Homo sapiens clone 23579 mRNA sequence	
40571	>10	N33558	Hs.103102	ESTs Weakly similar to WWP2 [H.sapiens]	
31178	>10	N64191	Hs.46584	ESTs	
29694	>10	N23009	Hs.43296	ESTs	
22201	>10	R54416	Hs.140932	ESTs	
28719	>10	AA282583	Hs.88817	ESTs	
32493	>10	T16497	Hs.85339	EST	
37179	>10	AA448004	Hs.99150	ESTs	
17980	>10	AA169173	Hs.72754	ESTs	
21934	>10	R44449	Hs.48778	ESTs	
36792	>10	AA435848	EST - RC_AA435848	ESTs	
34056	>10	AA194851	Hs.110575	ESTs	
39102	>10	AA620674	Hs.112882	EST	
26283	>10	AA253217	Hs.41271	ESTs	
23889	>10	T98529	Hs.16398	ESTs	
32456	>10	T15929	Hs.65284	ESTs	
15440	>10	W27301	Hs.111652	ESTs Moderately similar to PUTATIVE SERINE/THREONINE PROTEIN KINASE PKWA [Thermomonas curvula]	
19004	>10	H03299	Hs.30390	EST	
27839	>10	AA456309	Hs.58831	ESTs	
19848	>10	F10338	Hs.106309	ESTs Moderately similar to FOG [M.musculus]	
13112	>10	AA435896	Hs.16397	ESTs	

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FIGURE 7 (CONT.)

1850	>10	L17325	Hs.278	Human pre-TANK cell associated protein (1D12A2) mRNA complete cds
9101	>10	C17938	Hs.25536	ESTs
2807	>10	M55210	Hs.87428	Laminin gamma 1 (formerly LAMB2)
3383	>10	S37153	Hs.91787	Retinoblastoma-binding protein 1 (alternative products)
23142	>10	T26444	Hs.101248	ESTs
5367	>10	U95018	Hs.30941	Myasthenic syndrome antigen B (human fetal brain mRNA 3477 nt)
32205	>10	R44234	Hs.75169	ESTs
28515	>10	AA262972	Hs.87298	ESTs
15332	>10	W24127	Hs.16003	ESTs Weakly similar to keratin 8 type II cytoskeletal embryonic [M.musculus]
34183	>10	AA232251	Hs.128530	ESTs
6392	>10	X85753	Hs.25283	CELL DIVISION PROTEIN KINASE 8
33784	>10	Z40689	Hs.65973	ESTs
33474	>10	W87484	Hs.50429	ESTs
34984	>10	AA344854	Hs.96337	ESTs
14584	>10	AA821414	Hs.110903	Homo sapiens transmembrane protein mRNA complete cds
22640	>10	R83864	Hs.33416	EST
4339	>10	U38372	EST - U38372	
37567	>10	AA456988	Hs.41548	Human MHC Class I region proline rich protein mRNA complete cds
4937	>10	U68385	Hs.117313	Human Meis1-related protein 2 (MRG2) mRNA partial cds
30795	>10	N53043	Hs.47606	ESTs
30566	>10	N58432	Hs.48382	EST
33991	>10	AA181935	Hs.104050	EST
2285	>10	M11591	EST - M11591	
24315	>10	W84413	Hs.23017	ESTs
38752	>10	AA608852	Hs.112603	EST
5116	>10	U78271	Hs.7571	Human clones 23920 and 23921 mRNA sequence
15037	>10	U44798	Hs.93502	Human U1-sRNP binding protein homolog mRNA complete cds
37045	>10	AA446000	Hs.99043	ESTs
37627	>10	AA459392	Hs.105042	ESTs
21935	>10	R44477	Hs.22848	ESTs
18669	>10	F03869	Hs.27278	ESTs Highly similar to PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A [Bos taurus Sus scrofa]
22737	>10	R92512	EST - RC_R92512_s	
30727	>10	N51987	Hs.47390	EST
16086	>10	AA001879	Hs.59890	EST
23293	>10	T52201	Hs.9410	ESTs
5294	>10	U90065	Hs.79351	Human two P-domain K+ channel TWIK-1 mRNA complete cds
17769	>10	AA148923	Hs.93675	ESTs
25549	>10	AA101056	EST - RC_AA101056	
84	>10	AF001359	EST - AF001359_J	
4856	>10	U65093	Human msg1-related gene 1 (mrg1) mRNA complete cds	

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FIGURE 7 (CONT.)

7697	>10	AA214730	Hs.107256	ESTs	
36295	>10	AA24535	Hs.98416	ESTs	
17490	>10	AA125781	Hs.57489	ESTs	
36976	>10	AA442779	Hs.98983	ESTs	
10425	>10	AA010619	Hs.16446	ESTs	
41196	>10	R11654	Hs.20526	ESTs	
42285	>10	T94409	EST - RC_T94409	EST	
33185	>10	W69435	Hs.58009	EST	
13974	>10	AA479299	Hs.21107	ESTs	
18868	>10	H61580	EST - RC_H61580	ESTs	
1378	>10	HG831-	EST - HG831-HT831	EST	
621	>10	D53813	Hs.26866	Human mRNA for rod photoreceptor protein complete cds	
5346	>10	U92459	Hs.86204	Human melatropic glutamate receptor 8 mRNA complete cds	
6029	>10	X66533	Hs.77890	GUANYLATE CYCLASE SOLUBLE BETA-1 CHAIN	
22196	>10	R53972	Hs.26026	ESTs	
24609	>10	Z36900	Hs.26615	ESTs	
37198	>10	AA448228	EST - RC_AA448228	EST	
26151	>10	AA250838	Hs.108509	ESTs	
5938	>10	X62535	Hs.74044	Diacylglycerol kinase alpha (80kD)	
16373	>10	AA019603	Hs.60992	ESTs	
26356	>10	AA609080	Hs.41585	ESTs	
20070	>10	H98854	Hs.20423	ESTs	
17717	>10	AA136541	Hs.71647	EST	
20059	>10	H98768	Hs.13121	ESTs	
40865	>10	N74604	Hs.124694	ESTs	
10194	>10	R63545	Hs.11553	ESTs Weakly similar to putative type III alcohol dehydrogenase (D.melanogaster)	
40200	>10	H87229	Hs.82963	Gonadotropin-releasing hormone (leulinizing-releasing hormone)	
34983	>10	AA347417	Hs.96869	EST	
23543	>10	T79203	Hs.14480	ESTs	
12770	>10	AA421778	Hs.8981	ESTs	
25085	>10	AA017518	Hs.115241	Homo sapiens G protein beta 5 subunit mRNA complete cds	
37746	>10	AA463627	Hs.95598	ESTs	
2370	>10	M16505	Hs.79076	STERYL-SULFATASE PRECURSOR	
31244	>10	N66062	Hs.49112	EST	
31716	>10	N75507	Hs.50628	ESTs Weakly similar to CLATHRIN COAT ASSEMBLY PROTEIN AP17 [Rattus norvegicus]	
28308	>10	AA598959	Hs.59183	ESTs	
2220	>10	L76687	Hs.83070	Homo sapiens Gb14 mRNA complete cds	
12404	>10	AA400292	Hs.23786	ESTs	
41050	>10	N92882	Hs.109494	ESTs Weakly similar to putative progesterone binding protein [H.sapiens]	
2407	>10	M18737	Hs.90708	GRANZYME A PRECURSOR	

FIGURE 7 (CONT.)

23462	>10	T68948	Hs.12992	ESTs	
16614	>10	F02418	Hs.107614	ESTs	
40553	>10	N32060	Hs.104010	Homo sapiens CAG-isl 7 mRNA complete cds	
27826	>10	AA455949	Hs.61232	ESTs	
207	>10	D12763	Hs.66	Suppression of tumorigenicity 2	
41064	>10	N63508	Hs.102923	EST	
10845	>10	AA084405	Hs.106313	ESTs Weakly similar to P24 protein [M.musculus]	
21813	10	R42039	Hs.23084	ESTs	
18463	10	AA233151	Hs.81796	ESTs	
17507	10	AA126419	Hs.74876	ESTs	
23957	10	T97487	Hs.18070	ESTs	
13317	10	AA448212	Hs.38095	ESTs	
29550	10	H90133	Hs.41352	ESTs	
39068	10	AA620411	Hs.141503	Small inducible cytokine A5 (RANTES)	
28620	10	AA280413	Hs.89843	Spleen focus forming virus (SFFV) proviral integration oncogene spl1	
37675	10	AA460377	Hs.99816	ESTs	
31437	10	N68921	Hs.49573	ESTs	
32657	10	T68867	Hs.76889	ESTs	
34952	10	AA342828	Hs.73734	PLATELET GLYCOPROTEIN V PRECURSOR	
26475	10	AA262264	Hs.87640	ESTs	
41827	10	T15445	Hs.99491	H.sapiens mRNA for F2593.3 kinase like protein from C.elegans	
20073	10	H98985	Hs.111911	ESTs	
42336	10	T99713	Hs.139933	ESTs	
26412	10	AA258224	Hs.86646	ESTs	
21352	10	R15890	Hs.21745	ESTs	
22583	10	R78239	Hs.29855	EST	
34020	10	AA191543	Hs.144302	EST	
25913	10	AA161105		EST - RC_AA161105	
82	10	AF000959	Hs.110903	Homo sapiens transmembrane protein mRNA complete cds	
37531	10	AA456140	Hs.98235	ESTs	
13314	10	AA448169	Hs.6728	ESTs	
31430	10	N68610		EST - RC_N68610	
30570	10	N49587	Hs.46633	EST	
7302	10	AA089688	Hs.103668	EST	
27732	10	AA452167	Hs.55778	ESTs	
22533	10	R73408	Hs.140996	ESTs	
31079	10	N62969	Hs.48982	EST	
35470	10	AA400393	Hs.97803	EST Weakly similar to precursor polypeptide [H.sapiens]	
37102	10	AA446889	Hs.119316	ESTs	
203	10	D12620	Hs.106242	CYTOCHROME P450 IVF3	

FIGURE 7 (CONT.)

11427	10	AA233277	Hs.74947	ESTs	
24159	10	W57862	Hs.21289	ESTs	
17870	10	AA151772	Hs.72185	ESTs	
5302	10	U90543	Hs.79041	Human butyrophilin (BTF-1) mRNA complete cds	
27256	10	AA417998	Hs.62781	ESTs	
2219	10	L76670	Hs.109610	Homo sapiens nkal7 mRNA complete cds	
30658	10	N55081	Hs.47915	EST	
8870	10	AB002387	Hs.21355	Human mRNA for KIAA0369 gene complete cds	
40870	10	N67262	Hs.358	Zinc finger protein 135 (clone pHZ-17)	
11811	10	AA258130	Hs.11530	ESTs	
33254	10	W72833	Hs.58187	ESTs	
17192	10	AA079094	EST - RC_AA079094		
24392	10	W88568	Hs.58589	Homo sapiens glycogenin-2 gamma (glycogenin-2) mRNA complete cds	
27456	10	AA430539	Hs.57760	ESTs	
25419	10	AA069386	EST - RC_AA069386		
7100	10	AA012985	Hs.50548	ESTs	
31588	10	N71571	Hs.50050	ESTs	
29995	10	N26401	Hs.43802	EST	
31973	10	N93875	Hs.55015	EST	
36158	10	AA418279	Hs.82813	Colony-stimulating factor 1 (M-CSF)	
12419	10	AA400888	Hs.7159	ESTs	
27076	10	AA401630	Hs.62592	ESTs	
28251	10	AA504512	Hs.76852	ESTs Weakly similar to ZK782.1 [C.elegans]	
4219	10	U32324	Hs.64310	Human interleukin-11 receptor alpha chain mRNA complete cds	
27991	10	AA465650	Hs.87306	ESTs	
37702	10	AA461119	Hs.99539	ESTs	
25251	10	AA040792	Hs.54421	Bradykinin receptor B2	
27064	10	AA401253	Hs.87677	ESTs	
37582	10	AA458668	Hs.95698	ESTs	
39519	9	F10840	Hs.12354	ESTs	
31053	9	N62724	Hs.48614	EST	
33338	8	W79524	Hs.58585	ESTs	
23368	9	T59005	Hs.10476	EST	
6240	9	AA397841	Hs.108879	ESTs	
21778	9	R41389	Hs.29159	EST	
31168	9	N63965	Hs.48903	ESTs	
3440	9	S72370	Hs.89890	Pyruvate carboxylase	
25930	9	AA164928	EST - RC_AA164928		
29571	9	N25657	Hs.93892	EST	
39771	9	H17463	Hs.101735	ESTs	

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FIGURE 7 (CONT.)

21481	9	R26141	Hs.24032	ESTs Highly similar to transmembrane receptor [M.musculus]
10887	9	AA101632	Hs.22971	ESTs
31431	9	N68666	Hs.76798	ESTs
30756	9	N52398	Hs.39252	ESTs
35829	9	AA411438	Hs.74635	Dihydropyrimidine dehydrogenase (E3 component of pyruvate dehydrogenase complex 2-oxo-glutarate complex branched chain keto acid dehydrog
24540	9	Z38435	Hs.19235	ESTs
37500	9	AA455474	Hs.100530	ESTs
19007	9	H03358	EST - RC_H03358	EST
42650	9	W92272	Hs.25601	Homo sapiens zinc-finger helixcase (hZFh) mRNA complete cds
16705	9	AA043675	Hs.62633	EST
40275	9	H94647	Hs.102329	ESTs
24372	9	W87423	Hs.35598	ESTs
9011	9	C01394	Hs.106823	Homo sapiens clone 24818 mRNA sequence
40780	9	N59568	Hs.108107	ESTs
17177	9	AA079331	EST - RC_AA079331	EST
20878	9	N70305	Hs.34492	ESTs
38140	9	AA486273	Hs.100472	ESTs
3490	9	S77763	Hs.75643	Homo sapiens NF-E2 protein (NF-E2) mRNA complete cds
39112	9	AA620724	Hs.112890	ESTs
27347	9	AA424940	Hs.43580	ESTs
14747	9	D60364	Hs.34882	ESTs
23599	9	T82307	EST - RC_T82307	EST
23979	9	T98262	EST - RC_T98262	EST
27759	9	AA453472	Hs.95111	ESTs
36691	9	AA432381	Hs.97357	ESTs Moderately similar to NITRIC OXIDE SYNTHASE INDUCIBLE [H.sapiens]
26782	9	AA284181	Hs.89310	ESTs
26816	9	AA285145	Hs.50446	ESTs
22334	9	R61290	Hs.25870	ESTs
22945	9	N22995	Hs.42829	ESTs
30518	9	T10134	Hs.9877	Homo sapiens mRNA for KIAA0688 protein complete cds
29715	9	N50656	It.93596	ESTs Highly similar to mosaic protein LR11 [H.sapiens]
37560	9	H98700	Hs.50897	ESTs
23264	9	AA457023	EST - RC_AA457023	EST
31001	9	T50052	Hs.9092	EST
17841	9	N62200	Hs.47566	ESTs
3478	9	AA156109	Hs.66180	ESTs
11605	9	S76992	Hs.104005	Vav 2 oncogene
19032	9	AA243139	Hs.4863	ESTs
28933	9	H04822	Hs.30494	EST
	9	N24182	Hs.93677	ESTs

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FIGURE 7 (CONT.)

26622	9	AA260431	Hs.88756	ESTs	
4289	9	U35376	Hs.37138	Human repressor transcriptional factor (ZNF85) mRNA complete cds	
42034	9	T56281	Hs.110440	Human metallothionein (MT)-I gene	
30447	9	N47439	Hs.44603	ESTs	
25238	9	AA039568	EST - RC_AA039568	ESTs	
20238	9	N30077	Hs.14855	ESTs	
30232	9	N34500	Hs.44600	EST	
17017	9	AA059920	EST - RC_AA059920	ESTs	
11645	9	AA259064	Hs.10839	ESTs Weakly similar to unknown [S.cerevisiae]	
30229	9	N34457	EST - RC_N34457	EST	
30737	9	N52137	Hs.47442	EST	
30555	9	N49259	EST - RC_N49259	EST	
981	9	HG2139-	EST - HG2139-HT208_I	EST	
30498	9	N48325	Hs.93956	EST	
40434	9	N21461	EST - RC_N21461	EST	
36788	9	AA435824	Hs.95594	Homo sapiens BAC clone RG113D17 from 7p14-p15	
28991	9	F04652	Hs.66195	ESTs	
25942	9	AA234187	Hs.87267	ESTs	
30466	9	N47951	Hs.57485	ESTs	
19317	9	H17476	Hs.11615	ESTs Weakly similar to dual specificity phosphatase [H.sapiens]	
13859	9	AA470066	Hs.24309	ESTs Highly similar to S-ACYL FATTY ACID SYNTHASE THIOESTERASE MEDIUM CHAIN [Rattus norvegicus]	
23445	9	T65992	Hs.11722	EST	
24448	9	W93273	Hs.9270	ESTs Weakly similar to isopentenyl-diphosphate Delta-isomerase [H.sapiens]	
7583	9	AA167824	Hs.63559	ESTs Highly similar to PROTEIN CDC27HS [Homo sapiens]	
22778	9	R84840	Hs.35372	ESTs Weakly similar to III ALU CLASS B WARNING ENTRY [III [H.sapiens]	
16439	9	AA024835	Hs.47584	Homo sapiens Shab-related delayed-rectifier K+ channel alpha subunit (KCNS3) mRNA complete cds	
42395	9	W42733	Hs.109870	ESTs	
19991	9	HQ0887	Hs.18357	ESTs	
23690	9	T87648	EST - RC_T87648	ESTs	
7111	9	AA018804	Hs.125175	ESTs Highly similar to RAS-RELATED PROTEIN RAB-14 [Rattus norvegicus]	
6400	9	X86163	Hs.54421	Bradykinin receptor B2	
42474	9	W63747	Hs.109818	H.sapiens TTF mRNA for small G protein	
11425	9	AA233257	Hs.25511	Homo sapiens mRNA for Hic-5 partial cds	
27039	9	AA400277	Hs.48049	ESTs	
32206	9	R44386	Hs.91703	ESTs	
13310	9	W19098	Hs.7921	ESTs	
36501	9	AA431337	Hs.98017	ESTs	
463	9	D38462	EST - D38462	ESTs	
31674	9	N74357	Hs.50482	ESTs	
31182	9	N64339	Hs.48956	EST	

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FIGURE 7 (CONT.)

13499	AA453458	Hs.7301	ESTs	
37514	AA455914	Hs.1019	Parathyroid hormone receptor, 1	
5998	X55644	Hs.75063	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 ENHANCER-BINDING PROTEIN 2	
962	HG180-		EST - HG180-HT180	
40790	N62328	Hs.3788	Glutamate receptor metabotropic 3	
25700	AA131512	Hs.103820	EST	
36880	AA435708	Hs.98895	ESTs	
2809	M55267	Hs.41848	EV12A PROTEIN PRECURSOR TROPIC VIRAL INTEGRATION SITE 2A PROTEIN	
5620	X14885	Hs.2025	Transforming growth factor beta 3	
16643	AA035325	Hs.47200	ESTs	
32051	R01450	Hs.91081	ESTs	
33550	W80617	Hs.50120	ESTs	
6177	X75535	Hs.110884	33 KD HOUSEKEEPING PROTEIN	
33000	W45531	Hs.94642	ESTs	
20668	H98701	Hs.4985	ESTs	
4590	U50534	Hs.30649	Human infant brain mRNA clone 13cDNAT3	
37199	AA448257	Hs.97127	ESTs	
24601	Z38844	Hs.25803	ESTs	
33589	W93074	Hs.59342	ESTs	
37389	AA453468	Hs.99330	ESTs	
5801	X55448	Hs.3118	H.sapiens mRNA for 2.19 gene	
28748	D25912	Hs.74832	ESTs	
40070	H72592	Hs.77554	ESTs	
40367	H98857	Hs.75520	Human mRNA for KIAA0041 gene partial cds	
33609	W93585	Hs.59476	ESTs	
24502	Z38214	Hs.26946	ESTs	
11129	AA156873	Hs.15970	ESTs	
7144	AA033659	Hs.95154	ESTs	
28584	C21221	Hs.68619	ESTs Highly similar to METALLOTHIONEIN-1A [Equus caballus]	
22165	R52822	Hs.22003	ESTs	
31987	N94551	Hs.55060	ESTs	
32470	T15955	Hs.65289	EST	
36642	AA599152	Hs.91379	PTD-ASSOCIATED SPLICING FACTOR	
40438	N21864	Hs.80500	Human mRNA for KIAA0061 gene partial cds	
34471	AA258843	Hs.111376	ESTs	
41571	R61005	Hs.115170	Homo sapiens mRNA for GalT4 protein	
31417	N68435	Hs.49516	ESTs	
23951	T87318	Hs.18037	ESTs	
7832	AA249260	Hs.28545	ESTs Moderately similar to zinc finger protein [R.norvegicus]	
27928	AA461083	Hs.26789	ESTs	

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FIGURE 7 (CONT.)

2017	8	L34219	Hs.1933	Cellular retinoiddehyde-binding protein
25530	8	AA098834	Hs.83428	Nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105)
20556	8	N55189	Hs.34081	ESTs
27036	8	AA400155	Hs.142935	ESTs
22651	7	R85266	Hs.33487	ESTs
31663	7	W95805	Hs.59736	EST
18374	7	H19472	Hs.31653	EST
10275	7	R79356	Hs.19280	ESTs Weakly similar to PROTEIN Q300 [Mus musculus]
39471	7	D60265	Hs.107854	ESTs
25100	7	AA019426	Hs.103343	EST
8828	7	AB002316	Hs.55746	Human mRNA for KIAA0318 gene partial cds
17132	7	AA075674		EST - RC_AA075674
15915	7	Y08858	Hs.82577	Human DNA sequence from clone 323P24 on chromosome Xp11.21-11.23 Contains SPIN (spindlin homolog (PROTEIN DXF34)) hypothetical prote
8216	7	AA393089	Hs.66723	ESTs
22512	7	R71489	Hs.29196	EST
19097	7	H08171	Hs.30842	ESTs
25048	7	AA011041	Hs.130843	ESTs
35353	7	AA398962	Hs.97699	ESTs
31278	7	N68399	Hs.49193	EST
23149	7	T26893	Hs.7569	EST
11680	7	AA262783	Hs.22057	ESTs
17547	7	AA127595	Hs.71018	ESTs
32054	7	W32094	Hs.55501	ESTs
36822	7	AA435978	Hs.98852	EST
35530	7	AA400893	Hs.41717	Human 3' cyclic nucleotide phosphodiesterase (HSPDE 1A3A) mRNA complete cds
3869	7	U14417	Hs.106185	Human Ral guanine nucleotide dissociation stimulator mRNA partial cds
9388	7	H09246	Hs.100739	ESTs
15154	7	U79527	Hs.111075	Human orphan G-protein coupled receptor Dez isoform a mRNA complete cds
21178	7	R08607	Hs.19748	EST
33081	7	W57731	Hs.56213	ESTs
13848	7	AA465664	Hs.21323	ESTs
18659	7	F03220	Hs.13258	ESTs
1979	7	L29339	Hs.1964	Solute carrier family 5 (sodium/glucose cotransporter) member 1
22609	7	R08945	Hs.29378	ESTs
2418	7	M19507	Hs.1817	Myeloperoxidase
28863	7	D80051	Hs.124418	ESTs
26764	7	AA263326	Hs.51501	ESTs
6544	7	X95877		EST - X95877
33524	7	W89188	Hs.59096	ESTs
18374	7	AA226877	Hs.87624	ESTs

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FIGURE 7 (CONT.)

10108	7	R25069	Hs.23790	ESTs	Human sapiens centrosomal Nek2-associated protein 1 (C-NAP-1) mRNA complete cds
26178	7	AA251153	Hs.27910	ESTs	Human cardiac myosin binding protein-C (MyBP-C) gene complete cds
36428	7	AA427605	Hs.99551	EST	
29808	7	N21032	Hs.42931	ESTs	
24837	7	Z41186	Hs.27997	ESTs	
24909	7	Z98482	Hs.27250	ESTs	
26333	7	AA250075	Hs.92280	ESTs	Human sapiens regulator of G protein signaling 10 mRNA complete cds
11507	7	AA235465	Hs.29161	ESTs	
40387	7	H99460	Hs.108873	ESTs	
16112	7	AA004377	Hs.91813	ESTs	Human butyrophilin (BTf2) mRNA complete cds
25413	7	AA065096	Hs.20887	ESTs	EST - RC_AA065096
13232	7	AA443944	Hs.67805	ESTs	
27236	7	AA417037	Hs.129672	ESTs	
21684	7	R38944	Hs.15301	ESTs	ESTs Weakly similar to weakly similar to ANK repeat region of Fowlpox virus BarnHI-ori7 protein [C.elegans]
9284	7	D82712	Hs.5091	ESTs	Human sapiens torsinB (DO1) mRNA partial cds
16886	7	AA057119	Hs.28029	ESTs	ESTs Highly similar to EPIDERMAL GROWTH FACTOR PRECURSOR [Mus musculus]
20083	7	H99879	Hs.36672	ESTs	
30851	7	N51029	Hs.22123	ESTs	
22362	7	R62447	Hs.23076	ESTs	
21581	7	R33245	Hs.23600	ESTs	
21636	7	R37501	Hs.110130	ESTs	Human sapiens chromosome 19 cosmid F22329
21223	7	R08175	Hs.1339	ESTs	Collagen type IV alpha 2
32218	7	R45654	Hs.25722	ESTs	ESTs Weakly similar to KRUPPEL-RELATED ZINC FINGER PROTEIN 1 [Homo sapiens]
13405	7	AA450118	Hs.47111	ESTs	
30827	7	N50740	Hs.44227	ESTs	ESTs Weakly similar to IIII ALU SUBFAMILY J WARNING ENTRY IIII [H. sapiens]
30117	7	N30824	Hs.105669	ESTs	EST - RC_N67238
31344	7	N67238	Hs.105715	ESTs	
38119	7	AA485714	Hs.82401	ESTs	CD69 antigen (early T cell activation antigen)
33297	7	W73761	Hs.24550	ESTs	
6892	7	Z30426	Hs.13021	ESTs	
9923	7	N44998	Hs.95464	ESTs	ESTs Moderately similar to transcription enhancer factor TEF1 [H. sapiens]
27842	7	AA463237	Hs.43005	ESTs	
34845	7	AA283420	Hs.85280	ESTs	Human interferon regulatory factor 7 (humif7) mRNA complete cds
29829	7	N21460	Hs.112083	ESTs	
15059	7	U53831	Hs.109558	ESTs	
40441	7	N22053	Hs.62542	ESTs	Acylxylase (neutrophil)
25095	7	AA018937	Hs.89949	ESTs	Epoxide hydrolase 1 (microsomal xenobiotic)
2941	7	M62840	Hs.79310	ESTs	Human GAP SH3 binding protein mRNA complete cds
1845	7	L25878			
42648	7	W92150			

FIGURE 7 (CONT.)

19592	7	H40696	Hs.33750	ESTs	
29801	7	N20939	Hs.38759	ESTs	
15417	7	W26982	Hs.39330	ESTs	
39877	7	H38627	Hs.107606	ESTs	
23967	7	T97910	Hs.18184	EST	
20041	7	H97012	Hs.11050	ESTs	Weakly similar to L8004.7 gene product [S.cerevisiae]
18314	7	AA214510	Hs.86518	ESTs	
22452	7	R67370	Hs.28758	ESTs	
30496	7	N48294	Hs.46950	EST	
26830	7	AA287057	Hs.48820	ESTs	
33432	7	W86075	Hs.38715	ESTs	
31384	7	N87990	Hs.49421	ESTs	
7053	6	Z84721	Hs.75792	Hemoglobin alpha 1	
33518	6	W88996	Hs.59134	EST	
5355	6	U94320	Hs.123021	Human Y5 receptor mRNA complete cds	
41311	6	R38516	Hs.124255	EST	
12545	6	AA406320	Hs.24702	ESTs	
23843	6	T82561	Hs.110422	ESTs	
21687	6	R38475	Hs.21408	ESTs	
17472	6	AA121704	Hs.69494	ESTs	
25648	6	AA126873	Hs.110341	ESTs	
32710	6	T87324	Hs.91021	EST	
3450	6	S73840	Hs.931	H.sapiens mRNA for fast 2a myosin heavy chain (3' end)	
979	6	HG20900		EST - HG20900-HT2152	
8151	6	AA346686		EST - AA346686	
35380	6	AA398522	Hs.97571	ESTs	Weakly similar to T04A8.9 [C.elegans]
23789	6	T91047	Hs.128785	ESTs	
940	6	HG1496		EST - HG1496-HT1496	
35896	6	AA412106	Hs.97349	ESTs	
15350	6	AA019034	Hs.94000	ESTs	
27547	6	AA436613	Hs.72157	ESTs	
22528	6	R73036	Hs.29323	EST	
25815	6	AA149889	Hs.96200	ESTs	Weakly similar to A-kinase anchor protein 95 AKAP95 [R.norvegicus]
8473	6	AA437346	Hs.2957	SHB adaptor protein (a Src homology 2 protein)	
35742	6	AA406058	Hs.97999	EST	
36538	6	AA430002	Hs.112044	ESTs	
17831	6	AA152323	Hs.71947	ESTs	
25072	6	AA015799	Hs.33792	ESTs	
15632	6	W66102	Hs.71218	ESTs	
20442	6	N50827	Hs.25275	ESTs	

FIGURE 7 (CONT.)

28357	AA609120	Hs.55185	ESTs Weakly similar to The KIAA0147 gene product is related to adenylyl cyclase. [H.sapiens]
25022	AA007591	Hs.110227	ESTs
29134	H68158	Hs.28310	ESTs
28148	AA488875	Hs.6433	Homo sapiens clone 24523 mRNA sequence
30744	N52185	Hs.105365	H.sapiens mRNA for arginine methyltransferase
27577	AA442090	Hs.118295	ESTs
33472	W87469	Hs.58992	ESTs
25887	AA130857	Hs.100119	ESTs
10549	AA027317	Hs.19138	ESTs Weakly similar to III ALU SUBFAMILY J WARNING ENTRY [H.sapiens]
32835	W23631	Hs.55428	ESTs
17025	AA070160	EST - RC_AA070160	
22039	T10070	Hs.4217	Homo sapiens mRNA for KIAA0987 protein partial cds
15803	X52332	Hs.104115	Human Kox1 gene for Zinc finger protein
34818	AA282143	Hs.58094	H.sapiens mRNA for melanoma growth regulatory protein MIA
11074	AA148983	Hs.29068	ESTs
12212	AA297746	Hs.22654	ESTs
16102	AA002150	Hs.59872	ESTs
31340	N67197	Hs.50125	EST
19459	H24317	Hs.6528	ESTs
17533	AA127058	Hs.71037	EST
22017	R46597	Hs.22703	ESTs
23587	T87519	Hs.16075	ESTs Weakly similar to no similarities to reported gene products [H.sapiens]
30298	N38130	Hs.44792	EST Weakly similar to hypothetical protein [H.sapiens]
28973	F04014	Hs.65995	ESTs
17042	AA070387	EST - RC_AA070387	
20817	N88628	Hs.37630	ESTs
18430	AA232138	Hs.118899	ESTs
28493	C14820	Hs.67188	EST
30407	N48302	Hs.46852	EST
32502	T16896	Hs.65373	ESTs
41324	R38804	Hs.13434	Homo sapiens clone 24418 mRNA sequence
18418	AA228096	Hs.60480	ESTs
23622	T84046	Hs.15345	ESTs
15342	W25781	Hs.6136	Homo sapiens clone 23688 mRNA sequence
15248	W01094	Hs.84628	ESTs
2247	M10321	Hs.110802	VON WILLERAND FACTOR PRECURSOR
31906	N02643	Hs.35986	Homo sapiens CASK mRNA complete cds
9062	C06238	Hs.95685	Homo sapiens clone 24700 unknown mRNA partial cds
38640	AA599142	Hs.112509	EST
42622	W87801	Hs.108209	ESTs

FIGURE 7 (CONT.)

32159	5	R40974	Hs.124270	ESTs	
35492	5	AA400514	Hs.97505	ESTs	
37630	5	AA459849	Hs.95485	ESTs	
27103	5	AA042282	Hs.63481	ESTs	Weakly similar to kynurenine/alpha-aminoadipate aminotransferase [R.norvegicus]
17209	5	AA082833	Hs.63481	EST - RC_AA082833	
589	5	D50930	Hs.5084	Human mRNA for KIAA0140 gene complete cds	
17489	5	AA122394	Hs.70811	ESTs	
6293	5	X80878	Hs.95262	Human R kappa B mRNA complete cds	
5067	5	U77845	Hs.21254	Human hTRIP (hTRIP) mRNA complete cds	
23060	5	T23513	Hs.7147	ESTs	
28902	5	D80990	Hs.45247	ESTs	
32328	5	R76401	Hs.92262	ESTs	
33218	5	W70259	Hs.48523	ESTs	
28751	5	D45455	Hs.65524	ESTs	
21400	5	R19360	Hs.14651	ESTs	
15557	5	W36290	Hs.9115	ESTs	
12631	5	AA412293	Hs.21258	ESTs	
32282	5	R62578	Hs.62264	ESTs	
10416	5	AA008809	Hs.37589	ESTs	
40308	5	H96306	Hs.32980	Human mRNA for BST-1 complete cds	
11599	5	AA242829	Hs.7508	ESTs	
33220	5	W70279	Hs.94811	ESTs	Weakly similar to 3-oxoacyl-[acyl-carrier protein] reductase [E.coli]
23100	5	T23867	Hs.7316	ESTs	
15333	5	W24154	Hs.6166	ESTs	
8331	5	AA412556	EST - AA412556		
9010	5	C01360	Hs.67384	Homo sapiens clone 23904 mRNA sequence	
4660	5	U53225	Hs.75283	Sortilin nexin 1	
25213	5	AA035444	Hs.100543	Homo sapiens clone 24505 mRNA sequence	
25242	5	AA039933	Hs.30941	Myasthenic syndrome antigen B [human fetal brain mRNA 3477 nt]	
28708	5	D20538	Hs.90165	EST	
7435	5	AA095412	Hs.26230	ESTs	
25538	5	AA095560	Hs.101442	ESTs Highly similar to ZINC FINGER PROTEIN 8 [Homo sapiens]	
271	5	D14823	EST - D14823		
5490	5	X04571	Hs.2230	Epidermal growth factor	
18812	5	F10040	Hs.13251	ESTs	
23393	5	T62918	Hs.11110	ESTs Weakly similar to ZINC FINGER PROTEIN 42 [H.sapiens]	
23446	5	T66282	Hs.12507	ESTs	
35204	5	AA398155	Hs.97600	ESTs	
31369	5	N67598	Hs.136395	ESTs	
5244	5	U85992	Hs.87187	Human clone IMAGE:35527 unknown protein mRNA partial cds	

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FIGURE 7 (CONT.)

20835	5	N69215	Hs.37456	ESTs	
16502	5	AA027059	Hs.61425	EST	
23691	5	T87683	Hs.16414	ESTs	
31842	5	N90168	Hs.54593	EST	
7845	5	AA249611	EST - AA249611	ESTs	
29297	5	H65459	Hs.38323	ESTs	
7953	5	AA284403	Hs.74750	Human sapiens mRNA for KIAA0554 protein partial cds	
36412	5	AA428464	Hs.98466	ESTs	
19357	5	H18929	EST - RC_H18929	ESTs	
16299	5	AA016258	EST - RC_AA016258	ESTs	
25312	5	AA047078	Hs.95278	ESTs Weakly similar to III ALU SUBFAMILY SO WARNING ENTRY III [H.sapiens]	
27617	5	AA448114	Hs.55409	ESTs	
42432	5	W46403	Hs.107293	ESTs	
38432	5	AA496983	Hs.78672	Laminin alpha 4	
32215	5	R45175	Hs.117183	ESTs	
15214	5	U93553	Hs.91310	Human alpha1-fetoprotein transcription factor (hFTF) mRNA complete cds	
15141	5	U78768	Hs.90957	Human TNF receptor associated factor 6 (TRAF6) mRNA complete cds	
20052	5	H97922	Hs.5376	Human LAR-interacting protein 1a mRNA complete cds	
7551	5	AA156838	Hs.107941	ESTs	
28451	5	AA259058	Hs.43516	ESTs	
42355	5	W20404	Hs.55405	ESTs	
39480	5	D60419	Hs.81915	STATMIN	
17369	5	AA101833	Hs.69293	EST	
14993	5	U22172	Hs.73046	Human DNA damage repair and recombination protein RAD52 pseudogene mRNA partial cds	
23400	5	T63336	Hs.105095	ESTs	
21153	5	R05315	EST - RC_R05315	ESTs	
14282	5	AA505141	IIIs.11923	ESTs	
21104	5	R01081	EST - RC_R01081	ESTs	
32825	5	W20364	Hs.55412	ESTs	
35018	5	AA346591	EST - RC_AA346591	ESTs	
25104	5	AA019599	Hs.103351	ESTs	
19235	5	H12725	Hs.31181	ESTs	
34079	5	AA347209	Hs.7841	Human mRNA for KIAA0324 gene partial cds	
21501	5	R26855	Hs.24120	ESTs	
18331	5	AA218543	Hs.10881	Human sapiens mRNA for KIAA0541 protein partial cds	
37529	5	AA456112	Hs.99410	ESTs	
15532	5	W28844	Hs.5298	ESTs Highly similar to PUTATIVE 2-HYDROXYACID DEHYDROGENASE IN BISC-CSPA INTERGENIC REGION [Escherichia coli]	
11858	5	AA262308	Hs.106385	ESTs	
29450	5	H80865	Hs.11026	Phosphatidylinositol glycan class F	
37294	5	AA450127	Hs.110571	ESTs Highly similar to MYELOID DIFFERENTIATION PRIMARY RESPONSE PROTEIN MYD118 [Mus musculus]	

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FIGURE 7 (CONT.)

35170	5	AA397830	Hs.98347	ESTs Weakly similar to rmp-1 [H.sapiens]
23201	5	T40652	Hs.8279	ESTs
27012	5	AA308913	Hs.45231	ESTs
28787	5	D45808	Hs.83792	Surfactant pulmonary-associated protein D
17777	5	AA146834	Hs.62788	ESTs Weakly similar to hypothetical L1 protein [H.sapiens]
20588	5	N58009	Hs.38218	ESTs
20356	5	N39453	Hs.27371	ESTs
23375	5	T59870	Hs.10615	EST
17030	5	AA070188	EST - RC_AA070188	
30752	5	N52340	Hs.118084	EST
25808	5	AA149228	Hs.95821	Human osteoclast stimulating factor mRNA complete cds
31345	5	N87268	Hs.50139	ESTs
30784	5	N52857	Hs.47558	ESTs
13707	5	AA460281	Hs.14697	ESTs
25199	5	H25751	Hs.57082	EST
39003	4	AA609920	Hs.112785	EST
41529	4	R54458	Hs.2899	Glypican 1
3151	4	M83652	Hs.53155	Properdin P factor complement
33134	4	W61264	Hs.57829	ESTs
29186	4	H24458	Hs.85053	Homo sapiens clone 24440 mRNA sequence
12863	4	AA425782	Hs.27573	ESTs
11949	4	AA279827	Hs.125035	ESTs
31925	4	N92924	Hs.125032	ESTs
35258	4	AA398428	Hs.97628	ESTs
39838	4	H27218	Hs.107635	ESTs
30796	4	N53046	Hs.91148	ESTs Moderately similar to IIII ALU SUBFAMILY J WARNING ENTRY IIII [H.sapiens]
19464	4	H24458	Hs.32085	EST
42486	4	W68410	Hs.106857	Calbindin 2 (29kD calretinin)
34274	4	AA236352	Hs.110821	ESTs
37848	4	AA459917	Hs.99506	EST
3169	4	M85085	Hs.693	Cleavage stimulation factor 3' pre-RNA subunit 2 64kD
10326	4	R96417	Hs.107795	ESTs
15063	4	U56814	Hs.88646	Homo sapiens DNase gamma mRNA complete cds
23571	4	T80628	Hs.108169	ESTs
14377	4	AA599583	Hs.15289	ESTs Weakly similar to HSM-2 [H.sapiens]
22255	4	R56239	Hs.6656	ESTs
36820	4	AA435968	Hs.98849	ESTs Weakly similar to thioraxoid [D.melanogaster]
35063	4	AA358015	Hs.99998	EST
12376	4	AA399271	Hs.19510	ESTs
31406	4	N88163	Hs.49455	EST

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FIGURE 7 (CONT.)

27430	4	AA429028	Hs.42678	ESTs	Moderately similar to IIII ALU SUBFAMILY SB WARNING ENTRY IIII [H.sapiens]
30352	4	N40170	Hs.45046	ESTs	
30599	4	N50039	Hs.47004	ESTs	
27894	4	AA460319	Hs.48469	ESTs	
31844	4	N90218	Hs.54607	ESTs	
24935	4	AFEX	AFEX-HUMGAPDH/M33187_M		
40906	4	N68829	Hs.131510	ESTs	
35220	4	AA398246	Hs.37594	ESTs	
10024	4	N94832	Hs.121699	ESTs	
4238	4	U33053	Hs.2409	Human lipid-activated protein kinase PRK1 mRNA complete cds	
26558	4	AA256396	Hs.88156	EST	
24716	4	Z38734	Hs.22550	ESTs	
19243	4	II13539	Hs.31222	ESTs	
41844	4	TI5833	Hs.100227	EST	
39774	4	HI17948	Hs.106311	Homo sapiens DGS-A mRNA 3' end	
20111	4	N21380	Hs.25497	H.sapiens mRNA for ROX protein	
24008	4	T98337	Hs.18824	ESTs	
8316	4	AA410529	Hs.30732	ESTs	
35072	4	AA358738	EST - RC_AA358738		
39784	4	H21819	Hs.14896	Homo sapiens clone 24580 mRNA sequence	
1517	4	J04501	Hs.772	Glycogen synthase 1 (muscle)	
9164	4	D38081	Hs.89887	Thromboxane A2 receptor	
35027	4	AA349998	Hs.96937	ESTs	
35185	4	AA398015	Hs.87590	Unlabeled	
25570	4	AA278425	Hs.85428	ESTs Weakly similar to hypothetical L1 protein [H.sapiens]	
19759	4	H54352	Hs.36873	ESTs	
34310	4	AA243416	Hs.75470	Homo sapiens mRNA expressed in osteoblast complete cds	
39961	4	H57317	Hs.108161	ESTs	
23249	4	T47919	Hs.8749	ESTs	
19119	4	H09077	Hs.30895	EST	
14158	4	AA480182	Hs.118598	ESTs	
22866	4	R99938	Hs.36189	EST	
16935	4	AA059392	Hs.66791	ESTs	
41950	4	T33137	Hs.7967	ESTs	
20404	4	N46594	Hs.30881	Homo sapiens liprin-alpha2 mRNA complete cds	
18406	4	AA227962	Hs.112075	ESTs Weakly similar to reverse transcriptase [M.musculus]	
10560	4	AA031308	Hs.24341	ESTs	
26098	4	AA242831	Hs.87506	ESTs	
34360	4	AA251547	Hs.104358	EST	
16830	4	AA054222	Hs.40400	ESTs	

FIGURE 7 (CONT.)

32668	4	T69284	Hs.2314	Mannose-binding lectin soluble (opsonic defect)
32912	4	W38051	EST - RC_W38051	
16230	4	AA011549	ESTs	
29696	4	H87909	ESTs	
8232	4	AA397529	EST - AA397529	
25584	4	AA112320	ESTs	
30878	4	N56892	ESTs	
40579	4	N34524	ESTs	
8026	4	AA301842	ESTs	Weakly similar to reverse transcriptase homolog [H.sapiens]
3094	4	M77481	Hs.105189	Human antigen (MAGE-1) gene complete cds
17480	4	AA121974	EST - RC_AA121974	
15766	4	W65777	ESTs	
34865	4	AA299903	ESTs	
29779	4	N20290	ESTs	
6547	4	X95808	Hs.9568	Human mRNA for KIAA0385 gene complete cds
24479	4	W96222	Hs.34192	ESTs
16135	4	AA004805	Hs.63668	Human Toll-like receptor 2 (TLR2) mRNA complete cds
11098	4	AA151243	ESTs	
14388	4	AA599742	Hs.21600	ESTs
36078	4	AA417275	Hs.98214	ESTs
23440	4	T65566	Hs.12859	ESTs
20863	4	N69989	Hs.19187	ESTs
20347	4	N35117	Hs.12250	ESTs
7795	4	AA247455	Hs.15220	ESTs
10729	4	AA054087	Hs.18858	ESTs
12734	4	AA419200	Hs.5737	ESTs
24446	4	W93119	Hs.19512	ESTs
30734	4	N52083	Hs.47418	EST
20841	4	N62353	Hs.109685	ESTs
21183	4	R06769	Hs.19795	ESTs
18138	4	AA192757	Hs.131687	ESTs
35310	4	AA398662	Hs.97302	ESTs
39497	4	D80154	Hs.56340	ESTs
29868	4	N22343	Hs.43145	ESTs
8707	4	AA479995	Hs.76862	Homo sapiens mRNA for KIAA0583 protein partial cds
18472	4	AA233299	Hs.72158	ESTs
24720	4	Z39754	Hs.23236	ESTs
40825	4	N63923	Hs.102746	ESTs
15375	4	W26395	Hs.56876	ESTs
32869	4	W35211	Hs.54801	ESTs

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FIGURE 7 (CONT.)

4641	4	US2426	Hs.74597	Homo sapiens GOK (STIM1) mRNA complete cds
11786	4	AA258616	Hs.31707	ESTs
21571	4	R33841	Hs.24709	ESTs Highly similar to NUCLEOLYSIN TIA-1 [Homo sapiens]
1600	4	K03474	EST - K03474	ESTs
21103	4	R01068	Hs.14603	ESTs
22993	4	T16358	Hs.108443	ESTs
38666	4	AA599661	Hs.103849	ESTs
27148	4	AA406231	Hs.100113	Human mRNA for KIAA0381 gene partial cds
26680	4	D20261	Hs.80067	ESTs
36397	4	AA426372	Hs.105804	Human mRNA for histone H1x complete cds
26915	4	AA330634	EST - RC_AA330634	ESTs
6912	4	Z35278	Hs.25336	H.sapiens PEBP2aC1 acute myeloid leukaemia mRNA
31825	4	N89848	Hs.54543	ESTs
10763	4	AA057620	Hs.30607	ESTs
17007	4	AA069696	Hs.67317	ESTs
33439	4	W86445	Hs.56844	ESTs
27657	4	AA447612	Hs.60435	ESTs
26288	4	AA253393	Hs.87734	ESTs
8235	4	AA397616	Hs.107245	ESTs Moderately similar to potassium channel protein Raw3 [R.norvegicus]
12114	4	AA287097	Hs.25114	ESTs
879	4	D88155	Hs.97196	Human steroidogenic factor 1 mRNA complete cds
30793	4	N52978	Hs.51919	Plasminogen-like protein
13522	4	AA454115	Hs.6000	ESTs
20819	4	N88730	Hs.12160	ESTs
20019	4	H94266	Hs.9451	ESTs
32396	4	R95778	Hs.93008	EST
38162	4	AA487165	Hs.105706	EST
8487	4	AA442669	EST - AA442669	ESTs
18444	4	AA232646	Hs.68061	ESTs
16183	4	AA010070	Hs.60339	EST
33047	4	W49755	Hs.89359	ESTs Moderately similar to type Ia hair keratin a3 [H.sapiens]
14797	4	S82769	Hs.104133	GABAA receptor gamma 3 subunit [human fetal brain mRNA Partial 1535 nt]
26107	3	AA243172	Hs.87619	ESTs
24421	3	W82001	Hs.120969	ESTs
27665	3	AA447759	Hs.134724	ESTs
19154	3	H10047	Hs.22515	ESTs
10933	3	AA121380	Hs.27567	ESTs Weakly similar to similar to alpha-13-mannosyl-glycoprotein beta-1 2-N-acetylglucosaminyltransferase [C.elegans]
7254	3	AA074897	EST - AA074897	ESTs
18684	3	F04262	Hs.22137	ESTs
40997	3	N77904	Hs.44380	ESTs

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FIGURE 7 (CONT.)

14971	3	U10493	Hs.438	Human Mox1 protein (MOX1) mRNA complete cds
11217	3	AA180487	Hs.62440	ESTs
16782	3	AA047265	Hs.82582	Homo sapiens mRNA for osteoblast specific cysteine-rich protein complete cds
21477	3	R26054	Hs.23531	ESTs
21382	3	R16896	Hs.89615	PROTEIN KINASE C THETA TYPE
19508	3	H28966		EST - RC_H28966
30301	3	N36174	Hs.2507	5-HYDROXYTRYPTAMINE 2B RECEPTOR
21553	3	R33005	Hs.23153	ESTs Weakly similar to ETX1 (alternatively spliced) [H.sapiens]
6102	3	X70340	Hs.2023	Transforming growth factor alpha
23502	3	T70580	Hs.13759	ESTs
8333	3	AA412620	Hs.4248	ESTs
30500	3	N46329	Hs.30490	ESTs Highly similar to HYPOTHETICAL 70.7 KD PROTEIN F09C8.3 IN CHROMOSOME III [Caenorhabditis elegans]
21431	3	R22057	Hs.23336	ESTs
35920	3	AA412290	Hs.98124	ESTs
12065	3	AA283907	Hs.110480	Homo sapiens clone 23837 mRNA sequence
19156	3	H10068	Hs.25924	Homo sapiens clone 24468 mRNA sequence
24844	3	Z41301	Hs.23539	ESTs
33178	3	W68846	Hs.141719	EST
2062	3	L36818	Hs.75339	Inositol polyphosphate phosphatase-like protein 1 (51C protein)
15327	3	W23474	Hs.23352	ESTs
16874	3	F10565	Hs.12345	ESTs
9039	3	C02049	Hs.106291	ESTs
37470	3	AA454935	Hs.96568	ESTs
19167	3	H10841	Hs.22928	ESTs
34868	3	AA303078	Hs.94479	Human GT334 protein (GT334) gene mRNA complete cds
30591	3	N49952	Hs.138717	ESTs
26997	3	AA398468	Hs.93090	ESTs
18547	3	F03004	Hs.27109	ESTs
17867	3	AA157291	Hs.72183	ESTs
15280	3	W07019	Hs.35088	ESTs
20465	3	N51599	Hs.14633	ESTs
11047	3	AA142849	Hs.22660	ESTs
19451	3	H23747	Hs.31697	ESTs
41621	3	R69233	Hs.101504	ESTs
2822	3	M55621	Hs.117946	N-acetylglucosaminyltransferase I
28675	3	D20188	Hs.74876	ESTs
13928	3	AA478441	Hs.11590	ESTs
28473	3	H83694	Hs.40478	ESTs
25829	3	AA151621	Hs.110964	ESTs
28532	3	C20680	Hs.68513	EST

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FIGURE 7 (CONT.)

32376	3	R91391	Hs.64391	ESTs	
12064	3	AA283648	Hs.11387	ESTs	Weakly similar to KIAA0009 [H.sapiens]
15547	3	W32012	Hs.29353	ESTs	
40284	3	H95073	Hs.108734	ESTs	Highly similar to HYPOTHETICAL 55.1 KD PROTEIN IN FAB1-PES4 INTERGENIC REGION [Saccharomyces cerevisiae]
22861	3	R99595	Hs.36152	ESTs	
15525	3	W28763	Hs.16349	ESTs	Homo sapiens KIAA0431 mRNA partial cds
17968	3	AA167496	Hs.72695	EST	
3836	3	U12707	Hs.2157	EST	Wiskott-Aldrich syndrome (eczema-thrombocytopenia)
4528	3	U48251	Hs.75871	ESTs	Homo sapiens protein kinase C-binding protein RACK7 mRNA partial cds
29784	3	N20468	Hs.42849	ESTs	Weakly similar to line-1 protein ORF2 [H.sapiens]
7892	3	AA262100	EST - AA262100	ESTs	
15279	3	W05746	Hs.133302	ESTs	
42064	3	T63364	Hs.9225	ESTs	Highly similar to FIBRINOGEN-LIKE PROTEIN A PRECURSOR [Parastichopus porvimensis]
17943	3	AA165117	Hs.20508	ESTs	
4596	3	U50743	Hs.19520	ESTs	Sodium/potassium ATPase gamma subunit
16421	3	AA022541	Hs.61146	ESTs	
4914	3	U67611	EST - U67611	EST	
38171	3	AA487301	Hs.105713	EST	
20168	3	N24106	Hs.2759	ESTs	Cartilage linking protein 1
18791	3	F09892	Hs.12575	ESTs	
24281	3	W79773	Hs.16511	ESTs	
13996	3	AA480907	Hs.15769	ESTs	
20583	3	N57797	Hs.34421	ESTs	
37181	3	AA448158	Hs.99152	EST	
21450	3	R23146	Hs.23466	ESTs	
19834	3	H44866	Hs.31597	ESTs	
10163	3	R54534	Hs.7898	EST	Homo sapiens clone 23938 mRNA sequence
7059	3	Z96810	EST - Z96810	ESTs	
25762	3	AA136066	Hs.91797	ESTs	Retinoblastoma-binding protein 1[alternative products]
27426	3	AA428900	Hs.92897	ESTs	
29023	3	F03302	EST - RC_F09302	EST	
10989	3	AA132366	Hs.8023	EST	Homo sapiens mRNA for SPOP
6587	3	X97748	EST - X97748	ESTs	
8722	3	AA481309	Hs.30204	ESTs	
21476	3	R26065	Hs.23523	ESTs	
14096	3	AA487568	Hs.8135	ESTs	
35392	3	AA399562	Hs.97568	ESTs	
28608	3	C21509	Hs.112774	ESTs	
13350	3	AA449297	Hs.8944	ESTs	Weakly similar to type 1 procollagen C-proteinase enhancer protein precursor [H.sapiens]
41202	3	R12808	Hs.113619	ESTs	

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FIGURE 7 (CONT.)

15612	3	W51955	Hs.73372	ESTs	
33930	3	AA169539	Hs.95870	ESTs	
34215	3	AA233855	Hs.104252	UTROPIlin	
19208	3	H11734	Hs.110454	ESTs	Weakly similar to coded for by C. elegans cDNA cm10e3 [C.elegans]
24047	3	W15386	Hs.26750	ESTs	
14852	3	T52059	Hs.100383	ESTs	Highly similar to C-1-TETRAHYDROFOLATE SYNTHASE CYTOPLASMIC [Rattus norvegicus]
27815	3	AA455370	Hs.59729	ESTs	
22610	3	R81173	Hs.11482	ESTs	Highly similar to F11 antigen [H.sapiens]
37510	3	AA455896	Hs.2699	Glypican 1	
37825	3	AA470073	Hs.104836	ESTs	
13321	3	AA448238	Hs.16714	ESTs	
25999	3	AA235375	Hs.87421	EST	
9738	3	M13150	Hs.99500	MAST oncogene	
16248	3	AA013125	Hs.40871	ESTs	
27582	3	AA442856	Hs.61979	ESTs	Moderately similar to THREONYL-TRNA SYNTHETASE CYTOPLASMIC [H.sapiens]
16546	3	AA029452	Hs.95162	ESTs	
16981	3	AA064859	EST - RC_AA064859		
22128	3	R51021	Hs.23161	EST - RC_AA064859	Homo sapiens retinoic acid hydroxylase mRNA complete cds
23312	3	T54617	EST - RC_T54617		
16783	3	F09741	Hs.124205	ESTs	
10308	3	R86920	Hs.127585	ESTs	
22518	3	R71892	Hs.25996	ESTs	Highly similar to 40S RIBOSOMAL PROTEIN S27A [Homo sapiens Cavia porcellus]
8255	3	AA400226	Hs.25024	ESTs	Weakly similar to estrogen-responsive finger protein efp [H.sapiens]
16361	3	AA019218	Hs.40550	ESTs	Moderately similar to proto-cadherin 3 [R.norvegicus]
5453	3	X02910	Hs.2037	Tumor necrosis factor	
22509	3	R71383	Hs.29190	ESTs	
20055	3	H98657	Hs.27291	ESTs	
31091	3	N63076	Hs.138746	EST	
39050	3	AA610112	Hs.124849	ESTs	
2493	3	M22919	Hs.77365	MYOSIN LIGHT CHAIN ALKALI SMOOTH-MUSCLE ISOFORM	
30159	3	N32623	Hs.44069	ESTs	
28913	3	F01580	Hs.22583	ESTs	Highly similar to co-repressor protein [M.musculus]
12257	3	AA350030	Hs.4221	ESTs	
359	3	D26350	Hs.75119	Human mRNA for type 2 inositol 145-bisphosphate receptor complete cds	
23587	3	T81358	Hs.14906	ESTs	
14323	3	AA598575	Hs.12851	ESTs	
27231	3	AA416936	Hs.7491	Homo sapiens methionine synthase reductase (MTRR) mRNA complete cds	
34814	3	AA338728	Hs.133096	ESTs	
21233	3	R08359	Hs.19308	ESTs	
22650	3	T86475	Hs.16193	ESTs	

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FIGURE 7 (CONT.)

14236	3	AA496891	Hs.5011	ESTs	Weakly similar to The h1237 gene product is related to S.pombe rad21 gene product. [H.sapiens]
17617	3	AA131394	Hs.44572	ESTs	Weakly similar to The KIAA0147 gene product is related to adenyl cyclase. [H.sapiens]
24594	3	Z38804	Hs.22555	ESTs	Highly similar to OPIOID BINDING PROTEIN/CELL ADHESION MOLECULE PRECURSOR [Bos taurus]
7426	3	AA095895	Hs.111818	ESTs	Highly similar to OPIOID BINDING PROTEIN/CELL ADHESION MOLECULE PRECURSOR [Bos taurus]
34871	3	AA300151	Hs.125146	ESTs	Highly similar to OPIOID BINDING PROTEIN/CELL ADHESION MOLECULE PRECURSOR [Bos taurus]
17982	3	AA167051	Hs.83525	ESTs	Human brain mRNA homologous to 3'UTR of human CD24 gene partial sequence
24337	3	W86007	Hs.8876	ESTs	Human brain mRNA homologous to 3'UTR of human CD24 gene partial sequence
22589	3	R79580	Hs.29874	ESTs	Human brain mRNA homologous to 3'UTR of human CD24 gene partial sequence
24554	3	Z38522	Hs.27092	EST	Human brain mRNA homologous to 3'UTR of human CD24 gene partial sequence
22348	3	R61750	Hs.6136	ESTs	Human brain mRNA homologous to 3'UTR of human CD24 gene partial sequence
30217	3	N34288	Hs.44554	EST	Human brain mRNA homologous to 3'UTR of human CD24 gene partial sequence
10210	3	R67468	Hs.131828	ESTs	Human brain mRNA homologous to 3'UTR of human CD24 gene partial sequence
22156	3	R52145	Hs.25894	ESTs	Human brain mRNA homologous to 3'UTR of human CD24 gene partial sequence
16404	3	AA021284	Hs.60554	ESTs	Moderately similar to sodium-calcium exchanger form 3 [R.norvegicus]
29310	3	H66842	Hs.88729	ESTs	Moderately similar to sodium-calcium exchanger form 3 [R.norvegicus]
15956	3	Z21217	Hs.77695	ESTs	Human mRNA for KIAA0008 gene complete cds
9758	3	M25393	Hs.127610	ESTs	Human mRNA for KIAA0008 gene complete cds
20917	3	N72295	Hs.18004	ESTs	Acyl-Coenzyme A dehydrogenase C-2 to C-3 short chain
22964	3	T10362	Hs.57358	ESTs	Acyl-Coenzyme A dehydrogenase C-2 to C-3 short chain
9806	2	M79462	Hs.89633	ESTs	Acyl-Coenzyme A dehydrogenase C-2 to C-3 short chain
29807	2	N21031	Hs.42630	ESTs	Acyl-Coenzyme A dehydrogenase C-2 to C-3 short chain
39646	2	H02255	Hs.7268	ESTs	Acyl-Coenzyme A dehydrogenase C-2 to C-3 short chain
22733	2	R92181	Hs.34558	EST	Acyl-Coenzyme A dehydrogenase C-2 to C-3 short chain
23233	2	T41177	Hs.8410	ESTs	Acyl-Coenzyme A dehydrogenase C-2 to C-3 short chain
18549	2	F01360	Hs.6092	ESTs	Acyl-Coenzyme A dehydrogenase C-2 to C-3 short chain
31992	2	N91968	Hs.39635	ESTs	Acyl-Coenzyme A dehydrogenase C-2 to C-3 short chain
18661	2	F10452	Hs.12254	ESTs	Acyl-Coenzyme A dehydrogenase C-2 to C-3 short chain
24553	2	Z38521	Hs.9428	ESTs	Acyl-Coenzyme A dehydrogenase C-2 to C-3 short chain
19289	2	H18568	Hs.23748	ESTs	Acyl-Coenzyme A dehydrogenase C-2 to C-3 short chain
14185	2	AA480911	Hs.22393	EST	Acyl-Coenzyme A dehydrogenase C-2 to C-3 short chain
30723	2	N51935	Hs.47374	EST	Acyl-Coenzyme A dehydrogenase C-2 to C-3 short chain
34031	2	AA192514	Hs.83577	ESTs	Acyl-Coenzyme A dehydrogenase C-2 to C-3 short chain
18434	2	AA232206	Hs.50743	ESTs	Acyl-Coenzyme A dehydrogenase C-2 to C-3 short chain
14647	2	D20378	Hs.30731	EST	Acyl-Coenzyme A dehydrogenase C-2 to C-3 short chain
41048	2	N92734	Hs.115985	ESTs	Acyl-Coenzyme A dehydrogenase C-2 to C-3 short chain
38157	2	AA488558	Hs.105702	EST	Acyl-Coenzyme A dehydrogenase C-2 to C-3 short chain
33299	2	W73790	Hs.73803	ESTs	Acyl-Coenzyme A dehydrogenase C-2 to C-3 short chain
16816	2	AA035446	Hs.81783	ESTs	Acyl-Coenzyme A dehydrogenase C-2 to C-3 short chain
3276	2	M93718	Hs.76983	ESTs	Acyl-Coenzyme A dehydrogenase C-2 to C-3 short chain

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FIGURE 7 (CONT.)

33022	2	W46976	Hs.04667	EST	
31704	2	N75055	Hs.14632	ESTs	
38713	2	AA608577	Hs.112575	ESTs	
20396	2	N48293	Hs.12206	ESTs	
10310	2	R87373	Hs.75429	ESTs	
22388	2	R63895	Hs.1432	Protein Kinase C substrate 80K-H	
15936	2	Z11737	Hs.2664	Flavin-containing monooxygenase 4	
23667	2	T88826	Hs.142528	ESTs	
30903	2	N57730	Hs.48058	EST	
20938	2	N73988	Hs.37477	ESTs Weakly similar to No definition line found [C.elegans]	
5935	2	X62466	Hs.106338	CDW52 antigen (CAMPATH-1 antigen)	
19304	2	H16976	Hs.7973	ESTs	
8804	2	AB000463	Hs.16227	Homo sapiens mRNA for SH3 binding protein complete cds clone:RES4-23A	
41485	2	R49689	Hs.5260	ESTs Weakly similar to C08G8.3 [C.elegans]	
24685	2	Z39406	Hs.11797	ESTs Moderately similar to retinoid X receptor interacting protein [M.musculus]	
25403	2	AA063316	EST - RC_AA063316		
35773	2	AA406219	Hs.104747	ESTs	
16911	2	AA464287	Hs.24912	Homo sapiens bicuculal-D (BICD) mRNA complete cds	
42315	2	AA058658	Hs.60669	ESTs	
40632	2	T97353	EST - RC_T97353		
15722	2	N45221	EST - RC_N45221		
14842	2	W79046	Hs.15250	Homo sapiens DBI-related protein mRNA complete cds	
36088	2	T47519	EST - T47519		
15527	2	AA417344	Hs.98220	ESTs Moderately similar to located at OATL1 [H.sapiens]	
10302	2	W28788	Hs.63260	Phosphodiesterase 9A cGMP-specific rod alpha	
21243	2	R84933	Hs.133217	ESTs	
7759	2	R08773	Hs.20231	ESTs	
31872	2	AA234687	Hs.64147	ESTs Weakly similar to F59C6.4 [C.elegans]	
26799	2	N74336	Hs.91681	ESTs	
25857	2	AA284722	Hs.89121	ESTs	
16695	2	AA156504	Hs.95875	EST	
964	2	AA043115	Hs.9452	ESTs Weakly similar to ORF YDL077c [S.cerevisiae]	
12439	2	HG1804	EST - HG1804-HT1829		
18999	2	AA014452	Hs.32060	ESTs	
24223	2	H41235	Hs.109668	ESTs	
21052	2	W70158	Hs.28698	ESTs	
17463	2	N93764	Hs.10175	ESTs Weakly similar to hypothetical protein [H.sapiens]	
28949	2	AA121338	EST - RC_AA121338		
34140	2	F03032	Hs.65826	ESTs Weakly similar to reverse transcriptase homolog [H.sapiens]	
	2	AA215637	Hs.104188	ESTs	

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FIGURE 7 (CONT.)

7465	2	AA120886	EST - AA120886	
17376	2	AA102425	EST - RC_AA102425	
5130	2	U79288	Hs.85953	Homo sapiens clone 24440 mRNA sequence
30041	2	N27628	Hs.132744	Homo sapiens clone 24525 mRNA sequence
10684	2	H48488	Hs.143798	ESTs
8165	2	AA359093	EST - AA359093	
19202	2	H11509	Hs.22482	ESTs
20439	2	N50785	Hs.13269	ESTs
10431	2	AA011310	Hs.3757	ESTs
29707	2	H98244	Hs.42519	ESTs
39868	2	H37909	Hs.107680	ESTs
8988	2	C00185	Hs.10444	ESTs
41350	2	R40442	Hs.75952	Glutathione S-transferase M5
13121	2	AA436156	Hs.110837	ESTs
15747	2	W86550	Hs.132188	ESTs
18674	2	F03989	Hs.18995	ESTs Weakly similar to KIAA0412 [H.sapiens]
914	2	HG1019-	EST - HG1019-HT1019	
23804	2	T91086	EST - RC_T91086	
26556	2	AA276089	Hs.88550	ESTs
8567	2	AA453381	Hs.104900	ESTs
30457	2	N47685	Hs.64607	Human RACH1 (RACH1) mRNA complete cds
21975	2	R45441	Hs.23710	ESTs
17452	2	AA120766	Hs.70724	ESTs
31958	2	N93495	Hs.54960	ESTs
31495	2	N98850	Hs.49759	ESTs
32490	2	T16389	Hs.81248	Human RNA-binding protein CUG-BP1/NAB50 (NAB50) mRNA complete cds
39174	2	AA621067	Hs.112944	ESTs
21572	2	R34073	Hs.89740	Zinc finger protein 136 (clone pHZ-20)
15914	2	Y09846	Hs.81972	V-akt avian sarcoma viral oncogene homolog
12014	2	AA281769	Hs.7214	Human Hpast (IPAST) mRNA complete cds
39777	2	H18412	Hs.75253	Human clone ID 193225 NAD (H)-specific isocitrate dehydrogenase gamma subunit mRNA alternatively spliced partial cds
9484	2	H50178	Hs.108081	ESTs Highly similar to PROTEIN PHOSPHATASE PP2A 55 KD REGULATORY SUBUNIT NEURONAL ISOFORM [Oryzotagus cuticulus]
19147	2	H09751	Hs.117619	ESTs
36276	2	AA424179	Hs.124027	ESTs
16475	2	AA025903	Hs.57911	ESTs
21304	2	R11208	Hs.20755	ESTs
11199	2	AA176446	Hs.10024	ESTs
18093	2	AA187955	Hs.85564	ESTs
19190	2	H11274	Hs.31040	EST
15710	2	W76399	EST - W76399	

FIGURE 7 (CONT.)

18707	2	F04627	Hs.23540	ESTs	
6477	2	X91504	Hs.64904	Transcription factor COUP 2 (a.k.a. ARP1)	
20823	2	N68869	Hs.15118	ESTs	
16336	2	AA018601	Hs.75649	EXTRACELLULAR SIGNAL-REGULATED KINASE 3	
19680	2	H48457	Hs.35104	ESTs	
24833	2	Z41087	Hs.19066	ESTs	
24058	2	W23709	Hs.109047	ESTs	
29180	2	AA251230	Hs.112272	ESTs	
37177	2	AA447988	Hs.7765	ESTs	
14047	2	AA482597	Hs.26054	ESTs	
10770	2	AA059883	Hs.22552	ESTs	
41094	2	T47601	Hs.138805	ESTs	
19217	2	I112243	EST - RC_H12243		
36532	2	AA429889	Hs.68882	Acroisin	
23378	2	T60072	Hs.10688	ESTs	
1450	2	J03071	Hs.115352	Growth hormone 1	
8007	2	AA293072	Hs.97283	ESTs Moderately similar to IIII ALI CLASS B WARNING ENTRY IIII [H.sapiens]	
17266	2	AA084723	Hs.24812	ESTs	
24819	2	Z40923	Hs.89491	DNA-BINDING PROTEIN A	
6532	2	X95325	Hs.86641	ESTs	
26850	2	AA287651	Hs.108788	ESTs	
34175	2	AA227523	EST - RC_AA282169		
34620	2	AA282169	Hs.77978	ESTs	
27085	2	AA402495	Hs.15420	ESTs	
20173	2	N24730	Hs.26419	EST - RC_AA129060	
17574	2	AA129060	Hs.44076	Homo sapiens clone 24510 mRNA sequence	
22330	2	R60920	Hs.19978	ESTs	
30070	2	N26696	Hs.44076	EST	
20487	2	N52322	Hs.19978	ESTs	
724	2	D63703	Hs.30729	Peroxisomal biogenesis factor 6	
4132	2	U27655	Hs.82294	Human RGP3 mRNA complete cds	
8557	2	AA432705	Hs.23954	ESTs Weakly similar to D2045.9 [C.elegans]	
33659	2	W95626	Hs.59718	EST	
13375	2	AA449716	Hs.5723	ESTs	
30891	2	N57007	Hs.94074	EST	
13988	2	AA480045	Hs.7934	ESTs	
22308	2	R59906	Hs.100530	ESTs	
23167	2	T33184	Hs.12840	Homo sapiens germline mRNA sequence	
20873	2	N70134	Hs.31476	ESTs	
7231	2	AA059327	Hs.6580	Homo sapiens clone 23718 mRNA sequence	

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FIGURE 7 (CONT.)

24582	2	Z38752	Hs.28530	ESTs	
11320	2	AA213867	Hs.22222	ESTs	
16388	2	AA020781	Hs.60847	ESTs	
24608	2	Z38886	Hs.25046	ESTs	
7809	2	AA248085	Hs.12469	Homo sapiens clone 23930 mRNA sequence	
13163	2	AA437225	Hs.22410	ESTs	
20549	2	N54991	Hs.37581	ESTs	Weakly similar to transposon LRE2 reverse transcriptase homolog [H.sapiens]
1139	2	HG3227-	EST - HG3227-HT3404		
35572	2	AA401489	EST - RC_AA401489		
6964	2	Z49105	Hs.137591	H.sapiens HD21 mRNA	
27704	2	AA449704	Hs.77637	Homo box A4	
3196	2	W69725	Hs.10711	ESTs	
30963	2	N59373	Hs.26812	ESTs	
13988	2	AA476637	Hs.24441	ESTs	
16164	2	AA007509	Hs.75395	Human mRNA for TPRD complete cds	
18083	2	AA181928	Hs.70954	Homo sapiens mRNA for foxA7 protein	
20107	2	N21207	Hs.129942	ESTs Moderately similar to RETROVIRUS-RELATED POLYPROTEIN [Mus musculus]	
23004	2	T16556	Hs.6053	ESTs	
16238	2	AA011678	Hs.40470	ESTs	
18189	2	AA195042	Hs.85978	ESTs	
37567	2	AA457377	EST - RC_AA457377		
2174	2	L42611	Hs.11759	KERATIN TYPE II CYTOSKELETAL 6D	
38958	2	AA609707	Hs.112751	ESTs	
37919	2	AA478162	Hs.104965	ESTs	
28905	2	D81123	Hs.57475	ESTs	
33315	2	W74418	Hs.55410	ESTs	
7421	2	AA095600	EST - AA095600		
3745	2	U08117	Hs.80776	Human phospholipase c delta 1 mRNA complete cds	
19545	2	H37834	Hs.32699	ESTs	
21204	2	R07632	Hs.17949	ESTs	
8416	2	AA428531	EST - AA428531		
17589	2	AA128926	EST - RC_AA128926		
19572	2	H39195	Hs.22223	ESTs	
22760	2	R93714	Hs.33833	ESTs Highly similar to ALPHA-2-MACROGLOBULIN PRECURSOR [Homo sapiens]	
19354	2	H18829	Hs.121515	ESTs	
40618	2	N39565	Hs.108540	ESTs	
20913	2	N23708	Hs.43429	ESTs	
22571	2	R78565	Hs.138395	EST	
7598	2	AA174185	Hs.3354	Homo sapiens ezrin-radixin-moesin binding phosphoprotein-50 mRNA complete cds	
25385	2	AA050099	Hs.109727	ESTs	

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FIGURE 7 (CONT.)

14176	2	AA490620	Hs.11809	ESTs	
37400	2	AA453578	Hs.120994	ESTs	Weakly similar to T20D3.5 [C.elegans]
29487	2	H85120	Hs.80881		N-ACETYL-LACTOSAMINE SYNTHASE
10197	2	R64199	Hs.50785		Homo sapiens vesicle trafficking protein sec22b mRNA complete cds
322	2	D21241		EST - D21241_xpt1	
22224	2	R55192	Hs.25699	ESTs	
19488	2	H27675	Hs.25604	ESTs	
10568	2	AA029703	Hs.36574	ESTs	
10872	2	AA089357	Hs.15780	ESTs	Moderately similar to ATP-BINDING CASSETTE TRANSPORTER 2 [Mus musculus]
29987	2	N26172	Hs.43760	ESTs	
30799	2	N53143	Hs.64001	ESTs	
9638	2	L07592	Hs.106415		Human peroxisome proliferator activated receptor mRNA complete cds
21069	2	N98461	Hs.17706	ESTs	
27195	2	AA411473	Hs.65311	ESTs	
9241	2	D79565		EST - D79565	
9218	2	D81469	Hs.58896	ESTs	
22238	2	R55763	Hs.107287	ESTs	
7512	2	AA136389		EST - AA136389	
17438	2	AA115508	Hs.2780		Jun D proto-oncogene
24932	2	AFFX-		AFFX-HSAC07X00351_M	
28911	2	F01525	Hs.3786		Glutamate receptor metabotropic 3
10944	2	AA125969	Hs.34769	ESTs	Weakly similar to F35G12.9 [C.elegans]
42324	2	T98199	Hs.142702	ESTs	
34756	2	AA287665	Hs.0245	ESTs	
12743	2	AA421050	Hs.24545	ESTs	
21275	2	R10075	Hs.14890	ESTs	
13876	2	AA459389	Hs.26350		Homo sapiens mRNA for tyrosyl sulfotransferase-2
13009	2	AA430474	Hs.16466	ESTs	
7403	2	AA094921	Hs.79788	ESTs	
11151	2	AA159961	Hs.25819	ESTs	
35669	2	AA404707	Hs.54865	ESTs	
17701	2	AA135941	Hs.71626	ESTs	
18713	2	F04686	Hs.21782	ESTs	
24144	2	W52312	Hs.30303	ESTs	Highly similar to ZINC FINGER PROTEIN 45 [Homo sapiens]
30741	2	N52175	Hs.22222	ESTs	
23042	2	T23433	Hs.7105	ESTs	
18479	2	AA233483	Hs.87159	ESTs	
8314	2	AA410355	Hs.103081	ESTs	Highly similar to RIBOSOMAL PROTEIN S6 KINASE [Homo sapiens]
7990	2	AA291786	Hs.32822	ESTs	Weakly similar to HYPOTHETICAL PROTEIN KIAA0168 [H.sapiens]
10388	2	AA005355		EST - RC_AA005355	

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FIGURE 7 (CONT.)

9407	2	H20086	EST - H20086	
42791	2	AFX-	AFX-HUNGAPDH3197_M	
26302	2	AA255470	ESTs	
20722	1	N51924	Hs.88040	
24865	1	AFX-	Hs.47370	
38850	1	AA603262	AFX-Lyx-5	
13746	1	AA461300	EST - RC_AA603262	
6893	1	Z30843	ESTs	
31403	1	N68117	Hs.123123	H.sapiens mRNA for chloride channel (putative) 2139bp
17830	1	AA152312	Hs.41119	ESTs
10583	1	AA033874	Hs.72047	ESTs
20913	1	N72116	Hs.12035	ESTs
35607	1	AA022267	Hs.57435	Natural resistance-associated macrophage protein 2
9920	1	N44758	Hs.133475	ESTs Weakly similar to zinc finger protein [H.sapiens]
9468	1	H46074	Hs.141935	ESTs Weakly similar to transformation-related protein [H.sapiens]
29469	1	H82929	Hs.31562	ESTs
18121	1	AA191310	EST - RC_H82929	EST - RC_H82929
14705	1	D59382	Protein phosphatase 2 (formerly 2A) regulatory subunit A (PR 65) beta isoform	
16543	1	F04444	EST - RC_D59382	ESTs
16359	1	AA029430	Hs.6217	ESTs
40818	1	AA019197	Hs.61557	EST
35205	1	N63772	Hs.40763	ESTs
7831	1	AA388161	Hs.144550	Homo sapiens DNA sequence from PAC 434014 on chromosome 1q32.3-4.1. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydro
17794	1	AA249175	Hs.97602	ESTs
11347	1	AA161125	Hs.96334	ESTs Weakly similar to GOLIATH PROTEIN [Drosophila melanogaster]
17919	1	AA150260	Hs.72062	EST
22184	1	AA224245	Hs.26612	ESTs
14827	1	R53520	Hs.72384	EST
28091	1	T35288	Hs.102755	ESTs
28615	1	AA481788	Hs.80421	ESTs
17813	1	D59267	Hs.87593	ESTs
24655	1	AA151480	Hs.59782	ESTs
15611	1	Z39191	Hs.91202	ESTs
39598	1	H62865	Hs.27262	ESTs Weakly similar to Lph17p [S.cerevisiae]
15700	1	W73859	Hs.35098	ESTs
22045	1	R46905	Hs.38132	ESTs
36770	1	AA435753	Hs.78061	Homo sapiens mesoderm-specific basic-helix-loop-helix protein (POD1) mRNA complete cds
9877	1	N31127	Hs.24796	EST
22467	1	R68284	EST - RC_AA435753	EST - RC_AA435753
			Hs.40098	ESTs
			Hs.28399	ESTs

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FIGURE 7 (CONT.)

32400	1	R97176	Hs.110783	ESTs	
10802	1	AA069425	Hs.20573	ESTs	
23033	1	T17353	Hs.108894	Homo sapiens clone 23918 mRNA sequence	
17563	1	AA129856	EST - RC_AA129856		
14867	1	T58588	Hs.100419	ESTs	
20266	1	N32118	Hs.107365	ESTs Highly similar to THREONYL-TRNA SYNTHETASE CYTOPLASMIC [Homo sapiens]	
14447	1	AA609045	Hs.11759	ESTs	
37984	1	AA479819	EST - RC_AA479819		
12892	1	AA426521	Hs.18528	Homo sapiens mRNA for NA14 protein	
11970	1	AA280687	Hs.4069	ESTs	
19738	1	H53059	Hs.15548	ESTs	
14471	1	AA609346	Hs.20102	ESTs	
14855	1	T54762	Hs.9786	ESTs	
24725	1	Z39781	Hs.8004	Homo sapiens Duo mRNA complete cds	
5796	1	X55019	Hs.99975	Cholinergic receptor nicotinic delta polypeptide	
20259	1	N31598	Hs.12727	ESTs	
18441	1	AA232508	Hs.77480	ESTs	
18468	1	AA233177	Hs.87134	ESTs	
10164	1	R54743	Hs.19400	ESTs Weakly similar to MITOTIC MAD2 PROTEIN [S.cerevisiae]	
8830	1	AB002319	Hs.8663	Human mRNA for KIAA0321 gene partial cds	
15287	1	W07461	Hs.121559	ESTs Highly similar to DIPHTHINE SYNTHASE [Saccharomyces cerevisiae]	
16477	1	AA026031	Hs.61312	ESTs	
21969	1	R45334	Hs.21175	ESTs	
22340	1	R61522	Hs.26892	ESTs	
12884	1	AA426259	EST - RC_AA426259		
8682	1	AA477891	Hs.104478	ESTs	
22594	1	R70793	Hs.25900	ESTs	
19131	1	H09331	Hs.122791	ESTs	
17103	1	AA074997	EST - RC_AA074997		
35620	1	AA402493	Hs.10552	ESTs Highly similar to c-Jun leucine zipper interactive [M.musculus]	
35401	1	AA399593	Hs.97682	EST	
10901	1	AA112307	Hs.25224	ESTs	
19546	1	H37901	Hs.32706	ESTs	
15378	1	W26448	Hs.15071	ESTs Highly similar to VACUOLAR ATP SYNTHASE SUBUNIT D [Bos taurus]	
30292	1	N35978	Hs.82364	ESTs	
39087	1	AA620607	Hs.111591	ESTs	
37896	1	AA477463	Hs.77039	Ribosomal protein S28	
8836	1	AB002325	Hs.105917	Human mRNA for KIAA0327 protein complete cds	
18150	1	AA005428	Hs.60140	ESTs	
23955	1	T97467	Hs.18065	ESTs Weakly similar to alternatively spliced product using exon 13A [H.sapiens]	

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FIGURE 7 (CONT.)

37612	1	AA469939	Hs.105323	ESTs	
14782	1	S72370	Hs.89890	Pyruvate carboxylase	
23540	1	T79178	Hs.14463	ESTs	
41552	1	R58352	Hs.101253	Human mRNA for KIAA0286 gene complete cds	
21836	1	R42569	Hs.22444	EST	
11467	1	AA234089	Il.14593	ESTs	
18347	1	AA219230	Hs.86815	ESTs	
8215	1	AA389673	Hs.84344	ESTs Weakly similar to No definition line found [C.elegans]	
13505	1	W28366	Hs.7252	Human sapiens clone 24800 mRNA sequence	
22764	1	R93802	Hs.33687	ESTs	
14966	1	U07620	Hs.89661	Human MAP kinase mRNA complete cds	
24213	1	W69184	Hs.23973	ESTs	
8165	1	AA358888	Hs.104135	Human sapiens mRNA for DRIM protein	
32724	1	T90750	Hs.15230	ESTs Weakly similar to F25H2.2 [C.elegans]	
8212	1	AA386236	Hs.98757	Human sapiens transcription factor SUPT3H (SUPT3H) mRNA complete cds	
9834	1	M92269	Hs.22554	Homeo box B5 (2.1 protein)	
7229	1	AA059213	Hs.91898	ESTs	
15849	1	W58725	Hs.75074	H.sapiens mRNA for MAP kinase activated protein kinase	
42306	1	T96538	Hs.45080	Human K+ channel beta 1a subunit mRNA alternatively spliced complete cds	
9159	1	D31483	Hs.90062	Human sapiens clone 23565 unknown mRNA partial cds	
20040	1	H96712	Il.125198	ESTs	
42218	1	T86444	Hs.110095	ESTs	
15526	1	W28790	Hs.8124	ESTs	
17190	1	AA150182	Hs.42262	ESTs Weakly similar to HYPOTHETICAL 88.1 KO PROTEIN K02D10.1 IN CHROMOSOME III [C.elegans]	
17595	1	AA129529	Hs.71165	EST	
31314	1	N56866	Hs.49278	EST	
9777	1	M57888	Hs.95945	GRANZYME H PRECURSOR	
15373	1	W26376	Hs.74563	THY-1 MEMBRANE GLYCOPROTEIN PRECURSOR	
23547	1	T79448	Hs.14577	EST	
12076	1	AA284362	Hs.8448	ESTs Weakly similar to No definition line found [C.elegans]	
11956	1	AA279991	Hs.124691	ESTs	
15391	1	W26651	Hs.15961	ESTs	
9287	1	D82557	Hs.18104	ESTs	
16419	1	AA022466	Hs.81141	EST	
21713	1	R39930	Hs.21034	ESTs	
12805	1	AA427537	Hs.32419	ESTs	
30257	1	N34961	Hs.75873	H.sapiens mRNA for Zyxin	
28134	1	AA487622	Hs.64095	ESTs	
16380	1	AA019750	Hs.40787	ESTs Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [H.sapiens]	
10553	1	AA028904	Hs.33215	ESTs	

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FIGURE 7 (CONT.)

18053	1	AA180054	Hs.73677	ESTs	Weakly similar to IIII ALU SUBFAMILY SQ WARNING ENTRY IIII [H.sapiens]
39820	1	H24085	Hs.25443	ESTs	
7374	1	AA033378	Hs.101810	ESTs	
13109	1	AA435838	Hs.7985	ESTs	
19378	1	H19873	Hs.31670	ESTs	
24325	1	W84733	Hs.3978	ESTs	
22316	1	R60224	Hs.7065	ESTs	
24249	1	W73069	Hs.12600	ESTs	
16514	1	AA027948	Hs.44608	ESTs	
21421	1	R21741	Hs.23258	EST	
8397	1	AA428178	Hs.71725	ESTs	
8412	1	AA428090	Hs.26102	ESTs	
10072	1	R14782	Hs.31931	ESTs	
10349	1	AA001908	Hs.18180	ESTs	
14492	1	AA009635	Hs.27497	ESTs	
14930	1	T92512	EST	EST - T92512	
15681	1	X81001	Hs.141503	Small inducible cytokine AS (RANTES)	
16706	1	AA043800	Hs.62645	ESTs	
16744	1	AA045643	Hs.82868	EST	
16950	1	AA062980	Hs.65960	ESTs	
17836	1	AA155779	Hs.29759	ESTs	Weakly similar to IIII ALU SUBFAMILY SX WARNING ENTRY IIII [H.sapiens]
18834	1	F10207	Hs.13269	ESTs	
19178	1	H10992	Hs.100910	EST	
19767	1	H54720	Hs.35941	ESTs	
21341	1	R14959	Hs.21871	EST	Moderately similar to ninein [M.musculus]
21466	1	R24518	Hs.23674	EST	
21602	1	R36624	Hs.135137	ESTs	
21748	1	R40697	Hs.21250	EST	
21860	1	R43089	EST	EST - RC_R43089	
21891	1	R43590	Hs.13280	ESTs	
21937	1	R44508	Hs.22653	ESTs	
22006	1	R46244	Hs.23110	ESTs	
22054	1	R49116	Hs.25067	EST	
22222	1	R55042	Hs.105645	ESTs	
22292	1	R59385	Hs.141053	Homo sapiens bastrophin (VIM2) mRNA alternatively spliced product complete cds	
22383	1	R63453	Hs.23282	ESTs	
22446	1	R67259	Hs.25968	EST	
23103	1	T23839	Hs.7344	ESTs	
23972	1	T94562	Hs.17338	EST	
24291	1	W80642	Hs.16851	ESTs	

FIGURE 7 (CONT.)

24640	1	Z39086	Hs.21403	ESTs	
27519	1	AA435535	Hs.90695	ESTs	
32067	1	R06424	Hs.04896	ESTs	
32204	1	R44210	Hs.31440	EST	
32692	1	T79942	Hs.90330	ESTs	
33714	1	Z39430	Hs.65749	ESTs	
33733	1	Z39668	Hs.65782	ESTs	
33873	1	AFX-	AFX-DapX-3		
35434	1	AA400034	Hs.97760	EST	
35950	1	AA412498	Hs.104778	ESTs	
36463	1	AA428865	Hs.98563	EST	
36615	1	AA431469	Hs.98737	ESTs	
37329	1	AA452138	Hs.3781	Homo sapiens BAC clone RG118D07 from Tq31	
37700	1	AA461090	Hs.124826	EST	
38285	1	AA489840	Hs.105302	ESTs	
38887	1	AA509422	Hs.112705	EST	
38933	1	AA606606	Hs.112732	ESTs	
38994	1	H42037	Hs.114150	ESTs	
40244	1	H91660	Hs.30250	Homo sapiens short form transcription factor C-MAF (c-maf) mRNA complete cds	
40645	1	N47652	Hs.102624	EST	
40819	1	N63787	Hs.109304	ESTs	
41445	1	R45611	Hs.137696	ESTs	Weakly similar to IIII ALU SUBFAMILY SQ WARNING ENTRY IIII [H.sapiens]
41700	1	R85829	Hs.101863	EST	
41776	1	T03170	Hs.100165	EST	
13254	1	AA446587	Hs.6775	ESTs	Highly similar to ALANINE AMINOTRANSFERASE [Homo sapiens]
8171	1	AA362708	Hs.5009	ESTs	Weakly similar to mTERF [H.sapiens]
23030	1	T17291	Hs.9995	ESTs	
8406	1	AA427510	Hs.104287	ESTs	
16767	1	AA046650	Hs.40342	ESTs	
25010	1	AA005315	Hs.51282	ESTs	
14629	1	T35529	EST - T35529		
34584	1	AA280934	Hs.132872	ESTs	Moderately similar to IIII ALU SUBFAMILY SC WARNING ENTRY IIII [H.sapiens]
15909	1	Y07868	Hs.38842	H.sapiens mRNA for Pltn isolate 1	
9922	1	N44971	Hs.107164	Spectrin beta non-erythrocytic 1	
15381	1	W25456	Hs.107725	ESTs	Weakly similar to LIS-1 protein [H.sapiens]
22168	1	R53024	Hs.25985	ESTs	
11690	1	AA252762	Hs.31235	ESTs	
22999	1	T16510	Hs.6624	ESTs	
24490	1	Z38153	Hs.26921	ESTs	
19993	1	H91255	Hs.15227	ESTs	

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FIGURE 7 (CONT.)

19689	1	H48625	Hs.36291	ESTs	
12450	1	AA01809	Hs.19855	ESTs	
24366	1	W87260	Hs.124800	ESTs	
22565	1	R77631	Hs.29126	ESTs	
18872	1	F10542	Hs.12292	ESTs	
15358	1	W26105	Hs.8961	ESTs	
24186	1	W61319	Hs.37482	ESTs	Highly similar to COATOMER ZETA SUBUNIT [Bos taurus]
23863	1	T93078	Hs.17265	ESTs	
23846	1	T93078	Hs.17117	EST	
15143	1	U79257	Hs.65921	Human clone 23932 mRNA sequence	
9711	1	L44334	Hs.10432	ESTs	Weakly similar to BENOMYL/METHOTREXATE RESISTANCE PROTEIN [Candida albicans]
22544	1	R74235	Hs.60844	Homo sapiens mRNA for KIAA0573 protein partial cds	
41506	1	R52088	EST - RC_R52088	EST - RC_R52088	
39345	1	C21105	Hs.7768	Homo sapiens FGF-1 intracellular binding protein (FIDP) mRNA complete cds	
22272	1	R56922	Hs.26590	ESTs	
16434	1	AA024494	Hs.81199	ESTs	
17255	1	AA084412	EST - RC_AA084412	EST - RC_AA084412	
22692	1	R88711	Hs.34183	ESTs	
38830	1	AA609189	Hs.116415	ESTs	
9179	1	D50312	Hs.102308	Human mRNA for uKATP-1 complete cds	
42547	1	W73946	EST - RC_W73946	EST - RC_W73946	
36195	1	AA421144	EST - RC_AA421144	EST - RC_AA421144	
29355	1	H70121	Hs.79592	ESTs	
34608	1	AA281765	Hs.104441	ESTs	
20779	1	N67553	Hs.16917	ESTs	
11081	1	AA149826	Hs.34274	ESTs	
12151	1	AA291269	Hs.24642	ESTs	
39935	1	H52379	EST - RC_H52379	EST - RC_H52379	
7157	1	AA037199	Hs.9899	ESTs	
17858	1	AA156596	Hs.72146	ESTs	
34885	1	AA302831	Hs.57732	Homo sapiens p38beta2 MAP kinase mRNA complete cds	
16445	1	AA232648	Hs.87068	ESTs	
22524	1	R72597	EST - RC_R72597	EST - RC_R72597	
19224	1	H12448	Hs.124570	ESTs	Weakly similar to unknown protein [H.sapiens]
18803	1	F09988	Hs.5244	ESTs	
13810	1	AA454669	Hs.23294	ESTs	Weakly similar to weak similarity to HSP90 [C. elegans]
18070	1	AA180352	Hs.72733	ESTs	
17937	1	AA164750	Hs.72489	ESTs	
39115	1	AA620735	Hs.112893	EST	
22517	1	R71892	Hs.25996	ESTs	Highly similar to 40S RIBOSOMAL PROTEIN S27A [Homo sapiens Cavia porcellus]

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FIGURE 7 (CONT.)

16906	1	AA058555	Hs.63392	EST	
14251	1	AA07049	Hs.32501	ESTs	
23923	1	T96407	Hs.17812	ESTs	
21177	1	R06569	Hs.19721	ESTs	
25705	1	AA131921	Hs.71030	ESTs	
18805	1	H57725	Hs.124031	ESTs	
19008	1	H47656	Hs.33991	EST	
36693	1	AA432389	Hs.98702	ESTs	
14036	1	AA482107	Hs.5473	ESTs	
20859	1	N68825	Hs.16762	ESTs	
23949	1	T93113	EST - RC_T93113		
18265	1	AA207122	Hs.85316	ESTs	
35275	1	AA398530	Hs.97363	ESTs	
10262	1	R77869	Hs.110493	ESTs	
21757	1	R40789	Hs.21299	ESTs	
21541	1	R31607	Hs.24420	ESTs	
16873	1	AA056258	Hs.63264	EST	
19846	1	H46006	Hs.31677	ESTs	
23719	1	T89160	Hs.138506	ESTs	
19508	1	H41581	Hs.31592	ESTs	Moderately similar to HYPOTHETICAL 59.1 KD PROTEIN ZK637.1 IN CHROMOSOME III [Caenorhabditis elegans]
17382	1	AA102731	Hs.109072	ESTs	
16864	1	AA055871	Hs.63238	ESTs	
10897	1	AA111881	Hs.9192	ESTs	
17028	1	AA070178	EST - RC_AA070178		
19220	1	H12318	Hs.24324	ESTs	
9726	1	L44574	Hs.125235	ESTs	
24570	0	Z38681	Hs.27150	ESTs	
22167	0	R53021	Hs.25873	ESTs	
42537	0	W73417	Hs.103183	EST	
18806	0	F10005	Hs.12599	ESTs	
16585	0	AA033948	Hs.4236	ESTs	
17309	0	AA086232	Hs.68717	EST	Moderately similar to murine transposase [H.sapiens]
22813	0	R97419	Hs.35718	ESTs	
18429	0	AA022953	Hs.61172	EST	
22013	0	R46526	Hs.25377	EST	
8439	0	AA431277	Hs.32419	ESTs	
22834	0	T10042	Hs.4205	ESTs	
13063	0	AA432385	Hs.1191	Human mRNA for KIAA0073 gene partial cds	
10122	0	R31745	EST - R31745		
18195	0	AA195263	Hs.85001	EST	

FIGURE 7 (CONT.)

33249	0	W72557	Hs.57836	ESTs
16966	0	AA063378	Hs.144270	ESTs
16363	0	AA223929	Hs.89902	EST
34154	0	AA219304	Hs.74581	ALPHA-2-MACROGLOBULIN PRECURSOR
16222	0	AA011210	Hs.85044	ESTs
17174	0	AA079306	EST - RC_AA079306	

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Primary Key	fold upregulated of Tumor over normal colon	Accession	Unigene Descriptor	CRF structural info
16074	>10	AA001507	ESTs	other
25047	>10	AA011031	ESTs	other
25082	>10	AA017257	ESTs	other
16490	>10	AA028418	ESTs	other
25178	>10	AA031268	H. sapiens mRNA for kinesin-2	other
25215	>10	AA035540	APOLIPOPROTEIN AI REGULATORY PROTEIN-1	other
25282	>10	AA044825	ESTs	other
16810	>10	AA053636	ESTs	other
16835	>10	AA054438	ESTs	SS
10747	>10	AA055841	ESTs	other
10748	>10	AA055892	ESTs	other
16993	>10	AA065300	Human mRNA for KIAA0035 gene partial cds	other
17051	>10	AA070801	ESTs	TM
10840	>10	AA084104	ESTs	other
7296	>10	AA089561	ESTs	other
7325	>10	AA090842	ESTs Weakly similar to HYPOTHETICAL 36.7 KD PROTEIN C2F7.02C IN CHROMOSOME 1 [Schizosaccharomyces pombe]	other
17419	>10	AA113349	EST	?
17541	>10	AA127458	ESTs	other
17559	>10	AA128407	ESTs	other
25669	>10	AA128978	ESTs	?
17600	>10	AA130596	ESTs	other
10992	>10	AA132523	Human sapiens BAC clone RG119C02 from 7p15	other
17654	>10	AA133250	ESTs	TM
17734	>10	AA137246	ESTs	other
25801	>10	AA148530	EST - RC_AA148530	TM
25836	>10	AA149007	EST	?
11121	>10	AA156358	Human TAR DNA-binding protein-43 mRNA complete cds	?
11160	>10	AA164289	ESTs	other
25825	>10	AA164494	ESTs Weakly similar to CYCLIC-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF-6 [H. sapiens]	other
25934	>10	AA165355	Human clone cds unknown protein mRNA complete cds	?
17687	>10	AA169379	ESTs	other
18008	>10	AA171895	Human sapiens clone 24749 and 24750 mRNA sequences	TM
33953	>10	AA173200	Human HOKA1 mRNA long transcript and alternatively spliced forms complete cds	other
33980	>10	AA180223	CAMP-DEPENDENT PROTEIN KINASE TYPE II- ALPHA REGULATORY CHAIN	other
34013	>10	AA180688	EST - RC_AA180688	other
34014	>10	AA191348	ESTs	other
34015	>10	AA191353	ESTs	TM
34070	>10	AA196549	ESTs	other
18260	>10	AA206601	ESTs	?
34105	>10	AA207123	ESTs	SS
34107	>10	AA209469	ESTs	other
18330	>10	AA216722	Human mRNA for apolipoprotein E receptor 2 complete cds	TM
18362	>10	AA223912	Ribonuclease L (2'5'-oligoadenylate synthetase- dependent) inhibitor	other
18392	>10	AA227751	ESTs	SS
34188	>10	AA228030	ESTs	TM
34197	>10	AA232315	Human sapiens clone 23797 and 23917 mRNA partial cds	other
25948	>10	AA234365	Human sapiens survival of motor neuron protein interacting protein 1 (SIP1) mRNA complete cds	?
25951	>10	AA234558	EST	?

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11581	>10	AA236533	Ev-1	other
26059	>10	AA236685	ESTs	other
26100	>10	AA242035	Human mRNA for KIAA0391 gene complete cds	other
11603	>10	AA243052	ESTs Highly similar to GONADOTROPIN-RELEASING HORMONE RECEPTOR [Rattus norvegicus]	other
7785	>10	AA243375	EST - AA243375	other
34372	>10	AA251973	ESTs	?
26240	>10	AA252282	Human mRNA for KIAA0152 gene complete cds	TM
34382	>10	AA252512	ESTs	other
34391	>10	AA252703	EST - RC_AA252703	other
26274	>10	AA253011	ESTs	?
34400	>10	AA253400	ESTs	other
26291	>10	AA253422	ESTs	?
26355	>10	AA256379	ESTs	other
11813	>10	AA258150	ESTs	other
34518	>10	AA278721	ESTs	?
26545	>10	AA278979	ESTs	other
26574	>10	AA279504	ESTs	other
34554	>10	AA280016	DNA polymerase gamma	other
34561	>10	AA280296	ESTs	TM
26628	>10	AA280641	ESTs Highly similar to 60S RIBOSOMAL PROTEIN L39 [Rattus norvegicus]	TM
11989	>10	AA280670	ESTs	SS,
34575	>10	AA280738	ESTs	TM
26677	>10	AA281636	ESTs	?
26700	>10	AA282197	EST	?
34672	>10	AA284372	ESTs	other
34692	>10	AA285079	ESTs	other
12143	>10	AA290991	ESTs	other
8092	>10	AA316272	ESTs	TM
34904	>10	AA321746	EST	other
8111	>10	AA323787	ESTs	other
8125	>10	AA330771	Human protein-tyrosine phosphatase (HU-PP-1) mRNA partial sequence	TM
26916	>10	AA331393	ESTs	other
26926	>10	AA342402	ESTs	other
26935	>10	AA347193	ESTs Weakly similar to NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4 [Caenorhabditis elegans]	TM
35038	>10	AA350541	ESTs Moderately similar to URACIL-DNA GLYCOSYLASE 1 PRECURSOR [H. sapiens]	TM
35049	>10	AA350857	ESTs	other
35106	>10	AA371561	EST Weakly similar to putative p150 [H. sapiens]	?
35197	>10	AA398120	ESTs	other
35277	>10	AA398538	ESTs	other
35309	>10	AA398660	EST	other
35322	>10	AA398710	H. sapiens RNA for CLCN3	TM
27037	>10	AA400198	ESTs	TM
35495	>10	AA400527	ESTs	?
27048	>10	AA400670	Homo sapiens mRNA for KIAA0582 protein partial cds	other
35500	>10	AA400715	ESTs	other
12480	>10	AA403116	Homo sapiens U-snRNP-associated cyclophilin (USA-Cyp) mRNA complete cds	other
35693	>10	AA405485	ESTs Weakly similar to similar to I complex testis-specific protein [C. elegans]	other
35697	>10	AA405512	ESTs	other
35766	>10	AA406169	Homo sapiens KIAA0431 mRNA partial cds	other
35769	>10	AA406206	ESTs	other
35798	>10	AA410231	ESTs	other

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35801	>10	AA410291	ESTs	other
35803	>10	AA410295	ESTs	other
35822	>10	AA411144	ESTs	TM
35874	>10	AA412024	EST	?
35958	>10	AA412550	ESTs	other
36052	>10	AA417027	EST	TM
36258	>10	AA423962	ESTs Weakly similar to !!! ALU SUBFAMILY J WARNING ENTRY !!! [H.sapiens]	other
36288	>10	AA424502	ESTs	other
36307	>10	AA424803	EST	?
36371	>10	AA426017	ESTs	TM
36395	>10	AA426353	ESTs	other
36405	>10	AA426408	Homo sapiens mRNA for KIAA0530 protein partial cds	other
36506	>10	AA429610	ESTs	other
36571	>10	AA430726	EST - RC_AA430726	SS,
36695	>10	AA433910	ESTs	other
36739	>10	AA435610	EST - RC_AA435610	?
36753	>10	AA435686	ESTs	other
36845	>10	AA436198	ESTs	?
13136	>10	AA436590	ESTs	SS, TM
13143	>10	AA436619	ESTs	SS,
36958	>10	AA442060	ESTs	other
36982	>10	AA442082	ESTs	?
36981	>10	AA442845	EST	?
13237	>10	AA443971	ESTs Weakly similar to !!! ALU SUBFAMILY J WARNING ENTRY !!! [H.sapiens]	?
13242	>10	AA445994	ESTs	other
37057	>10	AA446131	ESTs	other
37068	>10	AA446312	ESTs Weakly similar to !!! ALU CLASS C WARNING ENTRY !!! [H.sapiens]	other
37074	>10	AA446344	ESTs	SS,
37084	>10	AA446486	Homo sapiens Ran binding protein 2 (RanBP2alpha) mRNA partial cds	?
37135	>10	AA447540	EST	?
37159	>10	AA447714	EST - RC_AA447714	other
37168	>10	AA447772	ESTs	?
37246	>10	AA449311	Homo sapiens mitotic checkpoint protein kinase (BUB1) mRNA complete cds	other
37310	>10	AA451707	ESTs	other
37453	>10	AA454610	ESTs	?
37456	>10	AA454832	ESTs	TM
27767	>10	AA454660	ESTs	?
37492	>10	AA455248	EST - RC_AA455248	other
37546	>10	AA456641	ESTs	TM
37601	>10	AA456864	ESTs	other
37611	>10	AA456996	Human signaling lymphocytic activation molecule (SLAM) mRNA complete cds	SS, TM
37615	>10	AA459101	Human serine/threonine kinase mRNA partial cds	other
37653	>10	AA460017	ESTs	other
37677	>10	AA460530	Homo sapiens orphan G protein-coupled receptor HC38 mRNA complete cds	other
37777	>10	AA464860	Homo sapiens Jnk2 kinase mRNA complete cds	other
6548	>10	AA465016	Homo sapiens serine protease-like protease (nest) mRNA complete cds	?
37816	>10	AA469954	EST	?
37829	>10	AA470084	ESTs	other
28015	>10	AA477421	ESTs	other
37978	>10	AA478284	EST - RC_AA478284	other
37978	>10	AA478285	ESTs Highly similar to RING CANAL PROTEIN [Drosophila melanogaster]	other

FIGURE 8 (cont.)

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37963	>10	AA479348	H sapiens mRNA for SYT	other
14094	>10	AA485223	ESTs	TM
38121	>10	AA485724	EST - RC_AA485724	other
20122	>10	AA485928	ESTs Weakly similar to LOK (M.musculus)	other
38167	>10	AA487237	EST - RC_AA487207	other
38172	>10	AA487424	EST - RC_AA487424	other
38178	>10	AA487492	Homo sapiens clone 23592 mRNA sequence	other
38182	>10	AA487501	ESTs	other
38184	>10	AA487669	ESTs	other
28141	>10	AA488432	ESTs	?
38211	>10	AA489687	ESTs	other
38235	>10	AA489930	ESTs	other
38260	>10	AA489791	EST - RC_AA489791	other
38318	>10	AA490500	Homo sapiens ribonuclease P protein subunit p20 (RPP20) mRNA complete cds	other
38330	>10	AA490882	ESTs	other
38456	>10	AA504343	ESTs	SS.
38460	>10	AA504462	ESTs	other
38553	>10	AA521471	ESTs	other
38560	>10	AA593545	ESTs	?
38590	>10	AA598548	Human mRNA for transcriptional activator hSNF2b complete cds	other
38601	>10	AA598738	ESTs	?
28323	>10	AA599639	ESTs	other
38828	>10	AA509177	ESTs	TM
38838	>10	AA509215	EST - RC_AA509215	?
38867	>10	AA509318	Human cbl-b mRNA complete cds	TM
38871	>10	AA509333	EST	?
38970	>10	AA509749	ESTs	other
38994	>10	AA509839	ESTs Moderately similar to "H1 ALU SUBFAMILY J WARNING ENTRY "H1 [H.sapiens]	?
39045	>10	AA510077	ESTs	other
39062	>10	AA520333	EST	?
39080	>10	AA520552	EST - RC_AA520552_r	?
39110	>10	AA520709	ESTs Weakly similar to HYPOTHETICAL 80.6 KD PROTEIN TGS10.7 IN CHROMOSOME II [C.elegans]	other
39176	>10	AA521091	ESTs	other
39218	>10	AA521330	ESTs	other
39221	>10	AA521345	Homo sapiens protein phosphatase with EF-hands-1 (PPEF-1) mRNA complete cds	other
39232	>10	AA521409	ESTs	other
21	>10	AB000905	H sapiens histone H4 gene	?
8963	>10	AFFX-HUMTFRRM115 D7	AFFX-HUMTFRRM11507_M	?
33890	>10	AFFX-HUMTFRRM115 C7	AFFX-HUMTFRRM11507_5	?
39302	>10	C14944	ESTs	other
39329	>10	C20797	EST	?
28644	>10	D12153	ESTs	other
218	>10	D13540	PROTEIN-TYROSINE PHOSPHATASE 2C	other
236	>10	D13645	Human mRNA for KIAA0202 gene complete cds	other
9127	>10	D30037	PHOSPHATIDYLINOSITOL	other
459	>10	D38293	Human mRNA for clathrin-4Aa protein complete cds	TM
39405	>10	D50975	ESTs	other
39433	>10	D52037	Human thymidine kinase 2 (TK2) mRNA complete cds	other
39438	>10	D52692	Human Ca2+-dependent activator protein for secretion mRNA complete cds	TM
14708	>10	D59388	EST	?

FIGURE 8 (cont.)

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39488	>10	D60631	ESTs	other
39504	>10	D60632	ESTs	other
765	>10	D60696	Prostaglandin E receptor 3 (subtype EP3) (alternative products)	?
787	>10	D60699	Human mRNA for KIAA215 gene complete cds	other
789	>10	D60671	Human mRNA for KIAA217 gene partial cds	other
39529	>10	F02202	ESTs	?
39535	>10	F02450	ESTs Moderately similar to unknown protein [H.sapiens]	TM
18676	>10	F04022	ESTs	other
18718	>10	F04915	ESTs	other
18762	>10	F09458	ESTs	other
18782	>10	F09739	ESTs	other
29080	>10	F13655	ESTs Moderately similar to H11 ALU SUBFAMILY SB1 WARNING ENTRY H11 [H.sapiens]	other
19001	>10	H02890	ESTs	other
19164	>10	H10285	EST	?
39725	>10	H11323	ESTs	other
19203	>10	H11593	ESTs	other
19328	>10	H17808	ESTs	other
19387	>10	H20128	ESTs	?
39787	>10	H20131	ESTs	SS
19389	>10	H20165	EST	?
39832	>10	H26279	EST - RC_H26279	other
19591	>10	H40888	ESTs	other
29229	>10	H48459	Human mRNA for KIAA2185 gene complete cds	other
19727	>10	H52702	ESTs	?
19787	>10	H56679	ESTs	other
39995	>10	H82474	EST	SS, TM
29331	>10	H88116	ESTs	TM
29344	>10	H68839	EST	?
40064	>10	H72283	Human mRNA for KIAA265 gene partial cds	other
40083	>10	H73466	MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3	other
19949	>10	H78263	ESTs	TM
40204	>10	H88296	EST - RC_H88296	other
29523	>10	H88353	ESTs Weakly similar to line-1 protein ORF2 [H.sapiens]	?
29551	>10	H90134	ESTs	?
29645	>10	H95840	ESTs	?
20057	>10	H98079	ESTs	other
976	>10	HG2036-HT2090	EST - HG2036-HT2090	?
1158	>10	HG3344-HT3521	EST - HG3344-HT3521	?
1210	>10	HG37-HT37	EST - HG37-HT37	?
1346	>10	HG4716-HT5158	EST - HG4716-HT5158	?
1349	>10	HG4747-HT5195	EST - HG4747-HT5195	?
1445	>10	J03027	MHC class I protein HLA-G	?
1570	>10	K01383	EST - K01383	?
1684	>10	L07541	Replication factor C (activator 1) 3 (38kD)	other
1852	>10	L17328	Human FEZ2 mRNA partial cds	TM
1856	>10	L18920	MELANOMA-ASSOCIATED ANTIGEN 2	?
1863	>10	L19161	TRANSLATIONAL INITIATION FACTOR 2 GAMMA SUBUNIT	other
2070	>10	L37378	Homo sapiens guanylyl cyclase (RatGC-2) mRNA complete cds	SS, TM
2123	>10	L40396	Homo sapiens (clone 422171) mRNA fragment	other
2144	>10	L41349	Phosphopase C beta 4	SS
9723	>10	L44542	ESTs	other
2188	>10	L47276	EST - L47276	other

FIGURE 8 (cont.)

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2343	>10	M15353	Eukaryotic translation initiation factor 4E	other
2627	>10	M29610	Glycophorin E	TM
2857	>10	M58597	Fucosyltransferase 4 (alpha (13) fucosyltransferase myeloid-specific)	TM
3021	>10	M68941	Protein tyrosine phosphatase non-receptor type 4	other
3163	>10	M84424	Cathepsin E	?
3195	>10	M85917	Oxysterol binding protein	other
20088	>10	N20054	ESTs Weakly similar to putative p150 [H.sapiens]	?
29795	>10	N20641	ESTs Highly similar to HYPOTHETICAL MYELOID CELL LINE PROTEIN 3 [Homo sapiens]	other
40427	>10	N21147	ESTs	other
40444	>10	N22140	ESTs Highly similar to TUBULIN GAMMA CHAIN [Euplates otocervinus]	other
22893	>10	N23003	ESTs	TM
40498	>10	N25086	Homo sapiens citrate synthase mRNA complete cds	SS
40559	>10	N33024	ESTs	SS
30190	>10	N33264	EST	?
30207	>10	N33920	H.sapiens mRNA for drubiquitin	other
20304	>10	N34686	Homo sapiens clone 23915 mRNA sequence	?
20307	>10	N34830	ESTs	other
30285	>10	N35115	ESTs	other
40594	>10	N35388	ESTs	other
40604	>10	N38893	Homo sapiens KIAA0428 mRNA complete cds	other
40631	>10	N45124	ESTs	other
40660	>10	N49104	NUCLEAR FACTOR RBP140	other
30810	>10	N50138	EST	?
30617	>10	N50646	ESTs	other
30631	>10	N50807	EST	?
30790	>10	N52935	EST	?
20564	>10	N55443	ESTs	TM
40760	>10	N57927	ESTs Weakly similar to ELL [H. musculus]	other
30838	>10	N58561	Cathepsin B	other
20614	>10	N59230	ESTs	SS
20657	>10	N62889	ESTs	other
31136	>10	N63512	ESTs Weakly similar to M01F1.4 [C.elegans]	TM
40827	>10	N64051	Homo sapiens Werner syndrome gene complete cds	other
31310	>10	N66831	EST	?
40876	>10	N67607	Human Rho-associated coiled-coil containing protein kinase p16OROCK mRNA complete cds	other
20791	>10	N68057	Homo sapiens telomeric repeat binding factor (TRF1) mRNA complete cds	?
40905	>10	N68738	ESTs	other
40911	>10	N69114	H.sapiens mRNA for orphan nuclear hormone receptor	other
40913	>10	N69218	ESTs	other
31484	>10	N69466	ESTs	other
31619	>10	N73449	ESTs	other
41005	>10	N79516	ESTs	TM
31818	>10	N89774	Homo sapiens mRNA for KIAA292 gene partial cds	other
31872	>10	N91109	EST	other
41040	>10	N91948	ESTs	other
31944	>10	N93193	ESTs	other
41065	>10	N93618	ESTs	other
32034	>10	N96926	ESTs Moderately similar to DMR-N9 PROTEIN [H.sapiens]	other
41107	>10	R01634	ESTs	other
41163	>10	R08176	ESTs	other
21238	>10	R08564	Plasminogen-like protein	other

FIGURE 8 (cont.)

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21240	>10	R08513	ESTs	other
21412	>10	R20670	ESTs	other
21519	>10	R27975	EST - RC_R27975	other
41381	>10	R42278	H sapiens mRNA for TRES	?
32189	>10	R43183	ESTs	TM
32195	>10	R43471	ESTs Weakly similar to ORF YOR258w [S cerevisiae]	other
21902	>10	R43822	EST	?
21946	>10	R44707	ESTs	TM
22072	>10	R49406	ESTs	?
32240	>10	R50976	Ribonuclease L (2'5'-oligoadenylate synthetase-dependent) inhibitor	other
32258	>10	R55823	ESTs	other
22258	>10	R56432	ESTs	other
22282	>10	R59187	ESTs	other
32277	>10	R61493	Human mRNA for rod photoreceptor protein complete cds	other
22372	>10	R62831	EST	?
22400	>10	R64109	ESTs	other
41583	>10	R64129	ESTs	other
10233	>10	R71427	ESTs Highly similar to PHENYLALANYL-TRNA SYNTHETASE ALPHA CHAIN CYTOPLASMIC [Saccharomyces cerevisiae]	other
41854	>10	R76437	THROMBOXANE-A SYNTHASE	TM
22557	>10	R76722	ESTs	other
22576	>10	R79111	ESTs	other
22593	>10	R79777	EST	?
41678	>10	R80675	EST	?
41719	>10	R89280	EST - RC_R89280	other
22783	>10	R96208	ESTs	other
41752	>10	R97063	ESTs	other
3375	>10	S50223	HKR-T1	other
3406	>10	S66896	SQUAMOUS CELL CARCINOMA ANTIGEN 1	other
3522	>10	S80267	Spleen tyrosine kinase	other
41793	>10	T03887	ESTs	?
23198	>10	T40530	ESTs Weakly similar to B0035.14 [C elegans]	other
23360	>10	T58531	ESTs	other
32635	>10	T61116	ESTs	other
42177	>10	T79786	ESTs	?
23623	>10	T84047	ESTs	?
23662	>10	T88674	ESTs	other
42242	>10	T89579	Human sapiens E2F-related transcription factor (DP-1) mRNA complete cds	other
23759	>10	T90313	ESTs	other
23832	>10	T92018	ESTs	other
32740	>10	T92950	ESTs	other
42790	>10	T95105	ESTs	?
3598	>10	U01157	Glucagon-like peptide-1 receptor	SS, TM
3659	>10	U04313	Protease inhibitor 5 (maspin)	other
3799	>10	U10690	Human MAGE-5a antigen (MAGE5a) gene complete cds	?
3870	>10	U14518	Centromere protein A (17kD)	other
3913	>10	U16261	Human MDA-7 (mda-7) mRNA complete cds	SS,
4029	>10	U21090	Human DNA polymerase delta small subunit mRNA complete cds	other
4157	>10	U28811	Human cysteine-rich fibroblast growth factor receptor (CFR-1) mRNA complete cds	other
4178	>10	U30246	Human bumetanide-sensitive Na-K-Cl cotransporter (NKCC1) mRNA complete cds	TM
15006	>10	U30246	Human bumetanide-sensitive Na-K-Cl cotransporter (NKCC1) mRNA complete cds	TM

FIGURE 8 (cont.)

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4193	>10	U31116	Human beta-keroglycan A3b mRNA complete cds	TM
4306	>10	U36798	Homo sapiens platelet cGMPDE mRNA complete cds	TM
4362	>10	U38817	Bloom syndrome	other
4386	>10	U40622	DNA repair protein XRCC4	other
4388	>10	U40714	Human tyrosyl-tRNA synthetase mRNA complete cds	other
4435	>10	U43944	MALATE OXIDOREDUCTASE	other
4477	>10	U45880	Human IAP-like protein ILP mRNA complete cds	other
4500	>10	U55766	Human Rev interacting protein Rip-1 mRNA complete cds	TM
4702	>10	U57341	EST - U57341	other
4713	>10	U57721	Human L-lysine hydrolase mRNA complete cds	other
4787	>10	U61145	Human enhancer of zeste homolog 2 (EZH2) mRNA complete cds	other
4862	>10	U65437	Human homodomain-containing protein (HAMP) mRNA complete cds	?
4845	>10	U69108	Homo sapiens mRNA for TRAF5 complete cds	other
4976	>10	U71088	Human MEK5 mRNA complete cds	other
4994	>10	U72514	Human C21 mRNA complete cds	other
5002	>10	U72761	Human karyopherin beta 3 mRNA complete cds	other
5021	>10	U73524	Human putative ATPGTP-binding protein (HEAB) mRNA complete cds	TM
5149	>10	U79716	Human rosin (RELN) mRNA complete cds	SS
5214	>10	U83303	H. sapiens mRNA for granulocyte chemotactic protein	?
5243	>10	U85946	Human brain secretory protein hSec10p (HSEC10) mRNA complete cds	other
52789	>10	W02779	ESTs Moderately similar to kinesin-73 (D melanogaster)	other
42354	>10	W19346	ESTs	other
42390	>10	W40150	Homo sapiens chromosome-associated polypeptide (HICAP) mRNA complete cds	other
33006	>10	W46286	ESTs Weakly similar to ZK1058.5 (C. elegans)	TM
33070	>10	W46891	ESTs Weakly similar to polypeptide N-acetylglucosaminyltransferase (H. sapiens)	other
33109	>10	W59961	Human mRNA for KIAA0369 gene complete cds	other
24197	>10	W67277	ESTs	other
24215	>10	W69425	ESTs	other
33301	>10	W73883	ESTs	other
33343	>10	W79834	ESTs Weakly similar to thotekin (M. musculus)	other
33377	>10	W81219	ESTs Weakly similar to F46B5.7 (C. elegans)	other
42602	>10	W86423	ESTs	TM
33556	>10	W90705	Murine leukemia virus (bmi-1) oncogene homolog	other
33616	>10	W93726	Protease inhibitor 5 (maspin)	other
33666	>10	W95876	ESTs	TM
5510	>10	X05360	Cell division cycle 2 G1 to S and G2 to M	?
5558	>10	X07876	Wingless-type MMTV integration site 2 human homolog	SS
5603	>10	X14253	Tarascarcinoma-derived growth factor 1	TM
5619	>10	X14850	HISTONE H2A.X	SS
5623	>10	X14975	T-CELL SURFACE GLYCOPROTEIN CD1E PRECURSOR	?
5692	>10	X17644	G1 to S phase transition 1	other
5789	>10	X54925	Matric metalloproteinase 1 (interstitial collagenase)	other
5799	>10	X55330	Aspartylglucosaminidase	SS
5802	>10	X55544	CYCLOC-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF-1	?
5857	>10	X58377	Human mRNA for edipogenesis inhibitory factor	other
5960	>10	X63575	ATPase Ca++ transporting plasma membrane 2 (NOTE redefinition of symbol)	TM
5963	>10	X63629	Cadherin 3 (P-cadherin)	SS, TM
5986	>10	X64810	Protein convertase subtilisin/kexin type 1	?
6041	>10	X67152	MITOTIC KINESIN-LIKE PROTEIN-1	other
6095	>10	X69962	Fragile X mental retardation 1	other

FIGURE 8 (cont.)

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6106	>10	X70683	SRY (sex determining region Y)-box 4	TM
6155	>10	X74331	DNA primase polypeptide 2A (58kD)	other
6167	>10	X74987	Recombinase L (75'-oligonucleotide synthetase-dependent) protein	other
6188	>10	X76029	NEUROMEDIN U-25 PRECURSOR	TM
6316	>10	X81889	H. sapiens mRNA for p0071 protein	other
6382	>10	X85133	H. sapiens RBQ-1 mRNA	other
6384	>10	X85137	Human kinesin-like spindle protein HKSP (HKSP) mRNA complete cds	other
6438	>10	X89388	URACIL-DNA GLYCOSYLASE 1 PRECURSOR	?
6449	>10	X89886	H. sapiens mRNA for NBK apoptotic inducer protein	TM
6478	>10	X91648	H. sapiens mRNA for put alpha extended 3'untranslated region	SS, TM
6479	>10	X91653	EST - X91653	?
6494	>10	X92589	H. sapiens mRNA for UDP-GalNAc:polypeptide N-acetylglucosaminyl transferase	TM
6713	>10	Y08564	EST - Y08564	?
6790	>10	Y12394	Human sapiens importin-alpha homolog (SRP1gamma) mRNA complete cds	other
24915	>10	YEL003w/	EST - YEL003w/	?
42773	>10	YEL019cMM521	EST - YEL019cMM521	?
24545	>10	Z38462	ESTs	other
33713	>10	Z39427	ESTs	other
33791	>10	Z40883	ESTs	other
42766	>10	Z99394	ESTs Moderately similar to H11 ALU SUBFAMILY SP WARNING ENTRY H11 [H. sapiens]	other
21558	>10	R33112	Human AF-6 mRNA complete cds	other
25718	>10	AA282576	ESTs	?
40113	9 9955090946	H78003	ESTs	?
13801	9 8879448276	AA092805	ESTs Weakly similar to PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE R10E11.3 [C. elegans]	other
37491	9 9513600842	AA455239	ESTs Highly similar to CHROMOSOME CONDENSATION PROTEIN OPY-27 [Caenorhabditis elegans]	other
23800	9 8272347693	T95789	ESTs	other
254	9 9188395324	D14657	Human mRNA for KIAA0101 gene complete cds	other
6885	9 8970927914	Z28331	Ubiquitin-conjugating enzyme E2H (homologous to yeast UBC8)	other
29683	9 8850706398	H97819	ESTs	SS,
26482	9 8765109024	AA262491	ESTs	other
23123	9 8699502095	T25306	EST	?
26525	9 8160399123	AA278352	ESTs	other
13110	9 7643356605	AA435840	Human sapiens mRNA for high mobility group protein HMGB2a	other
34863	9 7087597628	AA299784	EST	other
39432	9 7034550063	D51691	Phosphoribosylglycnamide formyltransferase phosphoribosylglycnamide synthetase phosphoribosylhydromidazole synthetase	?
31312	9 6513326388	N66845	ESTs Weakly similar to H11 ALU CLASS B WARNING ENTRY H11 [H. sapiens]	?
21112	9 6358446349	R01179	ESTs	?
31572	9 6254820695	N71294	ESTs	other
17903	9 6221229759	AA160259	EST	?
20747	9 6094813734	N66842	ESTs	other
4676	9 589223908	U55206	Human sapiens human gamma-glutamyl hydrolase (hGH) mRNA complete cds	TM
34363	9 5627081023	AA251587	Human sapiens mRNA for KIAA0530 protein partial cds	other
28094	9 540768688	AA620636	ESTs	other
3888	9 5372000133	U15128	Human beta-12-N-acetylglucosaminyltransferase II (MGAT2) gene complete cds	?
29386	9 506250529	D12184	ESTs	TM
7674	9 4458059039	AA203742	ESTs	other
4192	9 4329744134	U31099	Human DP prostanoicd receptor (PTGDR) mRNA partial cds	TM
4507	9 422874945	U47050	Human putative calcium influx channel (hcap3) mRNA complete cds	TM

FIGURE 8 (cont.)

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35606	9 412026255	AA02227	ESTs Moderately similar to N-nonomodulin (R norvegicus)	other
4970	9 3648551013	U70862	Human nuclear factor I-B2 (NFIB2) mRNA complete cds	?
19829	9 3432151573	H58813	EST	?
14837	9 2878504141	T40145	ESTs	TM
17336	9 2822140675	AA099585	ESTs	other
40541	9 2532636505	N30160	ESTs	other
29496	9 2487643833	H85434	EST	?
29943	9 1767074262	N24766	ESTs Moderately similar to (H) ALU SUBFAMILY J WARNING ENTRY !!! (H sapiens)	TM
17997	9 1629681314	AA169633	EST	other
21320	9 1243463316	R11673	ESTs	other
13883	9 1178796537	AA476917	ESTs Weakly similar to No definition line found (C.elegans)	other
30539	9 0866887776	N49072	ESTs	other
32778	9 0877919549	W02063	EST	?
26380	9 0809559378	AA257012	EST	?
15888	9 0595853607	X95832	Human Abi-2 mRNA complete cds	other
40812	9 0012874244	N63419	ESTs	other
903	8 9640387908	D90070	ATL-derived PMA-responsive (APR) peptide	other
22674	8 9515777733	R87160	ESTs	TM
40807	8 9510132281	H62995	TRANSCRIPTION INITIATION FACTOR IF BETA SUBUNIT	other
15244	8 9185644974	W00904	ESTs	TM
32296	8 8658778567	R87075	Zinc finger protein X-linked	other
18269	8 8575656769	AA209467	ESTs	other
19662	8 8507626284	H47391	ESTs	other
41807	8 8339255117	R87868	CLEAVAGE SIGNAL-1 PROTEIN	other
2548	8 8299864659	M25897	Platelet factor 4	TM
7736	8 8279341243	AA232121	Human tyrosyl-tRNA synthetase mRNA complete cds	other
34490	8 7844537272	AA262354	ESTs	other
38658	8 7668313482	AA599477	ESTs	other
7528	8 765157554	AA149543	ESTs	other
39939	8 7555031142	H53454	EST - RC_H53454	other
25111	8 7232892309	AA020787	ESTs	other
21655	8 716167279	R38239	EST	?
39663	8 665982652	H04756	ESTs Highly similar to NADH-UBIQUINONE OXIDOREDUCTASE B17 SUBUNIT (Bos taurus)	other
1042	8 652112324	HG2510 HT2608	EST - HG2510-HT2608	?
32330	8 6361115426	R77776	ESTs	other
25382	8 6239450487	AA059007	ESTs	other
27074	8 5900813076	AA401475	ESTs Weakly similar to C36B1.3 (C.elegans)	SS
3955	8 5298900183	U18259	MHC class II transactivator	other
4959	8 52646027	U70322	Human transportin (TRN) mRNA complete cds	other
2315	8 5259185808	M14123	EST - M14123_xp11	?
37253	8 4896914632	AA449357	ESTs	other
39624	8 471316877	F10836	ESTs	?
23213	8 4569920887	T40891	ESTs	?
2788	8 455596435	M54995	Connective tissue activation peptide III	TM
41154	8 4413390141	R07499	ESTs	?
32479	8 4093689549	T18282	WEE1-LIKE PROTEIN KINASE	other
41251	8 3587565415	R28279	Human clone 23548 mRNA sequence	other
19081	8 3583603183	H06701	ESTs Weakly similar to RHOMBOTIN-1 (H sapiens)	other
21098	8 3105877559	R00545	ESTs	other
14723	8 3061679053	D59854	ESTs	other
37154	8 2994822341	AA447666	Human CENP-F kinetochore protein mRNA complete cds	other

FIGURE 8 (cont.)

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8068	8 2835566361	AA313367	ESTs Highly similar to HYPOTHETICAL 847 kb PROTEIN ZK1098.1 IN CHROMOSOME III [Caenorhabditis elegans]	other
7435	8 281678048	AA129547	ESTs	other
16501	8 251796834	AA026968	ESTs	other
34527	8 2418163754	AA279091	ESTs	other
6700	8 1948675662	Y07867	H.sapiens mRNA for Pen isolate 1	other
2852	8 1928816537	M58480	Human 75-kD autoantigen (PK-Scl) mRNA complete cds	other
11188	8 1862492468	AA172372	ESTs	TM
42283	8 183311064	T95333	ESTs Weakly similar to coded for by C. elegans cDNA yk110g8.3 [C. elegans]	TM
5443	8 1783317544	X02530	Interferon (gamma)-induced cell line protein 1C from	SS.
40837	8 1534810594	N70607	ESTs	TM
23371	8 1499496068	T59505	EST - RC_T59505	?
26272	8 1339974519	AA252981	ESTs Weakly similar to K07C11.10 gene product [C. elegans]	other
17306	8 1332403782	AA086201	ESTs	other
18497	8 1182326373	AA233795	ESTs	other
235	8 0944363901	D13644	Human mRNA for KIAAC19 gene complete cds	other
24525	8 0860187097	Z38347	ESTs	TM
7826	8 0760028554	AA240884	EST - AA240884	TM
32142	8 0730258775	R38715	Homo sapiens clone 24540 mRNA sequence	other
39067	8 0557768803	AA620405	ESTs	other
6235	8 0448957236	X78416	Caseln alpha S1	TM
28617	8 0017588725	H88261	ESTs	other
28570	7 9852456973	C21104	Homo sapiens STAT-induced STAT inhibitor-2 mRNA complete cds	other
39344	7 9162087762	C21034	ESTs Moderately similar to induction factor eIF-2B gamma subunit [R. norvegicus]	other
18951	7 9002189759	H00580	ESTs	other
18953	7 8709160227	H00615	ESTs	other
18376	7 8564099916	AA225925	ESTs	other
19830	7 847878447	H58911	ESTs	other
36023	7 840835828	AA418881	ESTs	other
13347	7 8344414518	AA449238	ESTs	other
36614	7 8284591351	AA431466	ESTs	other
2192	7 8254072032	L48211	Homo Sapiens angiotensin II receptor gene complete cds	?
33016	7 8006574068	V46577	H sapiens mRNA for ESM-1 protein	other
17215	7 7941954038	AA083044	ESTs	other
34894	7 7658738105	AA311881	EST	?
40814	7 895001222	N39257	ESTs	other
36295	7 6834749899	AA424534	ESTs	other
19564	7 6744302788	H38833	ESTs	TM
16914	7 6686405336	AA055665	ESTs	SS.
35967	7 6378079107	AA412694	Human splicing factor SRp55-2 (SRp55) mRNA complete cds	other
21872	7 6364823402	R38635	ESTs	other
19918	7 6303275831	H59787	ESTs	?
10511	7 6297744492	AA024482	ESTs Highly similar to KERATIN TYPE I CYTOSKELETAL 14 [Homo sapiens]	other
17721	7 6057911016	AA136590	ESTs	?
42302	7 6031856697	T96130	EST	SS.
26134	7 6000819583	AA243763	ESTs	other
18766	7 5621799006	F09497	ESTs	other
34482	7 501590494	AA262439	ATL-derived PMA-responsive (APR) peptide	other
270	7 4512152125	D14822	EST - D14822	other
35975	7 4177746986	AA412738	ESTs	other
29842	7 4082809071	N21688	ESTs	?

FIGURE 8 (cont.)

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35389	7.3913043319	AA388555	ESTs	other
19979	7.3868157166	H88477	ESTs	other
5793	7.3865864025	X54942	CDC28 protein kinase 2	other
19978	7.350969715	H87770	EST - RC_H87770	other
1280	7.3691089318	HG4126-HT4395	EST - HG4126-HT4395	?
31571	7.3676263454	N71250	ESTs	other
23765	7.3541191734	T90443	ESTs Weakly similar to KIAA0376 [H.sapiens]	?
35123	7.3397933455	AA380927	EST	?
38252	7.33411119467	AA455247	ESTs	other
38218	7.3282021037	AA468861	ESTs	other
26418	7.2489407005	H77915	EST - RC_H77915	?
4834	7.1980951054	U63541	Human mRNA expressed in HCMCC livers and MoIT-4 proliferating cells partial sequence	other
42504	7.1813036522	V69803	ESTs	other
5111	7.158000189	X71125	H.sapiens mRNA for glutamine cyclotransferase	TM
41773	7.154479618	T03024	ESTs Weakly similar to ribosomal protein L7 [H.sapiens]	other
6951	7.1383626365	N71513	ESTs	other
28109	7.0941960224	AA485212	ESTs	other
908	7.0783044659	HG2160-HT2230	EST - HG2160-HT2230	?
29848	7.0610608511	N22107	ESTs	other
30628	7.0607950168	N50744	ESTs	other
22567	7.0225726353	R77771	ESTs	TM
9347	7.006323071	H03686	ESTs	TM
11698	7.0026773299	AA252894	ESTs	other
40584	7.0010096333	N34870	EST	?
193	6.9767029188	D10823	PROBABLE G PROTEIN-COUPLED RECEPTOR HM74	TM
18305	6.9740536051	AA214048	Collagen type IV alpha 4	other
6078	6.9699882397	X69141	FARNESYL-DIPHOSPHATE FARNESYLTRANSFERASE	other
26741	6.902658703	AA283198	ESTs	other
35069	6.892865685	AA358397	EST	?
23504	6.8977135883	T71042	ESTs	other
299	6.8824513029	D16815	Human sapiens orphan nuclear hormone receptor BD73 mRNA 3' end	other
40583	6.8689903023	N34855	ESTs	other
31428	6.8623762274	N68594	ESTs	other
6169	6.8606959727	X75091	SET PROTEIN	other
39524	6.8567355171	F01805	MALATE OXIDOREDUCTASE	other
34578	6.8430689439	AA280637	ESTs	other
38678	6.837527995	AA599920	Small inducible cytokine A5 (RANTES)	other
23936	6.8251471804	T96930	ESTs	other
9326	6.8181321394	D89377	Msh (Drosophila) homeo box homolog 2	other
19188	6.8087351958	H11255	ESTs Highly similar to ACTIN-LIKE PROTEIN [Bos taurus]	TM
18185	6.7882148811	AA194983	Human sapiens mRNA for osteoclastogenesis inhibitory factor (OCIF) complete cds	other
27029	6.757529124	AA399630	ESTs Weakly similar to KIAA0371 [H.sapiens]	other
41289	6.7519531681	R37265	EST	other
34511	6.7364448758	AA278299	EST - RC_AA278299	other
1566	6.7056207716	J05614	EST - J05614	?
23675	6.6932299748	AA129757	ESTs Highly similar to 60S RIBOSOMAL PROTEIN L22 [Rattus norvegicus]	other
5814	6.6584342828	X56088	CYTOCHROME P450 VII	SS
13861	6.6236291607	AA470145	ESTs	other
29794	6.6026313352	N20598	ESTs	other
39333	6.5902382643	C20910	Cyclin B1	other
3770	6.5835303599	U09609	Nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p48/p100)	other

FIGURE 8 (cont.)

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31831	5 5829933764	N59894	ESTs	?
33063	5 5806125026	W53000	Homo sapiens clone 24431 mRNA sequence	other
20326	5 5640084836	N35583	ESTs Weakly similar to PROBABLE E5 PROTEIN [Human papillomavirus type 58]	?
34384	5 5535703482	AA252537	ESTs	other
25599	5 5490481991	AA114291	Human (clone BB1) B1-cadherin mRNA complete cds	other
39749	5 53659363254	H14988	ESTs	other
42596	5 5230567072	W85900	ESTs	?
39006	5 5119482185	F10243	ESTs Weakly similar to [H] ALU CLASS B WARNING ENTRY [!!!] [H.sapiens]	?
14817	5 5105504748	C14983	ESTs	other
27831	5 45670814	AA456044	ESTs	?
34896	5 4496517783	AA312551	EST	?
27360	5 4434305006	AA425358	ESTs	other
20126	5 4326610424	N22015	ESTs	TM
6683	5 4324809977	Y00291	RETINOIC ACID RECEPTOR BETA 2	TM
30692	5 4196636207	N51563	ESTs	other
36472	5 4189542265	AA428633	EST	?
9578	5 3961788753	K07852	Homo sapiens orcaudal-D (BICD) mRNA complete cds	other
39670	5 3818496159	H05626	ESTs	other
22697	5 3652792447	R59218	ESTs	other
37308	5 3647804993	AA451694	EST	TM
16101	5 3517262802	AA002147	EST	?
20629	5 3486854401	N59798	ESTs	other
36100	5 3384148287	AA417740	ESTs	?
15488	5 3252580241	V28097	Homo sapiens clone 23711 unknown mRNA partial cds	other
30867	5 3131273544	AA432136	ESTs	other
30766	5 3115037824	N52627	EST - RC_N52627	?
32882	5 2745311453	W07683	ESTs	TM
18072	5 2675797205	AA180448	EST	?
18231	5 2652604863	AA199747	Human mRNA for KIAA0096 gene partial cds	other
38282	5 2514165678	AA489814	EST	?
28125	5 250317021	AA486073	ESTs	other
37464	5 2484456382	AA454747	ESTs	?
36618	5 1946328223	AA431478	ESTs	other
5082	5 1931116815	U78524	Human Gu binding protein mRNA partial cds	other
1441	5 1777287009	J02963	Integrin alpha 2b (platelet glycoprotein IIb of fibrin complex antigen CD41B)	other
42105	5 14875944	T87710	ESTs	?
6061	5 1394863141	X58314	Glutathione peroxidase 2 gastrointestinal	SS
32570	5 1156028796	T30222	ESTs Weakly similar to tetracycline transporter-like protein [M.musculus]	TM
32504	5 1019612076	T17063	EST	?
23335	5 0977927604	T56804	EST	?
10867	5 0970991075	AA088458	ESTs Weakly similar to [H] ALU SUBFAMILY J WARNING ENTRY [!!!] [H.sapiens]	other
30883	5 0911993489	N56923	EST	?
14528	5 0859008453	AA620295	ESTs	TM
28454	5 0685955036	H81306	EST	?
6758	5 0539173278	Y13153	Homo sapiens mRNA for kynurenine 3-monooxygenase	TM
21248	5 0525426545	R08871	ESTs	?
21940	5 0499984138	R44538	ESTs	?
29006	5 0455247653	F10927	Homo sapiens clone 23636 mRNA sequence	other
18774	5 0446826953	F09609	ESTs	?
30722	5 0172341891	AA435512	ESTs	SS
18062	5 0034342989	AA179845	ESTs Moderately similar to rabkinasin-6 [M.musculus]	other

FIGURE 8 (cont.)

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22689	5.9982817406	T16305	ESTs	other
41745	5.9905623398	R95863	ESTs	?
8787	5.9894877658	AA504307	X-LINKED HELICASE II	other
20530	5.984861785	N55013	ESTs	other
26470	5.9417784101	AA282178	ESTs	other
16574	5.9356497569	AA031926	EST	other
893	5.91689537305	D80007	Human mRNA for KIAA0185 gene partial cds	other
4093	5.914830973	U25182	Human endoxonin enzyme AGE37-2 mRNA complete cds	TM
1182	5.9086264407	HG3546-HT3744	EST - HG3546-HT3744	?
22850	5.8954735823	T10248	ESTs	other
38723	5.891006409	AA435524	EST	?
2114	5.8844986595	L40084	EST - L40384	other
26872	5.868238789	AA291137	ESTs	other
6602	5.8683883018	X98266	EST - X98266_cds2	other
42701	5.8594483433	Z38912	ESTs	other
28573	5.84591116	C21118	ESTs	other
18290	5.8189427895	AA211901	ESTs	other
732	5.8043917841	D83781	Human mRNA for KIAA0197 gene partial cds	other
5330	5.8014145811	U91327	EST - U91327	?
33503	5.7990715189	W88720	EST	?
2353	5.7787505864	M26167	Human platelet factor 4 version 1 (PF4vart1) gene complete cds	?
34705	5.7658902254	AA286907	ESTs Weakly similar to putative p150 [H.sapiens]	other
42663	5.7594091043	W93659	ESTs	other
38180	5.7539310793	AA487485	EST - RC_AA487485	other
4244	5.7476738806	U33286	Human chromosome segregation gene homolog CAS mRNA complete cds	other
32822	5.7418957453	V16834	ESTs	TM
3877	5.7245885557	U18991	Retinal pigment epithelium-specific protein (E51D)	?
24673	5.7202366155	Z38301	ESTs	TM
6328	5.7120261126	Z46629	SRY (sex-determining region Y)-box 9 (campomelic dysplasia autosomal sex-reversion)	other
38726	5.7030796258	AA508733	ESTs	?
33290	5.6882372058	C14573	Human mRNA for KIAA0029 gene partial cds	other
11405	5.6818873796	AA232231	ESTs	other
22538	5.6782005591	R73567	Homo sapiens matrix-L precursor (ADAM12) mRNA complete cds	TM
40747	5.6605393208	N56872	Homo sapiens clone 22 mRNA alternative splice variant alpha-1 complete cds	TM
31596	5.6554024604	N72094	ESTs	other
6329	5.6415652518	X82279	EST - X82279	?
31578	5.6273323861	N71361	ESTs	other
33207	5.6271818482	W70051	H.sapiens mRNA for M-phase phosphoprotein mop9	other
2545	5.6105880146	M25753	Cyclin B1	other
22580	5.5988402647	R79156	ESTs	other
33592	5.5935314518	W83127	ESTs	other
28843	5.5734698755	D60252	ESTs	other
6160	5.5688050619	X74784	CDC21 HOMOLOG	other
37987	5.561345667	AA478666	ESTs	other
42515	5.5217868811	W72116	Homo sapiens clone 23622 mRNA sequence	other
4732	5.5130666527	U58522	Human huntingtin interacting protein (HIP2) mRNA complete cds	other
3299	5.5099850678	M95623	Hydroxymethylglutathione synthase	?
28320	5.473406981	AA599574	ESTs	?
748	5.471280899	D84454	Human mRNA for UDP-galactose 4-epimerase complete cds	TM
39373	5.4635804954	C21517	ESTs	other
3117	5.4338413537	M81182	Peroxisomal membrane protein 1 (70kD Zellweger syndrome)	other

FIGURE 8 (cont.)

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21257	54343612441	R09196	ESTs Moderately similar to M-phase phosphoprotein 11 [H. sapiens]	other
31487	54318648859	H69507	ESTs	other
28954	54137130511	F03153	ESTs	other
38928	5328782721	AA609595	ESTs	other
29903	53722320822	N23366	EST	?
30925	53437432315	N58295	ESTs Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [H. sapiens]	?
19091	53344815609	H07864	ESTs	TM
28209	53138851018	AA491250	ESTs	other
9470	53118097884	H46617	EST - H46617	other
9435	53070056636	H30201	EST - H30201	?
28552	52954432572	C20914	ESTs	other
27411	52940164267	AA428137	ESTs	other
30615	52924125284	N50558	ESTs	other
28313	52657877167	AA599309	ESTs	TM
39321	52649035384	C20632	ESTs	?
29934	52531047395	N24194	ESTs	other
1094	52496703122	HG2846-HT2983	EST - HG2846-HT2983	?
35578	52481126384	F08925	ESTs	TM
11232	52466789424	AA186804	ESTs Weakly similar to unknown [S. cerevisiae]	other
2466	52426349328	M21539	Human small proline rich protein (sprt) mRNA clone 1292	other
26843	52387758661	AA287450	ESTs	?
40331	52353385567	H97562	ESTs Weakly similar to SPERMATID-SPECIFIC PROTEIN T2 [Sepia officinalis]	other
6035	52057983865	AA305116	EST - AA305116	other
29793	51955425722	H20593	ESTs Weakly similar to weak similarity to procollagen alpha chain 1(V) chain [C. elegans]	other
34109	51481650107	AA210722	EST	?
26408	51432577257	AA258177	ESTs Weakly similar to ROSA26AS [M. musculus]	other
19263	51427028707	H15054	ESTs	TM
24596	51416089352	Z35810	ESTs	other
28589	51365059753	C21245	H sapiens mRNA for apoptosis specific protein	other
5684	51121931412	X17098	Pregnancy-specific beta-1 glycoprotein 6	other
30710	51078347344	N51781	EST	?
35785	50973514948	AA406167	EST	?
26360	50883127861	AA258460	ESTs	?
2351	50849012082	M15796	Proliferating cell nuclear antigen	?
30262	50836877534	H35065	Human sapiens clone 24739 mRNA sequence	other
41792	50737512465	T03886	ESTs	?
35710	50703839864	AA434411	ESTs	other
39090	50545685407	AA520628	ESTs	TM
42185	50539926381	T78651	ESTs	?
18745	50480321557	F09134	ESTs	other
35746	50386841896	AA406063	ESTs	other
35356	50354809581	AA399053	EST	?
36769	50312706878	AA435750	EST	?
36900	50278911548	AA436866	H sapiens mRNA for M-chase phosphoprotein mpp9	other
27595	50244757301	AA443328	ESTs	TM
16290	50056611904	AA016145	ESTs	?
27117	50016146599	AA405098	ESTs Weakly similar to MCSEIN/EZRIN/RADUXIN HOMOLOG [D. melanogaster]	other
4304	49951554397	U36754	Eukaryotic translation initiation factor 3 (eIF-3) p36 subunit	other
33458	49907402071	V86635	Human sapiens mRNA for KIAA0536 protein complete cds	other
26693	49800090876	AA282120	EST	?
12659	49758138651	AA417030	Human sapiens protein regulating cytokinesis 1 (PRC1) mRNA complete cds	other

FIGURE 8 (cont.)
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29701	4 9706520307	H97970	EST	?
20483	4 9557253636	N52168	ESTs	TM
8720	4 9439110002	AA481218	EST - AA481218	other
34828	4 9431269475	AA292436	Homo sapiens semaphorin F homolog mRNA complete cds	SS, TM
14965	4 941821032	U15128	Human beta-12-N-acetylglucosaminyltransferase II (MGAT2) gene complete cds	?
16115	4 9377553532	AA004420	ESTs	?
42506	4 9348587118	W70074	EST	other
34781	4 9316837445	AA287833	ESTs	other
11870	4 9281056201	AA262587	ESTs	TM
23211	4 8256381854	T40880	ESTs	other
40811	4 9160502275	N39138	Homo sapiens mRNA for KIAA0584 protein partial cds	other
42611	4 9128605354	W87006	Homo sapiens putative RNA binding protein KOC (koc) mRNA complete cds	other
39652	4 9045174505	H03099	ESTs	other
17581	4 889674761	AA126395	EST	?
37239	4 8704375389	AA449121	ESTs	?
18712	4 8703518781	F04077	ESTs	other
30709	4 8611171953	N51752	ESTs Weakly similar to synapse-associated protein sap47-1 [D. melanogaster]	other
34179	4 8503613948	AA227903	ESTs Highly similar to GTP-BINDING PROTEIN LEPA [Pseudomonas fluorescens]	?
21433	4 825670988	R22183	EST	?
39731	4 8186142741	H11760	ESTs	other
31295	4 8116814607	N66553	ESTs	other
24647	4 804183055	Z39108	EST	?
31292	4 8008971817	N66815	ESTs	other
1285	4 7897542383	HQ4157-HT4427	EST - HG4157-HT4427	?
1106	4 7932425858	HG2981-HT3127	EST - HG2981-HT3127	?
18212	4 7812202505	AA190506	ESTs	other
34367	4 782207045	AA251758	Homo sapiens spleen mitotic checkpoint BUB3 (BUB3) mRNA complete cds	other
34802	4 7797760205	AA291468	ESTs	TM
34762	4 7775301548	AA287834	ESTs	other
11595	4 7696012848	AA242819	ESTs	other
8295	4 7639839111	AA405082	ESTs	?
17622	4 7586335576	AA131584	ESTs Weakly similar to SDF1 PROTEIN [Saccharomyces cerevisiae]	other
35781	4 7572463523	AA406335	ESTs	other
34754	4 7483874972	AA287842	Human mRNA for KIAA0078 gene complete cds	other
23237	4 7444854356	T47291	EST	?
37667	4 7280445357	AA460318	ESTs Highly similar to 60S RIBOSOMAL PROTEIN L26 [Rattus norvegicus]	other
11588	4 7257189975	AA238786	ESTs	other
38622	4 7190695733	AA598967	ESTs	?
5137	4 7057359474	U79296	Dihydrokocamide S-acetyltransferase (E2 component of pyruvate dehydrogenase complex)	other
25038	4 7002244728	AA010065	CDC28 protein kinase 2	other
18288	4 7000147312	H16567	ESTs	other
32503	4 6979488292	T17045	Collagen type I alpha-2	other
3278	4 6953739298	M94055	SODIUM CHANNEL PROTEIN BRAIN II ALPHA SUBUNIT	TM
9696	4 6942061018	L38961	Integral transmembrane protein I	TM
35400	4 6901390898	AA399591	Homo sapiens putative DNA methyltransferase (DNMT2) mRNA complete cds	other
35248	4 6862691303	AA398367	EST Weakly similar to HSP60 protein [M. musculus]	?
36387	4 6827499271	AA426270	ESTs	other
21509	4 6730072542	R27314	ESTs	other
31381	4 6729672124	N67889	ESTs	other
26723	4 6727894925	AA282781	ESTs Highly similar to PRE-MRNA SPLICING FACTOR RNA HELICASE PRP28 [Saccharomyces cerevisiae]	other

FIGURE 8 (cont.)

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36326	4 6703621086	AA425151	human GAP SH3 binding protein mRNA complete cds	other
17409	4 6688418667	AA113136	EST - RC_AA113136	other
4908	4 6552339935	U67156	Human mitogen-activated kinase kinase kinase 5 (MAPKKK5) mRNA complete cds	other
30594	4 6496236326	N49067	ESTs	other
38286	4 64639735	AA488847	ESTs Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Nycticebus coucang]	?
13073	4 6426509459	AA433950	ESTs	other
40435	4 6240181066	N21614	Human sapiens basic-leucine zipper transcription factor MafG (MAFG) mRNA complete cds	other
14474	4 6228694378	AA609427	ESTs Moderately similar to IRI ALU SUBFAMILY 5C WARNING ENTRY !!! [H.sapiens]	other
38213	4 6153099907	AA488847	ESTs Weakly similar to putative p150 [H.sapiens]	?
5312	4 606644180	U90716	Human cell surface protein NCAR mRNA complete cds	SS, TM
24225	4 6041550359	W70326	ESTs	?
35988	4 5868982366	AA401750	EST	?
26739	4 5863199051	H99626	EST	?
7203	4 5782992577	AA053096	EST - AA053096	other
2157	4 5772055869	L41839	Human sapiens protein-tyrosine kinase EPHB2 (EPHB2) mRNA complete cds	SS, TM
32066	4 5661024279	R11510	ESTs	?
8085	4 5648114738	AA314776	ESTs Weakly similar to LITHOSTATHINE 1 BETA PRECURSOR [H.sapiens]	SS,
224	4 5622018989	D13633	Human mRNA for KIAA0008 gene complete cds	other
34006	4 5609980241	AA188761	DNA polymerase gamma	other
33656	4 5557384389	W95477	ESTs	other
34065	4 5537335124	AA195517	ESTs Weakly similar to IRI ALU SUBFAMILY J WARNING ENTRY !!! [H.sapiens]	TM
6028	4 5357922087	X66503	Adenylocuccinate synthase	other
4166	4 5032930671	U29483	Cytochrome B561	?
40262	4 5024727522	H93562	ESTs	TM
22687	4 5018672549	R88209	ESTs	TM
41069	4 4977510482	N95969	H.sapiens mRNA for hFai protein	SS,
8264	4 4793100575	AA401334	ESTs	other
27588	4 472017297	AA443187	ESTs	other
35882	4 4717597552	AA412047	ESTs	?
34478	4 465518181	AA282080	Human bumetanide-sensitive Na-K-Cl cotransporter (NKCC1) mRNA complete cds	TM
15921	4 4548516436	Y12065	Human sapiens mRNA for nuclear protein hNap56	?
11278	4 4380038671	AA195399	ESTs	other
39222	4 4367850786	AA821348	ESTs Highly similar to DOULCHYL-PHOSPHATE BETA-GLUCOSYLTRANSFERASE [Saccharomyces cerevisiae]	other
34428	4 4364736766	AA256526	ESTs	other
8771	4 432067373	AA491188	ESTs	other
22193	4 4189810024	R53891	Human sapiens mRNA from chromosome Sq21-22 clone AJA	other
7896	4 4066170674	AA263032	ESTs	other
19902	4 3886145805	H66736	ESTs	other
9276	4 3868095209	D62374	ESTs	other
10716	4 3784529068	AA053319	ESTs	TM
13193	4 3751913512	AA442763	ESTs Highly similar to G2/MITOTIC-SPECIFIC CYCLIN B2 [Mesocricetus auratus]	other
5680	4 3723059417	X17620	NUCLEOSIDE DIPHOSPHATE KINASE A	other
35102	4 37147138	AA371509	EST - RC_AA371509	TM
17983	4 3612985487	AA189226	ESTs	other
24962	4 3497200925	AFPK-HUMTFRRM11507	AFPK-HUMTFRRM11507_5	?
31680	4 3410539669	N74438	ESTs	other
27168	4 330508894	AA410258	ESTs	other
28731	4 3231846659	D20981	EST	?
28348	4 3212284906	AA608752	ESTs	other

FIGURE 8 (cont.)

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16335	4 3019901487	AA018587	ESTs Weakly similar to III ALU SUBFAMILY SP WARNING ENTRY III (H.sapiens)	?
33036	4 2915644973	W48580	ESTs Weakly similar to transposon LRE2 reverse transcriptase homolog (H.sapiens)	other
30180	4 2897721925	N33144	ESTs	other
35591	4 2895541242	AA401758	ESTs Weakly similar to III ALU SUBFAMILY SQ WARNING ENTRY III (H.sapiens)	SS,
25340	4 2721717135	AA064554	EST	?
28106	4 2658103748	AA485084	ESTs	other
38690	4 2649184307	AA800121	ESTs	other
20203	4 2626499431	N26855	ESTs Moderately similar to III ALU SUBFAMILY SQ WARNING ENTRY III (H.sapiens)	other
10251	4 2608700594	R76185	ESTs Weakly similar to C01H6.7 [C.elegans]	SS,
12684	4 2604192389	AA417658	ESTs	SS,
31636	4 2509469427	N73680	Natural resistance-associated macrophage protein 2	TM
20769	4 2479765348	N67277	ESTs	other
1572	4 2353281083	K01884	EST - K01884	?
10923	4 2292322072	AA110036	ESTs	other
34380	4 2283782392	AA252414	ESTs	other
10132	4 2222816115	R35733	EST - R35733	other
16629	4 2181752119	AA036811	ESTs	other
25146	4 1969683794	AA026356	ESTs	?
28730	4 1965943098	D20859	ESTs Moderately similar to III ALU SUBFAMILY SQ WARNING ENTRY III (H.sapiens)	other
10200	4 1874912391	R64521	ESTs	other
38695	4 1545784653	AA600176	ESTs	other
31365	4 150549878	N67550	ESTs	other
42379	4 1496120668	W37999	ESTs	other
28050	4 1428703354	AA479139	Acid phosphatase 1 soluble	other
2620	4 1386565707	M29474	Human recombination activating protein (RAG-1) gene complete cds	?
6927	4 1340593744	AF008442	Homo sapiens RNA polymerase I subunit HRP439 mRNA complete cds	other
13379	4 1269549188	AA449741	ESTs Weakly similar to AF-6 PROTEIN [H.sapiens]	other
5134	4 1218251808	U78293	Human clone 23948 mRNA sequence	other
2625	4 1213948	M26581	Zinc finger protein 8 (clone HF.18)	other
38005	4 1160483666	AA479969	ESTs	other
38575	4 1127196584	AA431085	EST	?
18296	4 1121837207	AA213620	ESTs Weakly similar to putative p150 [H.sapiens]	?
29531	4 1111458313	H88953	EST - RC_H88953	TM
143	4 1095880506	AFFX- HUMTFRRM115 07	AFX-HUMTFRRM11507_5	?
10970	4 0967613396	AA129390	ESTs	other
25836	4 0952825397	AA152305	Interferon (gamma)-induced cell line protein 10 from	SS,
19735	4 0937927853	H53038	EST	?
40711	4 0909708431	N53564	ESTs	other
4149	4 0901471427	U28386	RAG (recombination activating gene) cohort 1	TM
5767	4 0862784557	X53793	MULTIFUNCTIONAL PROTEIN ADE2	other
5503	4 0861035825	X05232	Stromelysin	SS
20310	4 0641711856	N34893	ESTs Highly similar to HYPOTHETICAL 47.8 KD PROTEIN B0280.9 IN CHROMOSOME III [Caenorhabditis elegans]	other
456	4 059824556	D38145	Prostaglandin I2 (prostaglandin) synthase	SS,
7814	4 0559685576	AA248406	ESTs	other
40230	4 0447282719	H90161	ESTs	SS
33651	4 039204804	W95408	ESTs	other
16777	4 0231657929	AA048968	EST	?
19110	4 0094905222	H08778	ESTs	other
34442	4 0077010365	AA258093	HCR-T1	other
5099	4 004992433	U79247	Human clone 23599 mRNA sequence	TM

FIGURE 8 (cont.)

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8209	3 9990473163	AA384223	ESTs	other
24408	3 9976580074	V90145	ESTs	other
26596	3 9974918787	AA278943	ESTs	other
16485	3 9811264008	AA026269	Screen focus forming virus (SFFV) proviral integration oncogene edit	other
32969	3 9804901745	W42451	ESTs	TM
27005	3 9799768093	AA398695	ESTs Weakly similar to ED4F6 2 gene product [C. elegans]	other
26809	3 9526765967	N21043	EST	?
9586	3 9440163451	H91564	ESTs	TM
29024	3 8377933938	F09315	Homo sapiens mRNA for KIAA0563 protein partial cds	other
71694	3 0356365684	R39317	Homo sapiens protein-tyrosine kinase EPHB2+ (EPH82) mRNA complete cds	other
13207	3 829998104	AA443321	ESTs	other
37865	3 9143752629	AA476023	ESTs Highly similar to PUTATIVE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE C13A11.04C [Schizosaccharomyces pombe]	other
36201	3 9128828172	AA421164	ESTs	?
8961	3 8981160269	AFFX-HUMTFRM11507_3	AFFX-HUMTFRM11507_3	?
17444	3 8927133917	AA115933	ESTs	other
25869	3 8919834527	AA157287	ESTs Highly similar to HYPOTHETICAL 37.7 KD PROTEIN ZYG86.3 IN CHROMOSOME B1 [Caenorhabditis elegans]	TM
24862	3 89042252	Z41415	ESTs Highly similar to BONE MORPHOGENETIC PROTEIN 1 PRECURSOR [Mus musculus]	other
26685	3 889363205	AA281950	ESTs	?
42300	3 8850230368	T95850	ESTs	?
6495	3 8830844863	X92715	Zinc finger protein 74 (Cos52)	other
38604	3 8828045942	AA588803	ESTs	TM
36358	3 8826713718	AA425758	ESTs	other
30560	3 8732764451	N49284	MYB PROTO-ONCOGENE PROTEIN	other
14413	3 8724466158	AA800150	ESTs	other
23823	3 8574824967	T91805	Homo sapiens mRNA for ST1C2 complete cds	other
38158	3 8530968938	AA487021	EST	?
2572	3 8519747554	M27281	Vascular endothelial growth factor	other
40100	3 8464168967	H75933	Laminin receptor (2H5 epitope)	other
40258	3 8462922993	H93340	ESTs	TM
20944	3 8461621525	H74443	ESTs	other
20411	3 8459400968	N48963	Homo sapiens mRNA for KIAA0689 protein partial cds	other
10345	3 8457714481	AA001663	ESTs	other
31261	3 8451974374	N56248	EST	other
6513	3 8378410994	AA446990	ESTs	other
13877	3 8363409835	AA476504	ESTs	other
40748	3 8253562321	N56879	EST	?
14509	3 8152852163	AA609943	ESTs	other
10281	3 8065567331	R80333	ESTs	other
25284	3 8044158642	AA045074	ESTs Weakly similar to 52-kD SS-A/Ro autoantigen [H. sapiens]	other
6730	3 7900025129	Y09305	H. sapiens mRNA for protein kinase Dyrk4 partial	other
16033	3 7884582402	AFFX-HUMISGF3AM97935_M8	AFFX-HUMISGF3AM97935_M8	?
38242	3 7827164808	AA621523	ESTs	other
27354	3 7794760435	AA425221	ESTs	?
4552	3 777263605	U49188	Human placenta (Df(3)) mRNA complete cds	SS, TM
18385	3 7750189108	AA227218	Homo sapiens CAGF9 mRNA partial cds	other
16754	3 7677416053	AA046067	EST - RC_AA046067	other
12752	3 7671137403	AA421250	ESTs	other
42463	3 7601033106	W50180	ESTs	other

FIGURE 8 (cont.)
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10614	3.7581069016	AA037357	ESTs	?
867	3.7459337969	D87716	Human mRNA for KIAA0007 gene partial cds	other
7608	3.7336047135	AA180907	ESTs	other
31795	3.732738742	N80703	ESTs	other
35377	3.7273784603	AA399453	EST - RC_AA399453	?
27828	3.7243928524	R98192	ESTs	other
25240	3.7243198335	AA039713	ESTs	other
11008	3.7197391366	AA194289	ESTs Weakly similar to ASH1 [D.melanogaster]	?
4341	3.7162349944	U38545	Human ARF-activated phosphatidylcholine-specific phospholipase D1a (hPLD1) mRNA complete cds	other
28833	3.7147818393	D59787	EST - RC_D59787_1	?
3750	3.7121007154	U09279	Collagen type XIX alpha 1	SS,
17483	3.6943413512	AA122147	ESTs	TM
16854	3.6915208471	AA055552	ESTs Weakly similar to KIAA0319 [H.sapiens]	TM
3709	3.6891556771	U07550	Heat shock 10 kD protein 1 (chaperonin 10)	other
1808	3.6852978422	L00205	KERATIN TYPE II CYTOSKELETAL 6D	?
24577	3.6617721053	Z38727	Homo sapiens mRNA for KIAA0555 protein complete cds	TM
31032	3.6570916386	N52508	ESTs	other
4951	3.6536195433	U69546	Human RNA binding protein Etr-3 mRNA complete cds	other
37660	3.6523275307	AA460225	ESTs	other
20418	3.6495357091	N49209	ESTs	other
27895	3.6485167436	AA470155	Homo sapiens coatomer protein (COPa) mRNA complete cds	?
7971	3.6434397185	AA287423	ESTs	other
27606	3.64303453	AA443793	ESTs	other
24677	3.6427250633	Z39338	ESTs Highly similar to POLIOVIRUS RECEPTOR HOMOLOG PRECURSOR [Mus musculus]	other
11070	3.6406198277	AA148521	ESTs Weakly similar to putative p150 [H.sapiens]	TM
9328	3.6356048599	D69618	Homo sapiens importin-alpha homolog (SRP1 gamma) mRNA complete cds	other
36826	3.6346898002	AA435996	ESTs	other
17878	3.6300045785	AA134275	Human HIV1 tat element modulatory factor mRNA sequence from chromosome 3	other
36209	3.6274694477	AA421266	ESTs Weakly similar to LIS-1 protein [H.sapiens]	other
34120	3.6258090412	AA211815	EST	?
39152	3.6246442011	AA486737	H.sapiens mRNA for Sm protein F	TM
38463	3.6184693268	AA504491	ESTs Weakly similar to contains similarity to C3HC4-class zinc finger [C.elegans]	TM
20064	3.6183899978	H98653	ESTs	TM
31256	3.5992620732	N56152	EST	?
9713	3.5985228643	L44338	Homo sapiens mRNA for KIAA0525 protein partial cds	other
28622	3.5788056147	D11837	ESTs	?
38057	3.5736105703	AA481549	EST - RC_AA481549	other
28763	3.5688723791	D45568	EST	?
16996	3.5680705709	AA069038	EST - RC_AA069038	TM
28628	3.5604144617	D11888	ESTs Moderately similar to PROHIBITIN [H.sapiens]	?
25804	3.5442954572	AA148885	ESTs	?
2492	3.5423984239	M22898	Tumor protein p53 (Li-Fraumeni syndrome)	?
14904	3.5411970737	T83389	ESTs Highly similar to GEPHYRIN [Rattus norvegicus]	other
25265	3.5347588502	AA043765	H.sapiens RY-1 mRNA for putative nuclear acid binding protein	other
13605	3.5327912417	AA456437	ESTs Weakly similar to CLEAVAGE STIMULATION FACTOR 64 KD SUBUNIT [H.sapiens]	other
42307	3.5318436465	T86595	EST - RC_T86595	TM
1544	3.526202414	J05068	TRANSCOBALAMIN I PRECURSOR	SS,
42339	3.5195081035	W02072	ESTs Weakly similar to No definition line found [C.elegans]	other
42311	3.5183719631	T97257	ESTs	other
2023	3.5040279423	L34600	INITIATION FACTOR IF-2 MITOCHONDRIAL PRECURSOR	other

FIGURE 8 (cont.)
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4540	3 4955308569	U48807	Human MAP kinase phosphatase (MKP-2) mRNA complete cds	other
33707	3 4888594277	Z39297	Neuronal pentraxin II	other
17220	3 4755703461	AA083070	EST - RC_AA083070_s	SS,
24332	3 4725273806	V65782	ESTs	other
35897	3 4668063718	AA112067	ESTs	other
20158	3 4538150055	N23638	ESTs Weakly similar to coded for by C. elegans cDNA yk52e10.5 (C. elegans)	other
6338	3 4485832071	AA117152	Homo sapiens protein regulating cytokinesis 1 (PRC1) mRNA complete cds	other
387	3 4421427234	D28589	EST - D28589	other
12319	3 4356289717	AA398109	ESTs	SS, TM
38276	3 4313139432	AA489711	ESTs	TM
15643	3 4312194246	W58247	ESTs Highly similar to KINESIN-LIKE PROTEIN KIF4 [Mus musculus]	other
11218	3 4232832843	AA180488	ESTs	TM
16539	3 4178863379	AA029028	Human mRNA for KIAA0073 gene partial cds	?
26203	3 4162847487	H28581	ESTs	other
13838	3 4162403464	AA465342	ESTs	other
25565	3 4160353003	AA112389	H4(D10S17C)	SS,
34018	3 4145335853	AA181488	Human high-affinity copper uptake protein (HCTR1) mRNA complete cds	TM
251	3 4006042851	D14520	Basic transcription element binding protein 2	other
3778	3 4004518201	U08848	Zinc finger protein 139 (clone pHZ-37)	other
24535	3 3964397837	Z38409	ESTs	other
18858	3 3925194041	AA056759	Human mRNA for KIAA0128 gene partial cds	TM
16127	3 3921645927	AA004669	ESTs	other
36683	3 3841316491	AA432268	ESTs	other
26149	3 3809497785	AA250824	ESTs Weakly similar to ZINC FINGER PROTEIN 91 [H. sapiens]	other
4011	3 3798093471	U20536	Human cysteine protease Mch2 isoform alpha (Mch2) mRNA complete cds	other
41001	3 3794250205	N78844	ESTs	other
5660	3 3789306731	X18396	NAD-DEPENDENT METHYLENETETRAHYDROFOLATE DEHYDROGENASE	SS,
19204	3 3776332343	H11829	ESTs	other
42323	3 3768515879	T98152	Fibrin 2	SS,
26928	3 3725378868	AA342580	ESTs	SS,
20497	3 369285912	N52565	ESTs	other
19226	3 36674249	H12455	ESTs	other
36267	3 3606841839	AA424045	ESTs	other
32257	3 3599796018	R54726	DNA-REPAIR PROTEIN XRCC1	other
17365	3 3522214732	AA101851	ESTs	other
15296	3 3491193196	V10684	ESTs Moderately similar to Similar to S. cerevisiae hypothetical protein L3111 [H. sapiens]	other
17675	3 3485872272	AA134064	ESTs	TM
40332	3 3458489589	H97585	Homo sapiens mRNA from chromosome 6q21-22 clone A3-A	other
7219	3 3385684843	AA056319	Homo sapiens protein phosphatase 2A B56-epitope (PP2A) mRNA complete cds	other
10006	3 3322827322	N81193	Homo sapiens mRNA for KIAA0628 protein complete cds	?
33985	3 3276877441	AA181580	Homo sapiens importin beta subunit mRNA complete cds	other
8570	3 3263855302	H85169	Homo sapiens sodium/myo-inositol cotransporter (SLC5A3) gene complete cds	other
37551	3 3155406577	AA456679	ESTs	other
686	3 3111782759	D88613	Human mRNA for hGCMs complete cds	other
23650	3 3069426629	T86293	ESTs	other
18367	3 3007433533	AA224180	ESTs Moderately similar to ovarian-specific protein [H. norvegicus]	?
42494	3 2908070546	V69385	H. sapiens HUMA gene (Clone T33)	other
14310	3 2753564661	AA598412	ESTs Highly similar to HYPOTHETICAL TRP-ASP REPEATS CONTAINING PROTEIN IN PM18-PC11 INTERGENIC REGION [Saccharomyces cerevisiae]	SS, TM

FIGURE 8 (cont.)

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19233	3.274416299	H12634	ESTs	other
42263	3.2731066284	T94343	Homo sapiens M92 protein spliced isoform 2 mRNA complete cds	other
12909	3.271352097	AA424405	ESTs	other
36385	3.26960223617	AA424469	ESTs	other
21555	3.2686295446	R33073	EST	?
13767	3.265695616	AA463234	ESTs	TM
4738	3.2661591937	U58766	Human FX protein mRNA complete cds	other
7258	3.263106866	AA075427	ESTs	other
17041	3.2629042076	AA070364	EST - RC_AA070364	?
15504	3.2615745245	V226362	ESTs	other
23793	3.2611829896	T90971	EST - RC_T90971	other
18214	3.2572346955	AA196933	ESTs	TM
7401	3.257164123	AA094800	Human translation initiation factor eIF3 p55 subunit mRNA complete cds	other
18912	3.2553600001	F10913	Homo sapiens clone 23617 unknown mRNA partial cds	other
36317	3.2509495347	AA425089	Human mRNA for KIAA0334 gene complete cds	?
9410	3.2507270851	H20443	H. sapiens mRNA for TRES	other
2146	3.2464307696	L41390	EST - L41390	?
10663	3.240614336	F04258	ESTs Highly similar to (HORGANIC PYROPHOSPHATASE [Box taurus])	?
33891	3.2392191406	AFXX-HUMTFRRM11507	AFXX-HUMTFRRM11507_M	?
14435	3.2372161315	AA068730	ESTs Weakly similar to ELONGATION FACTOR 1-ALPHA [Glandia inresistens]	other
9584	3.2363829855	H88128	ESTs Highly similar to GTP-BINDING PROTEIN LEPA [Pseudomonas fluorescens]	other
22061	3.2340098572	R49218	ESTs	TM
35796	3.233287605	AA410223	EST - RC_AA410223	?
37403	3.2261852043	AA453613	ESTs	other
15796	3.2260359988	X16889	ALPHA-GALACTOSIDASE A PRECURSOR	SS
15840	3.2257832439	X70944	PTB-ASSOCIATED SPLICING FACTOR	other
7518	3.2232170427	AA147144	EST - AA147144	other
32335	3.2228388982	R78248	ESTs	other
3256	3.2180538038	M92439	130 KD LEUCINE-RICH PROTEIN	other
4400	3.2173698081	U41387	Human Gu protein mRNA partial cds	other
7681	3.2074414299	AA206983	Homo sapiens mRNA for DRIM protein	other
16678	3.2041209443	W68649	ESTs	TM
39590	3.2038953621	F06281	ESTs	other
26583	3.1980022253	AA291921	ESTs Weakly similar to putative p150 [H. sapiens]	?
9806	3.1920380384	M80627	Transcription factor 12 (HTF4 helix-loop-helix transcription factors 4)	other
27755	3.1900699454	AA453444	ESTs	other
29983	3.1882200623	N25011	ESTs	?
21350	3.1876957756	R15846	ESTs	other
11981	3.1870525747	AA280928	ESTs	other
23930	3.1817500097	T96690	ESTs Weakly similar to 118 ALU SUBFAMILY J WARNING ENTRY !!! [H. sapiens]	other
30399	3.1792054412	N45226	EST	?
22296	3.1781990049	R59312	ESTs	other
13494	3.1673900969	AA453431	ESTs	TM
12908	3.1530533441	AA427579	ESTs	other
22319	3.1469419301	R60567	ESTs	TM
31309	3.1466750523	N66818	ESTs	TM
31192	3.1458779523	N64406	ESTs	other
11288	3.144853134	AA196512	ESTs	TM
170	3.1430726349	D00596	Thymidylate synthase	?
5307	3.1347905628	U90549	Human non-histone chromosomal protein (HNC) mRNA complete cds	other

FIGURE 8 (cont.)

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26105	31311103325	AA243133	Homo sapiens serine/threonine kinase (STAK) mRNA complete cds	other
11659	31281786108	AA251909	Homo sapiens MAD3-like protein kinase mRNA complete cds	other
19177	3124406365	K10984	ESTs	TM
8389	31241545024	AA425230	ESTs	TM
34087	31216555797	AA205125	Protein serine/threonine kinase stg2	other
25001	31209327466	AA004718	ESTs Weakly similar to BAP31 protein [H.sapiens]	other
14149	31198500308	AA489665	ESTs	other
10167	31191800923	R55076	ESTs	other
17390	31071058868	AA102508	ESTs	other
42387	31044680628	W42028	ESTs	other
14835	31042015743	T94828	ESTs Weakly similar to GA BINDING PROTEIN BETA-2 CHAIN [H.sapiens]	other
41873	31030349819	R78618	ESTs Weakly similar to GTP-binding protein rab10 [R.norvegicus]	other
2750	31026223619	M35999	Integrin beta 3 (platelet glycoprotein Ila antigen CD61)	?
3190	31026223619	M86808	PYRUVATE DEHYDROGENASE E1 COMPONENT ALPHA SUBUNIT TESTIS-SPECIFIC FORM PRECURSOR	?
17406	30999394188	AA112979	Homo sapiens mRNA for VRK1 complete cds	other
598	30912414004	D59253	Homo sapiens mRNA for low molecular mass ubiquitin-binding protein complete cds	other
29348	30802365759	H69021	ESTs	other
14130	30744457534	AA489041	ESTs	other
14134	3069660341	AA489080	ESTs Highly similar to phosphorylation regulatory protein HP-10 [H.sapiens]	other
42421	30684159011	W45491	ESTs Weakly similar to T23G11.7 [C.elegans]	other
15723	30660746209	V79060	ESTs Highly similar to ribosome-binding protein p34 [R.norvegicus]	other
11140	30650815198	AA158132	ESTs Highly similar to YSA1 PROTEIN [Saccharomyces cerevisiae]	other
28531	30649767987	C20679	ESTs	other
2021	30628707497	L34409	Homo Sapiens (clone B383E13) chromosome 4p16.3 DNA fragment	?
14322	3058260163	AA810108	ESTs Highly similar to PROBABLE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE C21E11.05C [Schistosoma carolinensis]	SS,
29853	30545821815	N22162	ESTs	other
15862	30521475703	Z21420	ESTs	other
6341	30509806038	X95632	Human Abi Interactor 2 (Abi-2) mRNA complete cds	other
13229	30485366337	AA443811	ESTs	other
27315	3048622812	AA424038	ESTs	other
13621	30302306369	AA56821	ESTs Highly similar to BONE MORPHOGENETIC PROTEIN 1 PRECURSOR [Mus musculus]	other
35929	30269182409	AA412429	ESTs	other
17925	30253428426	AA184209	Homo sapiens RRM RNA binding protein GRY-rip (GRY-RSP) mRNA complete cds	other
5053	30249536782	U76992	Human Tat-SF1 mRNA complete cds	other
15080	30213293848	U54999	Human LGN protein mRNA complete cds	other
17757	30205801351	AA147224	EST	?
19050	30192378314	H05509	ESTs	other
26530	30176823278	AA278650	ESTs	other
16806	30158779832	AA053258	Homo sapiens mRNA for KIAA0648 protein partial cds	TM
29088	30149440394	F13700	Homo sapiens ribonuclease P protein subunit p40 (RPP40) gene complete cds	other
22960	30141662421	T10272	ESTs	other
33585	30121672451	W93000	ESTs	other
220	30109180714	D13627	Human mRNA for KIAA0002 gene complete cds	TM
4298	30024671064	U36448	Human Ca2+-dependent activator protein for secretion mRNA complete cds	TM
7445	29995643641	AA104023	ESTs	?
40903	29980347088	N68670	ESTs	?
18055	29973386648	AA176387	ESTs	other
7282	29962782596	AA083339	ESTs	other

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9348	2.9949017671	H03680	ESTs	TM
806	2.9877476516	D87009	Human (lambda) DNA for immunoglobulin light chain	?
38447	2.9876031644	AA504255	Human protein kinase ATR mRNA complete cds	other
41484	2.9870604981	R46837	ESTs	?
9682	2.9869352305	L19161	TRANSLATIONAL INITIATION FACTOR 2 GAAMBA SUBUNIT	other
18978	2.9801154057	AA083625	EST	?
37428	2.9756408909	AA454016	ESTs	other
2588	2.9725898298	M27878	Zinc finger protein 84 (MZF2)	other
15174	2.9695024379	U82987	Human Bcl-2 binding component 3 (bbc3) mRNA partial cds	other
33620	2.9657446567	W93943	ESTs	other
6784	2.9655061112	Y11581	Homo sapiens ribosomal protein S12 gene nuclear gene encoding mitochondrial protein complete cds	?
41077	2.9642389716	N95028	ESTs	TM
1932	2.9609985996	L24804	Human (p23) mRNA complete cds	other
39556	2.9588964022	F03738	ESTs	other
16108	2.9574232912	AA002258	ESTs	SS
32156	2.9574232912	R40381	ESTs	?
13617	2.9552306838	AA456646	ESTs	other
11989	2.955203991	AA281251	ESTs Weakly similar to Inthorax protein trxl (D.melanogaster)	other
6056	2.947654132	X58194	Pancreoelysin (human keratinocyte line HaCat) mRNA 2105 nt	TM
15446	2.9445456286	V027374	Homo sapiens 10kD protein (BC10) mRNA complete cds	other
38086	2.9445277634	AA482557	EST	?
13878	2.9444133384	AA476604	ESTs	other
6209	2.9422425032	X78770	H.sapiens PAP mRNA	other
358	2.9357591919	D28791	Phosphatidylinositol glycan class A (paroxysmal nocturnal hemoglobinuria)	?
1351	2.9266145582	HG4755-HT5203	EST - HG4755-HT5203	?
42824	2.9266145582	V87804	ESTs	other
34895	2.9242794509	AA311972	ESTs	other
20157	2.9214162978	N23393	ESTs	other
29248	2.9188102155	H52918	ESTs	?
4893	2.9178533564	U66615	Human SVM/SNF complex 155 KDa subunit (BAF155) mRNA complete cds	other
10104	2.9150324884	R23855	ESTs	TM
15035	2.9147218324	U46116	Protein tyrosine phosphatase receptor type gamma polypeptide	?
1605	2.9141775797	L00058	V-myc avian myelocytomatosis viral oncogene homolog	?
4536	2.9075603336	U48705	Receptor protein-tyrosine kinase EDDR1	?
10173	2.905710598	R56678	ESTs Weakly similar to cell division control protein CDC21 (H.sapiens)	?
26555	2.9056210172	AA279071	ESTs Weakly similar to TDBA11.2 (C.elegans)	other
4401	2.9047655582	U41515	Human deleted in split hand/split foot 1 (DSS1) mRNA complete cds	other
21009	2.8995011918	N90401	ESTs	TM
3602	2.894817322	U01317	HEMOGLOBIN EPSILON CHAIN	?
4833	2.8919254016	U63455	Sulfonylurea receptor (hyperinsulinemia)	?
36200	2.8912301426	AA421164	ESTs	?
26645	2.8898309441	AA281076	ESTs	other
35299	2.8887661574	AA396622	Transcription factor 6-like 1 (mitochondrial transcription factor 1-like)	other
9804	2.8880347344	M74558	Human SIL mRNA complete cds	other
5216	2.8879777815	U83410	Human CUL-2 (cul-2) mRNA complete cds	other
12313	2.8847621603	AA397816	ESTs	other
5528	2.8636060438	X62048	WEE1-LIKE PROTEIN KINASE	?
39586	2.8618258313	F09155	ESTs	TM
34758	2.8775214637	AA267880	EST	?
18199	2.8763649024	AA195318	ESTs	other

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10867	2.8720974689	H81476	ESTs	?
6061	2.8678372836	X59390	CD47 antigen (Rn-related antigen integrin-associated signal transducer)	SS, TM
5254	2.862067233	U86782	Human 26S proteasome-associated pad1 homolog (PDH1) mRNA complete cds	other
13579	2.8570620494	AA455967	Human neuronal PAS2 (NPAS2) mRNA complete cds	?
11117	2.8568053461	HG3075-HT3236	EST - HG3075-HT3236	?
20533	2.8564678641	N54407	ESTs	TM
38495	2.8562453397	AA505118	Human nucleoporin 98 (NUP98) mRNA complete cds	other
33729	2.8548155651	Z39654	EST	?
2028	2.85327776139	L35035	RIBOSE 5-PHOSPHATE ISOMERASE	other
27374	2.8520674335	AA425816	ESTs Weakly similar to Y53C12A.3 [C.elegans]	other
19404	2.8518690748	H20068	ESTs	other
26106	2.8504706329	AA243189	ESTs	SS,
4189	2.8439972255	U30930	UDP glycosyltransferase 8 (UDP-galactose ceramide galactosyltransferase)	TM
16708	2.8427388072	AA043944	ESTs	other
357	2.8350474214	D26156	Human mRNA for transcriptional activator hSNF2b complete cds	other
26045	2.8316740098	AA236276	ESTs	other
17796	2.8312342777	AA150435	ESTs	other
8059	2.8268722809	AA310967	ESTs Weakly similar to T04AB.11 [C.elegans]	other
42914	2.827999584	N69220	ESTs	other
27169	2.8263163852	AA410287	H. sapiens mRNA for basic transcription factor 2.34 kD subunit	other
21358	2.8262413945	R16079	ESTs	other
3572	2.8261469131	S87759	Protein phosphatase 2C alpha (human teratocarcinoma mRNA 2346 nt)	other
11877	2.8259099942	AA262727	ESTs	other
1653	2.8234017508	L05424	CD44 antigen (cell adhesion molecule)	?
24645	2.8131264428	Z39106	ESTs	other
35630	2.8126257031	AA411448	ESTs	TM
4433	2.8114422177	U43279	EST - U43279	?
20151	2.8109454503	N22895	Homo sapiens clone 1400 unknown protein mRNA partial cds	other
36548	2.8084431065	AA599267	EST - RC_AA599267	other
7777	2.8071817829	AA236820	ESTs	other
32845	2.80583194	VQ31668	EST	?
28258	2.8043934182	AA505133	ESTs	other
6853	2.798263202	Z22851	TRANSCRIPTION FACTOR P65	?
35944	2.7913872996	AA412483	ESTs	?
30648	2.7866522676	N50971	ESTs	?
18965	2.7857482775	H01411	ESTs	TM
8816	2.785444221	AA460077	ESTs	other
14945	2.7838257917	T99608	ESTs Weakly similar to F35G2.2 [C.elegans]	other
8375	2.7805657722	AA422160	H.sapiens NAP (nucleosome assembly protein) mRNA complete cds	other
34926	2.7792111121	AA342084	EST - RC_AA342084	other
320	2.7786978435	D21282	Human mRNA for KIAA0035 gene partial cds	other
27057	2.7781218063	AA400998	ESTs	SS,
36282	2.7746002184	AA424513	EST - RC_AA424513	other
6480	2.7735431318	X91788	H. sapiens mRNA for lcn protein	other
15424	2.7731675808	W27054	APOLIPOPROTEIN A1 REGULATORY PROTEIN-1	other
11802	2.7730818255	AA243007	ESTs	?
18175	2.77056686	AA194730	ESTs	?
25202	2.7698585998	AA034527	EST	?
1581	2.7697545972	L07493	Replication protein A (E. coli RecA homolog RAC51 homolog)	other
14568	2.767984858	AA621122	ESTs	other
25614	2.7633374335	AA115769	ESTs	other

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14182	2.7606046934	AA490825	ESTs	other
31599	2.7591187958	N72196	EST	other
18253	2.7471964081	AA208370	ESTs	other
6193	2.7442487702	X75082	Regulatory factor (trans-acting) 3	other
22911	2.7433449859	T03865	ESTs	other
35540	2.7432465806	AA401274	Homo sapiens RRM RNA binding protein Gyr-1b (GRY-RBP) mRNA complete cds	other
35955	2.7389431758	AA412528	ESTs Weakly similar to ORF2 consensus sequence encoding endonuclease and reverse transcriptase minus RNaseH (R norvegicus)	other
17642	2.7377607284	AA132693	ESTs Moderately similar to C-1-TETRAHYDROFOLATE SYNTHASE CYTOPLASMIC (H sapiens)	other
6131	2.7371784571	X72841	Human retinoblastoma-binding protein (RbAp48) mRNA complete cds	other
41429	2.7347564467	R44994	ESTs	other
17052	2.7323944161	AA070815	EST - RC_AA070815	other
34243	2.7294147034	AA235050	ESTs	?
22937	2.7284347248	T10065	Homo sapiens TLS-associated protein TASP-2 mRNA complete cds	other
5183	2.7243199196	U82130	Human tumor susceptibility protein (TSG101) mRNA complete cds	other
30837	2.7231409239	N54416	ESTs	other
16243	2.7228028265	AA012902	ESTs	TM
19954	2.7215193485	H80100	ESTs	other
6444	2.720441384	X89760	H.sapiens mRNA for TGIF protein	other
5916	2.7192579481	X61072	Human mRNA for T cell receptor clone IGRA17	SS,
6240	2.7168544194	X78627	H.sapiens mRNA for transt	?
42116	2.7144176166	T59924	EST - RC_T59924	other
7701	2.7107290468	AA215333	ESTs	TM
17568	2.7096978968	AA128905	ESTs	TM
42534	2.7086014274	W73189	Homo sapiens protein-tyrosine kinase EPHB2v (EPHB2) mRNA complete cds	SS, TM
29813	2.708372123	N21111	ESTs	other
36898	2.7067394943	AA609458	ESTs	other
10316	2.7055639457	R88880	ESTs Moderately similar to zinc finger protein (M. musculus)	other
14789	2.7040621985	S54641	HZF-16	other
32961	2.7012195407	W36366	Human mRNA for KIAA0005 gene complete cds	other
35273	2.6975345483	AA398507	ESTs	other
10180	2.6960696303	R50100	ESTs	?
32563	2.6955482902	T27697	Human mRNA for KIAA0036 gene complete cds	other
34502	2.6948574449	AA262768	ESTs	TM
13223	2.6912995353	AA443720	ESTs	other
8494	2.6908515739	AA443460	ESTs	other
7776	2.6900717525	AA236771	ESTs	other
10400	2.6898958961	AA007234	ESTs	other
1130	2.6897527619	HG3132-HT3308	EST - HG3132-HT3308	?
2379	2.6874247447	M16937	Human homeo box c1 protein mRNA complete cds	TM
18906	2.6881450774	F10668	Human SH3 domain-containing protein SH3P18 mRNA complete cds	?
34796	2.6853510115	AA291259	ESTs	TM
41955	2.6821408177	T33311	Neuronal pentraun II	other
2009	2.6791061739	L33881	Protein kinase C iota	?
33688	2.6775081286	Z38501	ESTs Weakly similar to PROBABLE ES PROTEIN (Human papillomavirus type 58)	other
1385	2.6771402807	HG884-HT884	EST - HG884-HT884	?
24758	2.6750080868	Z40075	ESTs	other
7620	2.6742248913	AA192484	ESTs Weakly similar to MITOCHONDRIAL INNER MEMBRANE PROTEASE SUBUNIT 2 (S. cerevisiae)	other
30733	2.6739544496	N52078	Homo sapiens mRNA for KIAA0637 protein complete cds	other
21256	2.6723253055	R09195	Homo sapiens mRNA for KIAA0564 protein partial cds	other
40526	2.669020458	N29325	ESTs Highly similar to 47 KD PROTEIN (Pseudomonas	other

FIGURE 8 (cont.)

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			chloroplast)		
25285	2.6685455406	AA045083	VITAMIN K-DEPENDENT GAMMA-CARBOXYLASE	other	
9296	2.667949532	D82775	ESTs Weakly similar to unknown [S cerevisiae]	SS	
12174	2.6669305328	AA282128	ESTs	other	
38357	2.6652770538	AA491265	EST	TM	
3154	2.6619596800	M83712	Cholinergic receptor nicotinic alpha polypeptide 5	TM	
7383	2.655440738	AA038834	ESTs Weakly similar to HYPOTHETICAL 16.8 KD PROTEIN IN SMY2-RPS101 INTERGENIC REGION [S cerevisiae]	other	
1923	2.6530372325	L23808	Matrix metalloproteinase 12 (macrophage elastase)	SS	
24908	2.6527048053	Z41840	ESTs	other	
34726	2.6495430564	AA287278	ESTs	SS	
30407	2.6495430564	N45983	ESTs	TM	
20408	2.6450891347	N48787	ESTs Moderately similar to III ALU SUBFAMILY SC WARNING ENTRY III [H sapiens]	other	
7158	2.6455059455	AA037208	ESTs	TM	
26286	2.6445109706	AA253351	ESTs	?	
19822	2.6431968212	H58684	ESTs	?	
12379	2.6428182941	AA399418	Homo sapiens mRNA for JN23 protein complete coding sequence (clone IMAGE 34591 and IMAGE 45355 and LUNLc110133Q7 (RZPD Berlin))	other	
22698	2.6396306055	R89287	ESTs	other	
24161	2.6394502284	W58015	ESTs	other	
9558	2.6370149706	H81497	ESTs	TM	
18104	2.6358767288	AA188801	ESTs	other	
24882	2.6357248889	Z41563	ESTs	other	
40038	2.6347874784	H59485	ESTs	other	
8965	2.6344845492	AB002359	Human mRNA for KIAA0361 gene KIAA0361 protein	other	
22148	2.6288326966	R51831	ESTs	other	
4627	2.6277060831	U51980	Human hPtp1B mRNA complete cds	other	
8394	2.6275394634	AA426156	ESTs	TM	
20422	2.6272599718	N49300	ESTs	other	
41602	2.6258613824	R67258	ESTs Moderately similar to molesin [M musculus]	other	
612	2.6257836582	D63480	Human mRNA for KIAA0146 gene partial cds	TM	
4821	2.619521444	U62801	Human protease M mRNA complete cds	SS, TM	
16807	2.617722828	AA053296	ESTs	other	
15288	2.6173997018	W07582	ESTs Moderately similar to rAB [R norvegicus]	other	
38023	2.6135617291	AA481058	ESTs	other	
23822	2.6120077647	T91715	ESTs Highly similar to HYPOTHETICAL 103.6 KD PROTEIN IN COX5B-PFK26 INTERGENIC REGION [Saccharomyces cerevisiae]	TM	
10951	2.6116018519	AA126719	ESTs	other	
6150	2.6113980879	X74262	RETINOBLASTOMA BINDING PROTEIN P46	other	
39336	2.6109987712	C20945	ESTs Highly similar to HYPOTHETICAL 54.2 KD PROTEIN IN CDC12-ORC8 INTERGENIC REGION [Saccharomyces cerevisiae]	other	
17793	2.6102158176	AA150242	ESTs Highly similar to modulator recognition factor 2 [H sapiens]	other	
26891	2.6085107387	AA292659	ESTs	other	
2175	2.607468576	L42621	Homo sapiens L-y-9 mRNA complete cds	TM	
10642	2.6048724507	AA040149	Human Chromosome 16 BAC clone CIT987SK-A-270G1	other	
15026	2.6031453592	U41816	Human C-1 mRNA complete cds	other	
7659	2.6019047419	AA215299	Homo sapiens chromosome 19 cosmid R30763	other	
6543	2.6011828937	X95654	Homo sapiens mRNA for SCP-1 complete cds	other	
20636	2.5993884878	N62122	ESTs	other	
11308	2.5993311375	AA207114	ESTs	other	
4386	2.5966362866	U24704	Human antisecretory factor-1 mRNA complete cds	other	
38615	2.5963996726	AA598938	EST - RC_AA598938	other	
11819	2.5961501969	AA258186	ESTs	other	

FIGURE 8 (cont.)

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37433	2.5957446266	AA454103	ESTs	other
28270	2.5939657529	AA521186	ESTs	TM
5587	2.5932338399	X13482	U2 SMALL NUCLEAR RIBONUCLEOPROTEIN A'	other
19041	2.5930132063	H59617	ESTs Highly similar to UBIQUITIN-CONJUGATING ENZYME E2-17 KD (<i>Drosophila melanogaster</i>)	other
10655	2.5925442731	AA040882	ESTs	?
14053	2.5899324577	AA485147	ESTs Highly similar to HYPOTHETICAL 83.6 KD PROTEIN R05D3.2 BY CHROMOSOME III (<i>Caenorhabditis elegans</i>)	other
31574	2.5883094453	N71303	EST	?
7614	2.5870699315	AA187579	ESTs Weakly similar to Yel007c-ap (<i>S. cerevisiae</i>)	other
37671	2.5847445397	AA479195	EST	?
7090	2.5845365105	AA099913	Human sapiens diphthamide biosynthesis protein-2 (DPH2) mRNA complete cds	other
17852	2.5841100415	AA156360	ESTs	other
24219	2.5823376094	W69980	ESTs	other
19070	2.5813645258	H05970	Human clone Z3960 mRNA sequence	other
17719	2.5803606155	AA136569	EST	?
38669	2.5791967991	AA599694	Human mRNA for KIAA0133 gene complete cds	TM
20982	2.5763957078	N79565	ESTs	TM
9158	2.5731038907	D31446	Human sapiens breakpoint cluster region protein 1 (BCRG1) mRNA complete cds	other
11362	2.5731137778	AA227261	ESTs	other
8613	2.5723119482	AA459555	Human sapiens mRNA for KIAA0546 protein partial cds	TM
13868	2.5715997844	AA476319	ESTs	SS
10303	2.5712815907	R86178	Ataxia telangiectasia mutated (includes complementation groups A C and D)	?
22299	2.567916035	R59801	EST	?
18267	2.5673459608	AA200591	EST - RC_AA200591	other
20555	2.5654242568	N55168	ESTs	other
39552	2.5645918108	F03605	PUTATIVE 60S RIBOSOMAL PROTEIN	other
27530	2.5631130948	AA435996	ESTs	other
1795	2.5608471476	L13434	Human chromosome 3p21.1 gene sequence complete cds	?
14745	2.5603154956	D60354	Human mRNA for KIAA0007 gene partial cds	other
2993	2.5587815672	M64929	Protein phosphatase 2 (formerly 2A) regulatory subunit B (PR 52) alpha isoform	other
19191	2.5545260975	H11297	ESTs	other
12986	2.5507998953	AA430032	ESTs Moderately similar to PTTG gene product (<i>R. norvegicus</i>)	?
15452	2.5488533884	W27451	Human Cdc5-related protein (PCDC5RP) mRNA complete cds	other
16003	2.5465671712	AA171692	ESTs	other
24198	2.5461854497	W67524	Human protein-tyrosine phosphatase (HU-PP-1) mRNA partial sequence	TM
42653	2.5447626827	W92703	ESTs	other
26446	2.544106171	AA258796	EST Weakly similar to putative p150 (<i>H. sapiens</i>)	?
30438	2.5368548574	M47204	ESTs Weakly similar to C50F4.12 (<i>C. elegans</i>)	other
36365	2.5362912735	AA429893	ESTs Weakly similar to probable CBP3 protein homolog (<i>C. elegans</i>)	other
26135	2.535658968	AA243765	ESTs	other
41885	2.5349932886	T23449	ESTs Moderately similar to ZNF127-Xp (<i>H. sapiens</i>)	SS
15457	2.5343495968	W27560	ESTs	other
27748	2.5320767519	AA453159	Human kinesin-like spindle protein HKSP (HKSP) mRNA complete cds	other
32315	2.5302979959	R59840	ESTs Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (<i>Nycticebus coucang</i>)	?
25310	2.5274401579	AA046745	ESTs	other
42720	2.5222453766	Z39436	ESTs	other
12939	2.5200945911	AA428204	ESTs	other
30746	2.5198420998	N52243	ESTs	other
2222	2.5193624578	L76703	Human sapiens protein phosphatase 2A B56-epsilon (PP2A) mRNA complete cds	?
11609	2.5191765545	AA243303	ESTs	TM

FIGURE 8 (cont.)

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9658	2 5185814336	L16991	Deoxythymidylate kinase	other
12210	2 5172044681	AA293774	ESTs Weakly similar to PROBABLE TRYPTOPHANYL-TRNA SYNTHETASE MITOCHONDRIAL (C. elegans)	other
3563	2 5169818533	S83364	EST - S83364	other
42407	2 5128230047	V444768	Homo sapiens nephrocytin (NPHP1) mRNA partial cds	?
32826	2 5128052161	V20391	Human mRNA for kinesin-related protein partial cds	other
9692	2 5119977118	L37747	LAMIN B1	?
27862	2 5094571267	AA458908	ESTs	TM
33691	2 509287494	Z39630	EST	other
17288	2 5088624644	AA085178	ESTs	SS,
9888	2 5078170902	H35449	ESTs Highly similar to HYPOTHETICAL 30.3 KD PROTEIN IN APE1/AP4-GVP1 INTERGENIC REGION [Saccharomyces cerevisiae]	other
5832	2 5073880985	X62153	Minichromosome maintenance deficient (S. cerevisiae)	other
15885	2 5053862932	X95073	H. sapiens mRNA for transin associated protein X	other
17952	2 5049193223	AA165677	ESTs Weakly similar to F16A11.1 [C. elegans]	other
12187	2 5042458391	AA293206	ESTs	other
6210	2 5042034458	X76942	Homo sapiens golin-245 mRNA complete cds	other
34047	2 5041917773	AA194166	ESTs Weakly similar to G1 TO S PHASE TRANSITION PROTEIN 1 HOMOLOG [H. sapiens]	other
16929	2 5034461307	AA058952	ESTs	other
26834	2 5028075682	AA287138	ESTs Weakly similar to ASPARTYL-TRNA SYNTHETASE [Thermus aquaticus thermophilus]	other
6157	2 5017270258	U80034	Human mitochondrial intermediate peptidase precursor (MPEP) mRNA mitochondrial gene encoding mitochondrial protein complete cds	other
38434	2 5005880672	AA497013	ESTs	?
33269	2 5000262771	W72967	ESTs	other
26991	2 4990009911	AA398284	ESTs	other
7590	2 4948786183	AA173505	ESTs Weakly similar to HYPOTHETICAL 46.1 KD PROTEIN IN PHO2-POL3 INTERGENIC REGION [S. cerevisiae]	other
14960	2 4896232864	UC5237	Human fetal Aiz-60-reactive clone 1 (FAC1) mRNA complete cds	other
13585	2 4866752902	AA455999	ESTs Highly similar to NEUROLYSIN PRECURSOR [Sus scrofa]	other
35901	2 4847673158	AA412151	ESTs	other
38185	2 4826740426	AA487508	Homo sapiens mRNA for KIAA0588 protein complete cds	other
34678	2 4824371274	AA284744	Annexin XI (56kD autoantigen)	other
1424	2 4811113231	J02645	Eukaryotic translation initiation factor 2A	other
16778	2 4800522256	AA047008	ESTs	other
21876	2 4789005203	R43286	EST - RC_R43286	?
17778	2 4685725489	AA149641	ESTs	other
24559	2 4682754649	Z38568	ESTs	other
7781	2 4679471166	AA242904	Homo sapiens proline-rich G1a protein 1 (PRGP1) mRNA complete cds	?
7474	2 4677129013	AA126592	ESTs Weakly similar to No definition line found [C. elegans]	other
34290	2 4675279697	AA235866	ESTs	other
5318	2 4673813483	U90905	Human clone 23574 mRNA sequence	TM
10218	2 4645666536	R68884	ESTs Highly similar to HYPOTHETICAL 44.2 KD PROTEIN IN SCQ2-MRF1 INTERGENIC REGION [Saccharomyces cerevisiae]	other
18109	2 4634292267	AA188981	Homo sapiens retinoblastoma-associated protein HEC mRNA complete cds	?
6485	2 4613518897	X92098	H. sapiens mRNA for transmembrane protein mp24	SS, TM
34964	2 4591845976	AA342959	EST - RC_AA342959	?
42558	2 4588830205	W74751	ESTs	other
27444	2 4585780563	AA430160	ESTs Weakly similar to F25H9.7 [C. elegans]	other
21284	2 4582503599	R10301	EST	?
8920	2 4588596729	AF006265	Homo sapiens cancer associated surface antigen (RCAS1) mRNA complete cds	other
30037	2 4544484116	N27439	ESTs	TM
27802	2 4527890177	AA443702	ESTs Weakly similar to WC2B12.7 [C. elegans]	TM

FIGURE 8 (cont.)

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3390	2 4525517032	S59184	RYK receptor-like tyrosine kinase	TM
25040	2 452352841	AA010188	ESTs	other
37713	2 4487800271	AA461317	ESTs	other
40477	2 4477660739	N24000	Homo sapiens BAC clone RG300E22 from 7q21-q31.1	other
29302	2 4470532391	H72914	ESTs	other
35521	2 4465885249	AA400831	ESTs	other
20324	2 4464518504	N35406	Phospholipase C beta 4	SS,
19620	2 4460334893	F02506	ESTs	other
21067	2 4406971835	R00186	EST	?
9950	2 4398530157	N71503	ESTs	other
31955	2 4363228422	N93629	ESTs	SS,
15120	2 4345895403	U73524	Human putative ATP/GTP-binding protein (HEAB)	TM
26813	2 4339770686	D59257	mRNA complete cds	other
36082	2 4295434916	AA482284	Human C-1 mRNA complete cds	other
34723	2 428289395	AA287115	ESTs	other
7860	2 427332589	AA285277	Homo sapiens brain expressed ring finger protein mRNA	other
19073	2 4231729031	AA180453	complete cds	other
36755	2 4222443392	AA435698	EST	other
18927	2 4187841215	F11087	EST - RC_AA435698	other
3457	2 4186224787	S74728	ESTs	other
38606	2 4177893475	AA588844	Ankuran	TM
20967	2 41519947	N76086	ESTs	other
24752	2 4141498374	Z40012	ESTs	other
28443	2 4138974256	AA621611	Homo sapiens mRNA for KIAA0587 protein complete	other
452	2 4135942278	D38076	cds	?
11701	2 4134095351	AA253031	ESTs	other
13655	2 412509306	AA458919	RAN binding protein 1	other
24822	2 4118066031	Z40958	Homo sapiens RRM RNA binding protein GRY- (GRY- RBP) mRNA complete cds	other
12672	2 4112720798	AA417067	ESTs Weakly similar to 26S proteasome subunit p4.5 [H sapiens]	other
4836	2 4106618618	U63717	ESTs	other
47700	2 4083828799	T83729	Human osteocalcin stimulating factor mRNA complete	other
10987	2 4078540866	AA132239	cds	?
35672	2 4073821434	AA404995	EST - RC_T83729	other
6224	2 406310553	X77748	ESTs Highly similar to HYPOTHETICAL 47.4 KD PROTEIN IN SHP1-SEC17 INTERGENIC REGION [Saccharomyces cerevisiae]	other
28395	2 404213441	AA610064	EST - RC_AA404895	other
36390	2 4032664297	AA426291	Glutamate receptor metabotropic 3	TM
21045	2 4031905697	N93403	ESTs	other
4558	2 4024665899	U49379	ESTs Weakly similar to No definition line found [C elegans]	other
12916	2 3996505067	AA427745	ESTs	?
20850	2 3998090334	N69514	Human diacylglycerol kinase epsilon. DGK mRNA	TM
29759	2 3986103066	H99972	complete cds	other
36786	2 3971859161	AA435815	ESTs Weakly similar to oxidoreductase [H sapiens]	other
31942	2 3947415736	N93185	ESTs	other
7097	2 393822714	AA011452	Human Ctl- associated RS cytoplasm CARS-Cyp mRNA	other
39462	2 3936147708	D60063	complete cds	other
14420	2 3919915706	AA600322	ESTs	other
34829	2 3916035475	AA262527	ESTs Highly similar to AAC-RICH MRNA CLONE AAC3 PROTEIN [Dictyostelium discoideum]	other
27431	2 3905463084	AA429038	EST - RC_AA262527	other
6387	2 3904071666	X85372	ESTs	TM
11342	2 3902176276	AA223874	H sapiens mRNA for Sm protein F	other
			Homo sapiens mRNA for KIAA0704 protein partial cds	other

FIGURE 8 (cont.)
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1487	2.368369765	J04088	Topoisomerase (DNA) II alpha (170kD)	other
9841	2.3641622016	M95724	Centromere autoantigen C	other
11454	2.3620201875	AA233854	ESTs	TM
29950	2.3607499489	N24902	Homo sapiens mRNA for E1B-55kDa-associated protein	TM
6386	2.3607187289	AA426176	ESTs Weakly similar to Similar to S cerevisiae hypothetical protein L3111 [H.sapiens]	other
32978	2.3605995259	VW42768	Human terminal transferase mRNA complete cds	other
27872	2.3784145648	AA459254	ESTs	other
11623	2.3769685069	AA243617	ESTs	other
26582	2.3766857777	AA279768	ESTs	other
22142	2.3761275381	R51382	Homo sapiens mRNA for KIAA0659 protein partial cds	other
13533	2.3758359586	AA454607	ESTs Highly similar to HYPOTHETICAL 402 kD PROTEIN K12H4.3 IN CHROMOSOME II [Caenorhabditis elegans]	other
11534	2.3747649776	AA236223	ESTs	other
5976	2.3709397882	X64229	DEK PROTEIN	other
6231	2.3680994679	X78121	Choroideremia	TM
2382	2.3677644584	M16967	Coagulation factor V	other
22887	2.3673034941	T03314	ESTs	TM
24371	2.3663729415	VW87415	ESTs Weakly similar to H1 ALU SUBFAMILY J WARNING ENTRY III [H.sapiens]	other
25286	2.3658134948	AA045261	ESTs	other
8054	2.3647542780	C02472	ESTs Weakly similar to EBV-INDUCED G PROTEIN-COUPLED RECEPTOR 1 PRECURSOR [Homo sapiens]	other
8163	2.3646144577	AA357394	ESTs	other
12233	2.3640777771	AA343513	ESTs Weakly similar to LINE/lg H-chain fusion protein [M.musculus]	SS
22824	2.3634007127	T06195	ESTs	other
14371	2.361524453	AA598219	ESTs Moderately similar to ALR [H.sapiens]	other
12401	2.3607283644	AA420229	ESTs	other
26169	2.3599033182	AA251089	ESTs Weakly similar to ORF YOR281c [S.cerevisiae]	?
23095	2.3592943521	T23539	ESTs Highly similar to zinc finger protein [M.musculus]	other
26524	2.3582182239	N53965	ESTs	other
20837	2.3577032218	N69263	ESTs Highly similar to HEXOKINASE TYPE I [Homo sapiens]	other
18201	2.3573132815	AA195358	Homo sapiens DNA sequence from PAC 434014 on chromosome 1q32.3-41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1 the ADORA2BP adenosine A2b receptor LONE pseudogene the IRF6	other
7813	2.3566868562	AA248297	ESTs	TM
21195	2.3547018746	R07210	ESTs	other
13377	2.3513919997	AA449720	Homo sapiens clone 24706 mRNA sequence	other
9714	2.3497245732	L44367	ESTs	other
41537	2.3480892052	R55673	ESTs	other
17352	2.34596172	AA100925	ESTs	other
11914	2.3446613991	AA278907	ESTs	?
24890	2.3440589932	Z41634	ESTs	other
28796	2.3434458024	D51272	EST - RC_D51272_s	?
36796	2.342525534	AA435870	ESTs Weakly similar to B0564.1 (C.elegans)	other
22491	2.3408264581	R70012	EST	other
4798	2.3403776443	U61535	Human calcium-binding protein cDNA complete cds	other
40847	2.3397210986	N86354	ESTs	other
15657	2.3392349306	W63627	Small inducible cytokine A5 (RANTES)	TM
24482	2.3374048148	Z36137	ESTs	other
42022	2.3336939603	T53138	Homo sapiens mRNA for hTCF-4	TM
38233	2.3314720199	AA488023	ESTs	other
41221	2.3310635524	R21531	ESTs Weakly similar to H1 ALU SUBFAMILY J WARNING ENTRY III [H.sapiens]	other
8053	2.3297250374	AA309880	ESTs	other

FIGURE 8 (cont.)

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363	2 3275393529	D26528	Human mRNA for RNA helicase complete cds	?
26678	2 3241677974	AA281733	ESTs	other
13407	2 3216524472	AA450200	ESTs	TM
17955	2 3180957399	AA106703	ESTs	TM
31858	2 3160641803	N90680	EST	?
24092	2 3151511584	W42845	Homo sapiens protein tyrosine phosphatase PIR1 mRNA complete cds	SS
16759	2 3118245547	AA046294	ESTs	other
7851	2 311355404	AA252430	Homo sapiens clone 23797 and 23517 mRNA partial cds	other
41176	2 3111508749	R09379	Natural resistance-associated macrophage protein 2	TM
3860	2 3104335895	U13813	Homolog of Drosophila slowpoke (potassium channel calcium-activated)	TM
40886	2 3077403929	N68149	ESTs Weakly similar to EBV-INDUCED G PROTEIN-COUPLED RECEPTOR 1 PRECURSOR (Homo sapiens)	other
19428	2 3068982601	H22949	EST	?
36080	2 3048383557	AA417282	EST - RC_AA417282	other
27264	2 3043527378	AA418389	ESTs	other
13600	2 3031968696	AA456286	ESTs	other
13552	2 3026088375	AA454943	ESTs	other
15664	2 3025773291	W67456	ESTs Moderately similar to YY1-associated factor 2 (H.sapiens)	other
26583	2 3025403178	AA279774	ESTs	?
37434	2 3013886299	AA454149	EST	?
7833	2 2992574443	AA249300	ESTs	other
3674	2 2885613315	U05237	Human fetal Aiz-50-reactive clone 1 (FAC1) mRNA complete cds	other
33694	2 2884566375	Z38770	ESTs	other
11178	2 2872286082	AA167436	ESTs	?
16977	2 2912855384	AA064616	ESTs	other
19799	2 2801199024	H57330	EST	?
6948	2 2900738182	X63337	EST - X63337	?
42097	2 2881548729	T66318	Isoleucine-tRNA synthetase	?
24247	2 2881065681	W73010	Ribosomal protein L37	other
40879	2 2870463637	N67816	ESTs Moderately similar to III ALU SUBFAMILY SX WARNING ENTRY !!! (H.sapiens)	other
5675	2 2860441014	X59405	Membrane cofactor protein (CD46 trophoblast-lymphocytic cross-reactive antigen)	?
22325	2 2850330577	R60777	ESTs	other
9021	2 2844572929	J05032	ASPARTYL-TRNA SYNTHETASE	other
9239	2 2823045248	D79100	ESTs	other
41897	2 2818672356	T47788	ESTs	other
31105	2 280917152	N63207	EST	?
39565	2 2794194837	F04320	Replication factor C 37-kD subunit	other
7404	2 2793872556	AA094969	Homo sapiens voltage dependent anion channel protein mRNA complete cds	other
6388	2 2788670475	X85373	H.sapiens mRNA for Sm protein G	other
20253	2 2729348551	N31952	ESTs Moderately similar to HYPOTHETICAL 66.5 KD PROTEIN F02A8.5 IN CHROMOSOME III (Caenorhabditis elegans)	other
14529	2 2722894932	AA620307	ESTs	other
21187	2 2718306964	R07320	ESTs	other
28203	2 2692501412	AA490989	ESTs	other
38320	2 2687130032	AA490611	ESTs	other
41625	2 2680307053	R89333	ESTs	other
4674	2 265734645	U54999	Human LGN protein mRNA complete cds	other
28661	2 2637023918	D80037	EST Weakly similar to C50B8.3 (C.elegans)	other
31082	2 2633840539	N82827	ESTs	other
26756	2 2627707292	AA283832	ESTs	other
11567	2 2614480815	AA236747	Homo sapiens mitogen activated protein kinase activated protein kinase gene complete cds	other

FIGURE 8 (cont.)

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25050	2.2605063659	AA011134	ESTs Weakly similar to renin [H.sapiens]	TM
41835	2.2593192037	T20681	Human serine kinase mRNA complete cds	other
26895	2.2582387069	AA292765	H.sapiens mRNA for M-phase phosphoprotein mpp5	other
40505	2.2581993488	N34891	Homo sapiens mRNA for KIAA2595 protein partial cds	other
3343	2.2568463074	M97938	SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 1-ALPHA/BETA	other
42435	2.2532463427	V46094	ESTs	?
5937	2.2489783488	X52534	High-mobility group (nonhistone chromosomal) protein 2	other
21241	2.2477801609	R09617	ESTs	TM
25756	2.2472586561	AA135868	ESTs	TM
34184	2.2459308213	AA227959	Human cysteine protease Mch2 (isoform alpha (Mch2) mRNA complete cds	other
8672	2.2450884129	AA477048	ESTs	other
7387	2.2447544716	AA093977	ESTs	other
28822	2.2424116577	D59352	ESTs	TM
18016	2.2410305445	AA173223	ESTs	other
20843	2.238288723	N69352	Homo sapiens mRNA for ATP-dependent RNA helicase A46 complete cds	other
10054	2.2387950133	R10266	ESTs Highly similar to HYPOTHETICAL GTP-BINDING PROTEIN IN PM40-PAC2 INTERGENIC REGION (Saccharomyces cerevisiae)	other
34094	2.2384154308	AA206088	ESTs	other
41246	2.2380827238	R27290	ESTs	other
22634	2.2346537819	R82837	ESTs	other
19686	2.2319351858	H48502	ESTs	SS
34568	2.2306030547	AA280609	ESTs Weakly similar to K02823 gene product (C.elegans)	other
28448	2.2295706871	AA521752	Human 26S proteasome-associated pad1 homolog (PDH1) mRNA complete cds	other
20909	2.2284835116	N71704	ESTs	other
651	2.2260763259	D78129	EST - D78129	SS, TM
40409	2.2244318492	H99877	Homo sapiens exportin 1 mRNA complete cds	other
20340	2.224062527	N38825	ESTs	other
22002	2.2233023294	H93005	EST - RC_H93005	other
37321	2.2209252793	AA451898	ESTs	other
8274	2.2208752623	AA402095	ESTs	other
20221	2.2197714612	N29345	ESTs	other
5782	2.2186801223	X54941	CDC28 protein kinase 1	other
4034	2.21808435	U21858	Human transcription initiation factor TFIID subunit TAF131 mRNA complete cds	other
36222	2.2148577598	AA421481	ESTs	other
16567	2.2146935655	AA031591	ESTs	other
4721	2.2134595068	U58046	Human mRNA for KIAA0139 gene complete cds	other
28656	2.2125017907	D19708	Human Gu protein mRNA partial cds	TM
20723	2.2113936194	N66093	ESTs	other
5714	2.2062571749	Y08612	H.sapiens mRNA for Nup68 protein	?
19240	2.205583996	H13265	ESTs	other
36447	2.2050784323	AA426188	ESTs	other
11688	2.202413216	AA252672	Homo sapiens diaphenamide biosynthesis protein-2 (DIP2) mRNA complete cds	other
21650	2.2018153311	R37938	Homo sapiens KIAA0440 mRNA partial cds	other
14152	2.2015953698	AA489790	Homo sapiens Ran-GTP binding protein mRNA partial cds	other
42657	2.1975280207	W62771	GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR	other
4642	2.1968027789	U52427	Human RNA polymerase II subunit rsRP87 mRNA complete cds	?
32779	2.1962611079	W02102	ESTs	TM
38341	2.1951559134	AA490987	ESTs	other
11803	2.1821143838	AA257871	ESTs	other
34835	2.190705129	AA262877	ESTs	TM
39065	2.1895804523	AA620599	ESTs	other

FIGURE 8 (cont.)

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4046	2 1877784122	U22376	MYB PROTO-ONCOGENE PROTEIN	?
11620	2 1876723705	AA242869	ESTs Weakly similar to house-keeping protein (M. musculus)	other
5061	2 1868660566	U78638	Human BRCA1-associated RING domain protein (BARD1) mRNA complete cds	other
33917	2 1804055739	AA157323	ESTs	TM
20674	2 1858972155	NG3392	ESTs	TM
41031	2 1768902734	N91246	ESTs	?
25114	2 1759894608	AA020923	EST	?
24711	2 1768363153	Z39645	ESTs	other
4733	2 1721706534	U58658	Human unknown protein mRNA within the p53 intron 1 complete cds	other
4871	2 1712100791	U66033	Human g-tyrosin-5 (GPC5) mRNA complete cds	other
29733	2 1687028853	H99398	EST	?
23155	2 1678113438	T30550	ESTs	other
34638	2 164515923	AA282887	EST	?
35541	2 1621400372	AA400986	Prothymosin alpha	other
1889	2 1598384252	L20591	Annexin III (lipocortin III)	?
15136	2 1591553983	U68111	PROTEIN PHOSPHATASE INHIBITOR 2	?
40131	2 1583553062	H78779	Homo sapiens histone deacetylase 3 (HDAC3) mRNA complete cds	other
19516	2 158045763	H29207	EST	other
4136	2 1577792237	U28014	ICH-2 PROTEASE PRECURSOR	other
20278	2 1548737104	N32919	ESTs	other
13292	2 1546709291	AA447621	ESTs Highly similar to 40 KD PROTEIN [Borna disease virus]	other
20696	2 154262609	NG3165	ESTs	other
6065	2 1528848242	X88580	Sp3 transcription factor	other
18238	2 1516362853	AA255389	ESTs	other
21627	2 1515099104	R37410	EST	?
3438	2 1502571642	S72024	Eukaryotic translation initiation factor 5A	?
34848	2 1498935434	AA283772	ACTIVATOR 1 35 KD SUBUNIT	other
5994	2 1488964343	X83657	Follicular lymphoma variant translocation 1	SS.
13250	2 1466065975	AA446459	ESTs	other
34370	2 1465845856	AA251829	ESTs Weakly similar to HYPOTHETICAL 27.4 KD PROTEIN IN MER2-CPR7 INTERGENIC REGION [Saccharomyces cerevisiae]	other
27996	2 145312871	AA470156	ESTs Weakly similar to dynein 74K chain cytosolic [R. norvegicus]	SS.
4408	2 13988685247	U41745	Human PDGF associated protein mRNA complete cds	other
4187	2 1395632138	U30888	Human (RNA-guanine transglycosylase) mRNA complete cds	other
10804	2 1306058886	AA09549	ESTs	other
34552	2 1340290702	AA279985	Human mRNA for KIAA0372 gene complete cds	other
18380	2 1331897018	AA227119	ESTs	other
5223	2 1298428563	U83843	EST - U83843	other
37415	2 1270169134	AA453807	EST	other
14582	2 1260941468	AA521340	ESTs Weakly similar to HYPOTHETICAL 39.6 KD PROTEIN IN MTD1-MUP133 INTERGENIC REGION [Saccharomyces cerevisiae]	other
27756	2 123647107	AA453447	ESTs	other
13787	2 1232868197	AA463745	ESTs Highly similar to PRE-MRNA SPLICING FACTOR RNA HELICASE PRP22 [Saccharomyces cerevisiae]	other
5173	2 1232706565	U81554	Homo sapiens signal recognition particle 72 (SRP72) mRNA complete cds	other
40029	2 1214337319	H68221	Human E2 ubiquitin-conjugating enzyme Ubch5B (UBCH5B) mRNA complete cds	other
19972	2 1193721042	H83639	ESTs	other
23301	2 117519655	T52847	ESTs	other
20504	2 1134521605	N52900	ESTs	other
40145	2 1132200572	H81391	Human mRNA for histamine N-methyltransferase complete cds	other
3461	2 1131164397	S75256	EST - S75256	SS.
41833	2 1124189285	T23611	ESTs	other

FIGURE 8 (cont.)
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39298	2.1092181518	C14805	EST - RC_C14805	other
36021	2.1084568145	AA418876	ESTs Weakly similar to TRANSFORMATION-SENSITIVE PROTEIN REF SSP 3521 [H. sapiens]	other
8382	2.1077406838	AA424199	ESTs Weakly similar to C50B8.3 [C. elegans]	other
26288	2.1075583303	AA596447	Homo sapiens exportin 1 mRNA complete cds	other
5807	2.1071008331	X55740	5' nuclease (CD73)	?
19747	2.1061096899	H53572	ESTs	other
38155	2.1052335506	AA486777	ESTs	TM
924	2.1037724222	HG1112-HT1112	EST - HG1112-HT1112	?
8544	2.1022261814	H72830	ESTs	other
8384	2.1005713227	AA424282	Human 75-kD autoantigen (PM-Sc1) mRNA complete cds	other
25185	2.1005132894	AA027837	Retinitis pigmentosa 3 (X-linked recessive)	SS, TM
24348	2.1000368838	V88489	Tropomyosin alpha chain (skeletal muscle)	?
41401	2.0994868367	R43334	Homo sapiens KIAA0410 mRNA complete cds	other
35340	2.0993762592	AA386900	EST - RC_AA386900	other
10898	2.0990741816	AA112053	ESTs Weakly similar to PRE-MRNA SPLICING HELICASE BRR2 [S. cerevisiae]	other
381	2.0974305874	D26473	Isovaleryl-CoA synthetase	other
27051	2.0971755	R49047	ESTs Weakly similar to H1 ALU SUBFAMILY J WARNING ENTRY III [H. sapiens]	other
3293	2.096563118	M94893	Testis specific protein Y-linked	TM
11528	2.0954548212	AA236018	ESTs Weakly similar to unknown [S. cerevisiae]	?
11890	2.0952685865	AA278323	Homo sapiens clone 24605 mRNA sequence	TM
13543	2.0952581265	AA458578	Homo sapiens clone 24477 mRNA sequence	other
15927	2.0952547855	H71829	ESTs	other
36511	2.0927695829	AA429632	ESTs	?
2130	2.0925292202	L40407	Homo sapiens thyroid receptor interactor (TRIP9) gene complete cds	?
7183	2.0924678077	AA046768	Homo sapiens clone TUA8 Cn-du-chat region mRNA	TM
5448	2.0921643187	X02751	Neuroblastoma RAS viral (v-ras) oncogene homolog	?
35956	2.0875765163	AA12533	ESTs	other
7525	2.0870133892	AA149259	ESTs	other
39592	2.0862891765	F09351	ESTs Weakly similar to weakly similar to S. cerevisiae PTM1 precursor [C. elegans]	TM
28029	2.0855738844	AA478476	ESTs	other
18425	2.0855157851	AA232103	ESTs	other
23494	2.0843308862	T70045	ESTs Weakly similar to HYPOTHETICAL 33.2 KD PROTEIN F26A3.7 IN CHROMOSOME 1 [C. elegans]	other
30882	2.0840312831	NS6906	EST	?
32597	2.0839196473	T47333	Human TRIP9 subunit TAF155 (TAF155) mRNA complete cds	other
33368	2.0838178514	W80814	ESTs	other
10259	2.0829121213	R77527	ESTs	other
21882	2.0825457608	R43365	ESTs	other
20590	2.0820571859	NS8146	ESTs	other
12907	2.0807802388	AA427577	ESTs	other
22958	2.0770069467	T10284	ESTs	other
42044	2.0762746251	T58753	ESTs	other
4210	2.0750074179	U31814	Human transcriptional regulator homolog RPD3 mRNA complete cds	other
39	2.074214716	AB003698	Homo sapiens mRNA for Cdc7-related kinase complete cds	other
14350	2.0739236064	AA598831	ESTs	TM
29840	2.0729224128	N21680	ESTs	other
25593	2.0715918096	AA113149	Homo sapiens IPL (IPL) mRNA complete cds	other
26071	2.0708411247	AA236850	Protein phosphatase 2A regulatory subunit B' alpha-1	other
26528	2.0699045563	AA278584	EST	?
12154	2.0692102056	AA291253	ESTs	other
18817	2.0684614007	F10077	ESTs	?

FIGURE 8 (cont.)

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6635	2 0674931973	X93565	H sapiens mRNA for SMT3B protein	other
6681	2 066065203	Y00971	Phosphonobispyrophosphate synthetase 2	other
22077	2 0647745388	R49482	ESTs	other
11752	2 0645929355	AA256042	ESTs	other
41257	2 0634413834	R31690	ESTs	SS,
6904	2 0622381932	Z34897	Histamine receptor H1	TM
16879	2 060262971	AA056538	ESTs	other
38040	2 0595449295	AA481403	ESTs	other
4111	2 0567536207	U26312	Human heterodimeric protein HP1Hs-gamma mRNA complete cds	other
32878	2 0546912272	W37448	ESTs	TM
21743	2 0543668448	R40576	ESTs Moderately similar to III ALU SUBFAMILY SX WARNING ENTRY!!!! [H.sapiens]	?
25968	2 0525018401	AA234935	ESTs	other
24658	2 0506511899	Z39211	Homo sapiens GDP-L-fucose pyrophosphorylase (GFPF) mRNA complete cds	other
38030	2 0505994824	AA481148	ESTs	other
61	2 0484706331	AC002115	Cytochrome c oxidase subunit Vlb	?
6306	2 0474040935	X81825	EUKARYOTIC PEPTIDE CHAIN RELEASE FACTOR SUBUNIT 1	?
6203	2 0473464771	AA382517	EST - AA382517	other
34357	2 0469305727	AA251430	ESTs Highly similar to RAS-RELATED PROTEIN RAB-10 [Caris (amicans)]	other
36972	2 0468599712	AA442767	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein beta polypeptide	other
28156	2 0459278083	AA489057	H sapiens mRNA for nuclear protein SA-2	?
24434	2 045085222	W92787	ESTs	other
33508	2 0449481783	W08772	Human DNA sequence from cosmid F0811 on chromosome 6. Contains Diox BING1 Tapasin RGL2 KE2 BING4 BING5 ESTs and CpG islands	other
37881	2 04489348104	AA600675	H sapiens mRNA for TRES	other
27125	2 0448698236	AA405505	Homo sapiens mRNA for putative RNA helicase 3' end	other
3780	2 0445300752	U09851	Zinc finger protein 148 (pH2-52)	other
9112	2 0443252757	D16611	Coproporphyrinogen oxidase (coproporphyrin oxidoreductase)	TM
6357	2 044244223	AA418921	ESTs Highly similar to RSP5 PROTEIN [Saccharomyces cerevisiae]	other
9133	2 0436113204	D30946	ESTs Highly similar to TRANSLOCATOR-ASSOCIATED PROTEIN GAMMA SUBUNIT [Rattus norvegicus]	TM
7519	2 0414123824	AA147425	EST - AA147425_a	other
14701	2 0413755305	D59324	ESTs	other
380	2 0411495076	D28423	EST - D28423	?
30571	2 0348528804	N49595	ESTs	other
825	2 0329522889	D87328	Holo-carboxylase synthetase (biotin-(propionyl)-Coenzyme A-carboxylase (ATP-hydrolyzing)) ligase	TM
27744	2 0318041265	AA452818	ESTs Weakly similar to HYPOTHETICAL PROTEIN H10034 [Haemophilus influenzae]	other
3997	2 0311206335	U19906	Arginine vasopressin receptor 1 (AVPR1)	?
22717	2 0302732387	R91394	EST - RC_R91394	?
377	2 0289078264	D28364	EST - D28364	other
28581	2 0274006652	C21163	EST	other
11790	2 0269672127	AA256678	ESTs Highly similar to POP3 PROTEIN [Saccharomyces cerevisiae]	other
37931	2 0269058272	AA478523	ESTs Weakly similar to III ALU SUBFAMILY J WARNING ENTRY!!!! [H.sapiens]	other
24678	2 0206818539	Z39349	ESTs Weakly similar to VACUOLAR ATP SYNTHASE 54 KD SUBUNIT [Saccharomyces cerevisiae]	other
10940	2 0209035614	AA122217	ESTs Weakly similar to HYPOTHETICAL 61.3 KD PROTEIN F25B5.5 IN CHROMOSOME III [C.elegans]	other
13964	2 0207518872	AA479048	ESTs	?
15665	2 0197735566	W67631	Homo sapiens clone 24538 mRNA sequence	TM
28379	2 0183373185	AA609710	ESTs	other
13349	2 0172119305	AA448269	ESTs Weakly similar to MITOCHONDRIAL PRECURSOR PROTEINS IMPORT RECEPTOR [Neurospora crassa]	SS,
7322	2 0167797945	AA090692	ESTs Weakly similar to The KIAA0138 gene product is novel. [H.sapiens]	other
29358	2 0165298752	H70641	EST - RC_H70641	?

FIGURE 8 (cont.)

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24230	2 016017562	W72276	ESTs	other
40212	2 0150778189	H88535	Human clone 121711 defective manner transposon	?
729	2 01573779	D83778	Human mRNA for KIAA0184 gene partial cds	other
17851	2 0144787235	AA165526	Human sapiens bifunctional ATP sulfurylase/adenosine 5'-phosphosulfate kinase mRNA complete cds	other
33943	2 0135709277	AA171739	ESTs	other
5870	2 0118426189	X59244	Zinc finger protein 43 (MTF6)	other
36319	2 0118529739	AA425107	ESTs	other
75654	2 0097423819	AA126851	ESTs Weakly similar to DNA-directed RNA polymerase (D. melanogaster)	other
16344	2 0090457727	AA018907	ESTs	?
8118	2 0090099575	AA320593	ESTs	other
29962	2 0087628088	N25228	ESTs	TM
32236	2 0078250756	R48327	Natural resistance-associated macrophage protein 2	TM
3279	2 0072427596	M94065	DIHYDROOROTATE DEHYDROGENASE PRECURSOR	TM
16255	2 0065069683	AA013348	ESTs	other
37872	2 0059235228	AA478215	EST - RC_AA478215	TM
41256	2 005858844	R31577	ESTs	other
34834	2 0050133743	AA289265	ESTs	other
23168	2 0039279023	T33215	ESTs	other
29851	2 0034762885	N22145	ESTs	other
32862	2	VQ32519	EST	?

FIGURE 8 (cont.)

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New Key Number	Accession	fold upregulated of Tumor over normal colon	Unigene Descriptor	
104660	AA007160	23	ESTs	SS
130016	AA055811	14	transmembrane glycoprotein	SS, TM
104954	AA074514	10	ESTs; Moderately similar to (define not available 4753768) [H.sapiens]	Other
105082	AA143763	7	ESTs; Weakly similar to Similarity to S. Pombe BEM1/BUD5 suppressor [C.elegans]	Other
109141	AA176428	7	ESTs	Other
108893	AA135894	6	retinoic acid induced 3	TM
108927	AA143493	5	ESTs; Weakly similar to PLECKSTRIN [H.sapiens]	Other
109027	AA157818	5	Human endogenous retroviral protease mRNA; complete cds	Other
133015	AA047036	4	ESTs	Other
114546	AA056263	4	ESTs; Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]	Other
104974	AA085918	4	H.sapiens HUNK1 mRNA	Other
108695	AA121315	4	ESTs	SS
105049	AA132554	4	ESTs; Moderately similar to myosin heavy chain 12 [H.sapiens]	Other
133834	AA147510	4	Homo sapiens serine protease mRNA; complete cds	Other
109244	AA194237	4	ESTs; Weakly similar to C17H11.6 [C.elegans]	Other
128411	AA007555	3	ESTs; Weakly similar to transformation-related protein [H.sapiens]	SS, TM
114509	AA043551	3	ESTs	Other
104888	AA053680	3	ESTs	Other
114542	AA055768	3	ESTs	SS
132718	AA056731	3	Sjogren syndrome antigen A2 (60kD; ribonucleoprotein autoantigen SS-A/Ro)	Other
104953	AA074157	3	ESTs	Other
132784	AA089589	3	GDP dissociation inhibitor 2	Other
130962	AA102051	3	transmembrane 4 superfamily member 6	SS, TM
134421	AA122386	3	collagen; type V; alpha 2	SS
105035	AA128486	3	ESTs	Other
105039	AA130349	3	ESTs	Other
105062	AA134968	3	ESTs	Other
133617	AA148318	3	Human mRNA for KIAA0069 gene; partial cds	TM

FIGURE 9

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		ESTs: Highly similar to CAMP-DEPENDENT PROTEIN KINASE TYPE II-ALPHA REGULATORY CHAIN	
130335	AA156499	3: [H.sapiens]	Other
105132	AA159501	3: HBV associated factor	Other
109042	AA159525	3: ESTs	Other
109043	AA159605	3: ESTs	Other
132669	AA188378	ESTs: Weakly similar to 60S RIBOSOMAL 3: PROTEIN L22 (H.sapiens)	Other
135398	AA194075	3: nuclear receptor coactivator 4	Other
109344	AA213696	3: ESTs	SS
133221	AA235289	ESTs: Highly similar to rap2 gene product 3: [H.sapiens]	Other
114496	AA035611	ESTs: Weakly similar to !!!! ALU SUBFAMILY SX WARNING ENTRY !!!! 2: [H.sapiens]	Other
128635	AA043959	2: tropomyosin 4	Other
129912	AA047344	ESTs: Weakly similar to similar to WW/rsp5/WWP domain containing proteins 2: [C.elegans]	Other
104927	AA058855	2: ESTs	SS
132821	AA070724	CD44 antigen (homing function and Indian 2: blood group system)	Other
108409	AA075578	zm88h3.s1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone 2: IMAGE:54545 3', mRNA sequence"	Other
133621	AA076138	2: H2A histone family; member Y	Other
108565	AA085342	ATPase; Ca++ transporting; cardiac 2: muscle; slow twitch 2	TM
104977	AA088228	2: ESTs	Other
103777	AA093131	Homo sapiens PAC clone DJ0157F23 from 2: 7p15	Other
108649	AA112540	2: ESTs	Other
114692	AA121998	ESTs: Weakly similar to Similar to 2: potassium channel protein. [C.elegans]	Other
105063	AA134985	2: ESTs	Other
133273	AA147725	2: dendritic cell protein	Other
128515	AA149044	ESTs: Highly similar to the KIAA0195 gene 2: is expressed ubiquitously. [H.sapiens]	SS
105182	AA191014	ESTs: Weakly similar to Ydr372cp 2: [S.cerevisiae]	Other
109277	AA196332	2: ESTs	Other
132608	AA199588	ARP3 (actin-related protein 3; yeast) 2: homolog	Other
109380	AA219015	2: ESTs	Other
130800	AA223385	ESTs: Weakly similar to katanin p80 2: subunit [H.sapiens]	Other
129945	AA232104	ESTs: Highly similar to (define not 2: available 4929579) [H.sapiens]	Other
105305	AA233609	2: spindle pole body protein	Other

FIGURE 9

(Cont.)

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128924	AA234962	2 ESTs	TM
114895	AA236177	2 partial cds	Other

FIGURE 9 (Cont.)

FIGURE 10
1 of 8

A	B	C	D	E
1	2451	Accession	Human alpha satellite and satellite 3 junction DNA sequence	7
2	27090	M21305	ESTs; Weakly similar to serine protease [H.sapiens]	7
3	232	AA11502	ESTs; Weakly similar to serine protease [H.sapiens]	7
4	25481	D13666	ESTs; Weakly similar to serine protease [H.sapiens]	7
5	27685	AA103530	ESTs; Weakly similar to heat shock protein hsp90 homolog [H.sapiens]	TM
6	39492	AA453763	ESTs	other
7	28050	F13873	ESTs	other
8	31485	AA489037	H.sapiens mRNA for nuclear protein SA-2	7
9	25606	N11781	ESTs	other
10	7600	AA132514	densely-regulated protein	other
11	25931	Z14816	collagen, type I, alpha 2	SS
12	12118	AA238200	ESTs	other
13	32813	AA291528	ESTs	other
14	26864	W46810	HMT1 (hHR23 methyltransferase; S. cerevisiae) like 2	other
15	22514	AA393004	H beta 58 homolog	other
16	25466	R78392	ESTs	other
17	32276	AA112019	lactate dehydrogenase A	TM
18	22430	T32108	matrix metalloproteinase 12 (macrophage elastase)	SS
19	30052	R22994	ESTs	other
20	28354	R11092	TFAR19 novel apoptosis-related gene	other
21	28354	N32586	ESTs; Weakly similar to Ydr33cp [S.cerevisiae]	other
22	28354	C14037	ESTs; Weakly similar to Ydr33cp [S.cerevisiae]	7
23	28604	H08555	Homo sapiens gene for NBS1, complete cds	TM
24	27592	AA449417	Homo sapiens gene for NBS1, complete cds	TM
25	28691	D51276	Homo sapiens mRNA for putative glucosyltransferase, partial cds	other
26	19100	H10933	STATMIN	other
27	5691	X60486	H4 histone family, member G	7
28	12289	AA394243	ESTs; Highly similar to RSPs protein [Saccharomyces cerevisiae]	other
29	23629	T85700	ESTs	other
30	23951	AA236572	ESTs; Weakly similar to DFG5 [H.sapiens]	other
31	477	D38593	Human mRNA for calguzarin, complete cds	7
32	11153	AA188897	ESTs	TM
33	27183	AA421562	Homo sapiens secreted cement gland protein XAG-2 homolog (XAG-2R)	SS
34	32899	W45728	ESTs; Highly similar to HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN	other
35	9576	J03464	collagen, type I, alpha 2	SS
36	10506	AA027089	ESTs; Highly similar to HYPOTHETICAL 1.4 KD PROTEIN IN URPS-SPT	other
37	22064	R51309	ESTs	other
38	39217	C21242	calpain 2	other
39	2813	M29540	CARCINOEMBRYONIC ANTIGEN PRECURSOR	TM
40	27553	AA440968	ESTs	TM
41	40031	H33442	calichest-O-methyltransferase	other
42	10131	R55183	polyubiquitin initiation factor 3, subunit 8 (48kD)	other
43	25154	AA043353	ESTs; Highly similar to UBQUITIN-CONJUGATING ENZYME E2-17 KD	other
44	25821	AA164643	ESTs; Weakly similar to Ks-167 intracellular antigen [H.sapiens]	other

FIGURE 10 (CONT)
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A	B	C	D	E
45	2604	A243297	ESTs: Weakly similar to PEANUT PROTEIN [Drosophila melanogaster]	other
46	27055	A40642	ESTs	other
47	1084	AA100710	non-specific cross reacting antigen	other
48	11358	AA332104	ESTs	other
49	17389	AA121315	ESTs	other
50	17415	AA122389	Collagen, type V, alpha 2	?
51	23772	182735	ESTs	TM
52	25531	AA070847	tropomyosin 4	other
53	25359	AA070138	histone macroH2A1.2	other
54	27039	AA06145	ESTs	SS, TM
55	27261	AA025144	Homo sapiens clone 23589 mRNA; complete cds	other
56	28785	DA0046	SFRS protein kinase 1	other
57	32182	R62725	collagen, type XI, alpha 1	other
58	3083	M77349	transforming growth factor, beta-induced; 6kD	SS
59	5519	X08700	collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal co	other
60	5582	X12576	keratin 18	other
61	11618	AA231802	Homo sapiens lysophospholipase (LPL) mRNA; complete cds	other
62	17686	AA147725	Homo sapiens GA17 protein mRNA; complete cds	other
63	18024	AA188370	ESTs: Highly similar to CS RIBOSOMAL PROTEIN L22 [Rattus norvegicu	other
64	20941	N90923	ESTs	other
65	13612	AA456889	ESTs: Highly similar to (define not available 412715) [H. sapiens]	TM
66	17789	AA157818	Human endogenous retroviral protease mRNA; complete cds	other
67	25344	AA075182	Sjogren syndrome antigen A2 (8kD; ribonucleoprotein autoantigen SS-A/R	?
68	25583	AA131182	ESTs	other
69	32170	R61297	eukaryotic translation initiation factor 3; subunit 6 (48kD)	other
70	35586	M18728	cytosolic protein complex; subunit alpha	SS
71	2396	M93036	non-specific cross reacting antigen	other
72	3251	AA372830	membrane component; chromosomal 4; surface marker (35kD glycoprotein	other
73	8158	D78032	ESTs: Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 GAMM	other
74	9207	U64661	Human poly(A)-binding protein processed pseudogene3	?
75	15951	W63827	ESTs: Moderately similar to IIII ALU SUBFAMILY SP WARNING ENTRY II	TM
76	15914	AA070485	Homo sapiens clone 23967 unknown mRNA; partial cds	other
77	25323	AA070827	ESTs: Weakly similar to KIAA18 [H. sapiens]	TM
78	25329	AA127058	ESTs: Weakly similar to predicted using GeneFindor [C. elegans]	TM
79	25549	AA131185	helioscous nuclear ribonucleoprotein A2/B1	other
80	25584	AA411971	Homo sapiens mRNA for KIAA494 protein; complete cds	TM
81	27466	R31180	ESTs	?
82	32012	AA408951	Homo sapiens chaperonin containing 1-complex polypeptide 1; beta subun	other
83	30087	AA598714	Lon protease-like protein	other
84	38457	F03974	H. sapiens mRNA for Sop2p-like protein	other
85	39421	U09587	glycyl-tRNA synthetase	other
86	3758	C00038	ESTs	TM
87	8952	AA431191	ESTs	other
88	12576			

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FIGURE 10 (CONT)
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	A	B	C	D	E
89	17827	2.8	AA13584	Homo sapiens putative G protein-coupled receptor (RAIG1). Retinoid acid I	TM
90	20752	2.8	N6921	ESTs; Weakly similar to neogenin [H.sapiens]	other
91	22954	2.6	T17185	ESTs	TM
92	25808	2.6	AA16161	ESTs	other
93	27169	2.6	AA416878	protease (prosome, macrophage) 26S subunit, non-ATPase, 11	other
94	28086	2.6	AA48082	ESTs; Moderately similar to ubiquitous TPR motif, Y isoform [H.sapiens]	other
95	28705	2.8	CS4289	ESTs	other
96	33593	2.6	Z39041	ESTs; Weakly similar to DNA-DIRECTED RNA POLYMERASE III LARGE	TM
97	37383	2.8	AA485521	E2F transcription factor 5; p13-binding	other
98	39170	2.6	C15324	ESTs	SS, TM
99	39251	2.5	D20002	HUMGS972 Human promyelocyte Homo sapiens cDNA clone pm2344.3	other
100	2767	2.5	M37583	H2A histone family, member Z	other
101	546A	2.5	X04347	heterogeneous nuclear ribonucleoprotein A1	other
102	9243	2.5	D8246	Homo sapiens mRNA for 5-aminimidazole-4-carboxamide-1-beta-D-ribo-	other
103	103	2.5	T35725	ESTs; Highly similar to HYPOTHETICAL 44.2 KO PROTEIN IN SC02-MR	other
104	14804	2.5	T48195	eukaryotic translation initiation factor 3, subunit 3 (gamma; 4KD)	other
105	16974	2.5	AA070724	CD44 antigen (homolog function and Indian blood group system)	other
106	20031	2.5	N21085	Homo sapiens androgen receptor associated protein 24 (ARQ24) mRNA; c	?
107	25484	2.5	AA112679	ESTs; Weakly similar to alternatively spliced product using exon 13A [H.sapiens]	TM
108	26330	2.5	AA347359	lysosyme (renal amyloidosis)	SS
109	26068	2.5	AA490212	histone macroH2A1.2	other
110	30071	2.5	N33011	replication protein A3 (14KD)	other
111	32740	2.5	V01800	von Hippel-Lindau syndrome	other
112	35870	2.5	AA416785	heterogeneous nuclear ribonucleoprotein A1	other
113	41908	2.5	T59161	Thymidylate beta 1	TM
114	60111	2.4	X66401	protease (prosome, macrophage) subunit, beta type, 8 [large multifunction	?
115	9201	2.4	D63078	ESTs; Weakly similar to NADH-UBIQUINONE OXIDOREDUCTASE CHAI	other
116	9218	2.4	D78891	ESTs	TM
117	10065	2.4	R32993	ESTs; Highly similar to LEUCYL-TRNA SYNTHETASE; CYTOPLASMIC [other
118	10253	2.4	R22411	DEK gene	other
119	11107	2.4	AA159501	ESTs; Moderately similar to RBCK2 [R.nervosus]	other
120	11846	2.4	AA262969	ESTs; Weakly similar to similar to Yeast hypothetical protein L6167, 12 like	other
121	12767	2.4	AA424348	ESTs; Weakly similar to unoporphyrinogen III synthase; UROJLIS [H.sapiens]	SS
122	13772	2.4	AA464703	ESTs; Weakly similar to alternatively spliced product using exon 13A [H.sapiens]	other
123	16728	2.4	AA053102	cadherin 17, LI cadherin (liver-liver)	SS, TM
124	17174	2.4	AA158243	ESTs; Highly similar to (define not available 412715) [H.sapiens]	other
125	21366	2.4	R24059	ESTs	other
126	25433	2.4	AA095969	GDP dissociation inhibitor 2	TM
127	25603	2.4	AA132032	Homo sapiens CAGH1a (CAGH1) mRNA, partial cds	other
128	25791	2.4	AA159980	ELK1, motif kinase	other
129	28153	2.4	AA252827	ESTs	?
130	26852	2.4	AA365527	ESTs; Weakly similar to T1.5-associated protein 1ASR [H.sapiens]	other
131	27122	2.4	AA416877	ESTs	other
132	28385	2.4	C14090	actin, gamma 1	other

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FIGURE 10 (CONT)
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A	B	C	D	E
133	26526	D25560	Homo sapiens DNA from chromosome 19-coxmid H2819 containing USF2;	other
134	26567	D51241	Homo sapiens mRNA for putative vacuolar protein ATPase membrane sec	SS, TM
135	26550	N24968	vacuolar H(+)-ATPase subunit	other
136	32892	V04457	ESTs; Moderately similar to neuronal thread protein AD7c-NTP [H.sapiens]	other
137	33811	AA173143	heterogeneous nuclear ribonucleoprotein G	other
138	40121	I03492	ESTs; Highly similar to villin [H.sapiens]	other
139	40141	H94877	ESTs; Moderately similar to putative G-binding protein [H.sapiens]	other
140	40167	H95237	collagen, type XI, alpha 1	other
141	446	D38073	minichromosome maintenance deficient (S. cerevisiae) 3	other
142	3530	S81914	DIFFERENTIATION-DEPENDENT GENE 2	other
143	7935	AQ25436	Homo sapiens tyrosinophosphatase (LPL) mRNA, complete cds	other
144	10958	AA121879	proteasome (prosome; macropain) subunit, beta type; 9 (large multifunction	other
145	10955	AA134138	ESTs; Highly similar to CYTOSOL AMINOPEPTIDASE [Bos taurus]	other
146	11015	AA143763	ESTs; Weakly similar to similarity to S. Pombe BEM1/BLDS suppressor [C	other
147	11895	AA278420	ESTs; Highly similar to (define not available 43735) [H.sapiens]	TM
148	13388	AA451676	ESTs	other
149	15484	V02391	proliferation-associated 2G4, 36kD	other
150	17619	AA135406	ESTs	other
151	18225	AA213686	ESTs	other
152	20450	N53927	ESTs; Weakly similar to phenylalanine binding protein [H.sapiens]	7
153	25308	AA065227	ESTs; Weakly similar to coded for by C. elegans cDNA Y1c1.3 [C. elegans]	other
154	25590	AQ282151	ESTs; Weakly similar to predicted using GeneWise [C. elegans]	other
155	27624	AA452112	Homo sapiens mRNA for putative thionin-like protein	other
156	27792	AA460359	ESTs; Weakly similar to DNA-DIRECTED RNA POLYMERASE II 14 KD P	7
157	28231	AA600153	DEK gene	other
158	28722	D59711	ESTs	other
159	30383	N47958	eukaryotic translation initiation factor 3, subunit 3 (gamma, 4kD)	other
160	32928	V07620	ESTs; Weakly similar to reverse transcriptase related protein [H.sapiens]	other
161	39585	H11320	Homo sapiens HR23B215 mRNA; partial cds	TM
162	40175	H06685	peptidylprolyl isomerase B (cyclophilin B)	other
163	40366	N26891	ESTs; Highly similar to (define not available 467914) [H.sapiens]	other
164	40733	N67422	ESTs; Weakly similar to 25 kDa trypsin inhibitor [H.sapiens]	other
165	4918	U08105	poly(A)-binding protein-like 1	7
166	5165	U01607	GRAVIN	other
167	12242	AQ372018	ESTs	other
168	13154	AA442768	Homo sapiens inner mitochondrial membrane translocase Tim23 (TIM23)	7
169	14276	AA598450	ESTs	other
170	15721	V09348	ESTs	other
171	20588	N62945	Homo sapiens hMm17A1b mRNA, complete cds	TM
172	24021	V42567	ESTs	TM
173	24250	V084712	galactanin	other
174	25245	AQ033768	ESTs	SS
175	25430	AA099429	SPlicing FACTOR U2AF 35 KD SUBUNIT	TM
176	25562	AA178904	heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)	other

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FIGURE 10 (CONT)

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	A	B	C	D	E
177	28745	2.2	D60485	caldesmon 1	other
178	31997	2.2	R20669	tumor rejection antigen (gp96) 1	other
179	32481	2.2	T47333	Human TFIID subunit TAF155 (TAF155) mRNA; complete cds	other
180	35636	2.2	T93807	high-mobility group (nonhistone chromosomal) protein 1	other
181	37703	2.2	AA170237	ESTs; Weakly similar to uroporphyrinogen III synthase, UROIIIH [H.sapien]	TM
182	215	2.1	D13627	Human mRNA for KIAA2 gene; complete cds	TM
183	2449	2.1	M21259	small nuclear ribonucleoprotein polypeptide E	?
184	3205	2.1	M68458	ER LUMEN PROTEIN RETAINING RECEPTOR 2	TM
185	4197	2.1	U31556	E2F transcription factor 5; p13-binding	other
186	4811	2.1	U62862	eukaryotic translation initiation factor 3; subunit 6 (484D)	other
187	5417	2.1	X01060	transferrin receptor (p57 CD71)	TM
188	6334	2.1	X33228	cadherin 17; L1 cadherin (liver-ectoderm)	SS, TM
189	6605	2.1	X58133	NEUTROPHIL GELATINASE-ASSOCIATED LIPOCALIN PRECURSOR	?
190	10471	2.1	AA024492	ESTs; Highly similar to KERATIN, TYPE I CYTOSKELETAL 14 [Homo sa]	other
191	11027	2.1	AA140316	Human mRNA for KIAA099 gene; partial cds	TM
192	11116	2.1	AA161292	INTERFERON-ALPHA INDUCED 11.3 KD PROTEIN	other
193	11540	2.1	AA238972	ESTs; Moderately similar to III ALU SUBFAMILY J WARNING ENTRY IIII	other
194	11937	2.1	AA280865	ESTs; Weakly similar to Similarity to Yeast hypothetical protein YOR3180	other
195	17312	2.1	AA111689	pigment epithelium-derived factor	other
196	18286	2.1	H18947	ESTs	other
197	20122	2.1	N26259	ESTs; Weakly similar to uroporphyrinogen III synthase, UROIIIH [H.sapien]	other
198	20946	2.1	N91492	Homo sapiens clone 626 unknown mRNA; complete sequence	other
199	20997	2.1	N98464	ESTs	other
200	27106	2.1	AA172452	ESTs	other
201	28036	2.1	AA488433	ESTs; Weakly similar to deduced amino acid sequence is highly homologous	other
202	28187	2.1	AA521256	ESTs; Highly similar to nuclear pore complex protein NUP17 [R.novgous]	other
203	28336	2.1	AA621604	ESTs	other
204	28719	2.1	D59370	ESTs	other
205	28886	2.1	F04674	Homo sapiens mRNA for KIAA2746 protein; partial cds	other
206	32124	2.1	R46608	eukaryotic translation initiation factor 3; subunit 7 (2cst, 66674D)	other
207	33433	2.1	W80444	ESTs; Highly similar to (define not available 4454524) [H.sapien]	other
208	33564	2.1	W96151	ESTs; Moderately similar to ganglioside-induced differentiation associated	?
209	35778	2.1	AA172270	ESTs	other
210	35868	2.1	A4608751	calhesin B	other
211	39301	2.1	D51317	Human transcriptional corepressor PC4 mRNA; complete cds	SS
212	39945	2.1	H74484	ESTs; Weakly similar to similar to Yeast hypothetical protein L8187.12 bba	SS, TM
213	39977	2.1	H76323	Homo sapiens E2F-related transcription factor (DP-1) mRNA; complete cds	other
214	40378	2.1	N27188	ESTs	other
215	41765	2.1	T28789	ESTs; Highly similar to TYROSINE-PROTEIN KINASE RECEPTOR EPH-	TM
216	1714	2	L09604	proteoglycan protein 2 (coronin epithelium-enriched)	TM
217	2001	2	L33930	Homo sapiens CD24 signal transducer mRNA; complete cds and 3' region	TM
218	3278	2	M94358	single-stranded DNA-binding protein	other
219	4145	2	U28749	high-mobility group (nonhistone chromosomal) protein isoform LC	TM
220	6149	2	AA394267	ESTs; Highly similar to HYPOTHETICAL 58.7 KD PROTEIN ZK757.1 IN C	other

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FIGURE 10 (CONT)
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	A	B	C	D	E
221	9844	2	N33807	ESTs: Highly similar to NEDD-4 PROTEIN [Homo sapiens]	other
222	14032	2	AA46002	ESTs: Weakly similar to CH-TOG PROTEIN [H. sapiens]	TM
223	15395	2	AA025873	ESTs: Moderately similar to (define not available 416878) [H. sapiens]	TM
224	17327	2	AA112840	ESTs	TM
225	23003	2	T30801	ubiquitin-conjugating enzyme E2E 1 (homologous to yeast UBC4/5)	other
226	25625	2	AA133569	ESTs: Weakly similar to neuronal thread protein AD7c-MTP [H. sapiens]	other
227	28073	2	AA490494	ESTs	other
228	28700	2	D51139	ribosomal protein S28	other
229	29055	2	H27188	collagen-binding protein 2 (colligen 2)	other
230	32191	2	R67083	cathepsin	SS, TM
231	32887	2	W45664	5' nucleotidase (CD73)	other
232	10782	1.6	AA074880	ESTs: Weakly similar to HYPOTHETICAL 95, KD PROTEIN IN CPA3A1P	other
233	21785	1.6	AA460454	ESTs: Weakly similar to KIAA512 protein [H. sapiens]	other
234	28706	1.6	D54286	Human mRNA for KIAA255 gene, complete cds	TM
235	36414	1.6	AA430166	ESTs	other
236	9979	1.5	N91087	ESTs: Weakly similar to F55A12.9 [C. elegans]	other
237	9987	1.5	N95507	ESTs: Weakly similar to KIAA318 [H. sapiens]	TM
238	10656	1.5	AA047280	ESTs	other
239	14877	1.5	U37546	apoptosis inhibitor 1	TM
240	27065	1.5	AA410294	Human mRNA for KIAA336 gene, complete cds	other
241	29278	1.5	H72948	biglycan	SS
242	31917	1.5	N98238	ESTs	other
243	36272	1.5	AA486533	ESTs	other
244	41396	1.5	R55342	COB8 antigen	other
245	41968	1.5	T87710	ESTs	?
246	8439	1.4	AA436304	Homo sapiens androgen receptor associated protein 24 (ARAZ4) mRNA, c	other
247	10311	1.4	AA001938	ESTs	other
248	10559	1.4	AA112149	ESTs	other
249	11278	1.4	AA213410	ESTs	SS
250	13548	1.4	AA486033	ESTs: Highly similar to HYPOTHETICAL 1,4 KD PROTEIN IN UBPS-SPT	other
251	14340	1.4	AA598553	Homo sapiens TCFL5 mRNA for transcription factor-like 5, complete cds	other
252	32180	1.4	R63777	ESTs	other
253	35187	1.4	AA398722	ESTs	other
254	37254	1.4	AA453483	ESTs	TM
255	1344	1.3	HG4757-HT5207	"Oncogene MIA-4", Fusion Activated"	other
256	5397	1.3	V01516	KERATIN, TYPE II CYTOSKELETAL 6D	SS, TM
257	16272	1.3	AA018922	core promoter element binding protein	other
258	23427	1.3	T76356	ESTs: Highly similar to POL. POLYPROTEIN [Simian sarcoma virus]	other
259	25718	1.3	AA150741	gene with multiple splice variants near HD locus on 4p16.3	other
260	35469	1.3	V93403	ESTs	other
261	36574	1.3	AA334454	ESTs: Weakly similar to orf, hypothetical protein [E. coli]	SS
262	41546	1.3	R82846	ESTs	other
263	2366	1.2	M17863	insulin-like growth factor 2 (somatomedin A)	TM
264	6388	1.2	X46371	lethal giant larvae (Drosophila) homolog 1	other

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FIGURE 10 (CONT)
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A	B	C	D	E
265	24427	ESTs		other
266	27089	238208		other
267	33177	AA411473	adducin 1 (alpha)	other
268	34852	W73195	ESTs	other
269	35325	AA347891	ESTs	?
270	36609	AA400270	ESTs	other
271	38477	AA435668	ESTs; Weakly similar to putative p15 [H sapiens]	other
272	40975	AA398939	ESTs	other
273	41874	R02547	ESTs	other
274	8235	T51150	ESTs	other
275	9772	AA401047	Homo sapiens mRNA for neuropilin; complete cds	other
276	14758	M81349	SERUM AMYLOID A-4 PROTEIN PRECURSOR	SS
277	15831	S63188	BPLP	other
278	20656	X90579	H sapiens DNA for cyp related pseudogene	?
279	24891	N6289	ESTs	other
280	25045	AA04502	cerebroside (3'-phosphoadenylylsulfate galactosylceramide 3') sulfotransferase	TM
281	31584	H13549	ESTs	other
282	31840	N74890	ESTs	TM
283	35293	N73784	Homo sapiens BimEL mRNA; complete cds	other
284	37583	AA400013	EST	other
285	37652	AA461489	ESTs	other
286	38397	AA479896	ESTs	other
287	38652	AA521342	ESTs	other
288	40397	AA609018	ESTs	other
289	40488	N29883	ESTs; Moderately similar to III ALU CLASS C WARNING ENTRY III [H sa]	other
290	41231	N40559	ESTs; Highly similar to LEUKOTOXIN SECRETION ATP-BINDING PROT	other
291	41333	R41772	EST	other
292	3255	R48580	ESTs	other
293	5742	M83143	"Homo sapiens plasminogen-like protein (PLGL) mRNA, complete cds"	?
294	6007	X53065	Acetabulum not listed in Genbank	?
295	15233	X66383	SERINE/THREONINE-PROTEIN KINASE PC1AIRE-1	other
296	15262	W04960	ESTs	other
297	15363	W7304	Homo sapiens mRNA for KIAA97 protein; complete cds	other
298	15608	W26847	ESTs; Highly similar to MITOCHONDRIAL RNA SPLICING PROTEIN MS	other
299	18435	W58725	mitogen-activated protein kinase-activated protein kinase 2	TM
300	21738	AA233898	ESTs	other
301	23508	R41998	ESTs	TM
302	28111	AA058881	Zm13a3.1; Stratiotes parviflorus (p33720) Homo sapiens cDNA clone INA	other
303	34743	H04088	ESTs; Weakly similar to III ALU SUBFAMILY J WARNING ENTRY III [H sa]	other
304	34801	AA302772	ESTs; Weakly similar to neuronal thread protein AD7c-NTP [H sapiens]	other
305	35355	AA342528	ESTs; Moderately similar to unknown [H sapiens]	other
306	38940	AA400521	ESTs	other
307	39221	AA46449	ESTs	other
308	1322	C21330	Domain	other
		HG4535-PT4940		

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FIGURE 10 (CONT)
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	A	B	C	D	E
309	9842	0.9	NR4146	ESTs	other
310	10084	0.9	R32822	ESTs	other
311	11701	0.9	AA255546	ESTs	other
312	12088	0.9	AA287568	Human mRNA for KIAA107 gene, complete cds	other
313	15287	0.9	W19098	ESTs	other
314	15901	0.9	Z20005	immunoglobulin superfamily, member 3	SS
315	21008	0.9	R45512	ESTs	other
316	22002	0.9	R09459	ESTs	other
317	23136	0.9	T40327	ESTs	other
318	26673	0.9	D43719	ESTs	other
319	29159	0.9	H60824	ESTs	other
320	32610	0.9	T09122	Human clone 23732 mRNA, partial cds	SS TM
321	32674	0.9	W02129	EST	other
322	35428	0.9	AA401409	ESTs	other
323	38504	0.9	AA399209	ESTs; Moderately similar to neuronal thread protein AD7c-NTP [H sapiens]	other
324	244	0.8	D14446	Fibrinogen-like 1	TM
325	14204	0.8	AA496980	ESTs	other
326	25360	0.8	AA056210	ESTs	other
327	6971	0.7	N07590	ESTs	other
328	20461	0.7	N44429	ESTs	other
329	41029	0.7	R06815	Hemogianase 12-dioxygenase (hemogianase adrese)	other
330	41885	0.6	T11012	fibrinogen, B beta polypeptide	SS TM

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FIGURE 11
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PRIMEKEY	Fold Upregulated in Tumors	Exemplar Accession	Complete Title	ORF Structural Info
134804	12.3	L37036	small inducible cytokine subfamily B (Cys-X-Cys); member 5 (epithelial-derived neutrophil-activating peptide 78)	TM
130617	11.4	M90516	glutamine-fructose-6-phosphate transaminase 1	TM
104209	10.6	AB000221	small inducible cytokine subfamily A (Cys-Cys); member 18; pulmonary and activation-regulated	SS
109991	10	H09813	ESTs	TM
124315	8.3	H94892	v-rat simian leukemia viral oncogene homolog A (ras related)	Other
132977	8.2	U28686	RNA binding motif protein 3	Other
130407	7.4	N29888	ESTs	Other
116176	6.6	AA463725	ESTs; Weakly similar to KIAA0226 [H.sapiens]	Other
119271	6.5	T16387	ESTs	Other
134711	6.5	X04011	cytochrome b-245; beta polypeptide (chronic granulomatous disease)	TM
134326	6.1	U16306	"Human chondroitin sulfate proteoglycan versican V splice-variant precursor peptide mRNA, complete cds"	Other
125852	5.9	H09290	ESTs; Weakly similar to unknown [H.sapiens]	SS, TM
112109	5.9	R48589	ESTs	TM
132528	5.9	AA283008	chromosome-associated polypeptide C	Other
134367	5.7	X54199	phosphoribosylglycinamide formyltransferase; phosphoribosylglycinamide synthetase; phosphoribosylaminoimidazole synthetase	Other
111829	5.2	R40057	prominin (mouse)-like 1	SS, TM
102165	5	U18321	Death associated protein 3	Other
130441	5	U35835	protein kinase; DNA-activated; catalytic polypeptide	Other
133282	5	U52960	SRB7 (suppressor of RNA polymerase B; yeast) homolog	Other
100783	4.9	HG3748-HT4 018	"Basic Transcription Factor, 44 Kda Subunit"	Other
122223	4.9	AA436158	ESTs	Other
104660	4.8	AA007160	ESTs	SS
113702	4.8	T97307	ESTs; Moderately similar to IIII ALU SUBFAMILY J WARNING ENTRY IIII [H.sapiens]	Other
101185	4.7	L19872	aryl hydrocarbon receptor	Other
105308	4.7	AA233744	ESTs	Other
107168	4.7	AA621540	ESTs	Other
101201	4.6	L22524	matrix metalloproteinase 7 (matrilysin; uterine)	SS
101809	4.5	M86849	"Homo sapiens connexin 26 (GJB2) mRNA, complete cds"	TM
101478	4.5	M23379	RAS p21 protein activator (GTPase activating protein) 1	Other
104685	4.5	AA012953	ESTs	Other
100365	4.4	D78611	mesoderm specific transcript (mouse) homolog	TM
126819	4.3	AA305536	"EST176522 Colon carcinoma (Caco-2) cell line II Homo sapiens cDNA 5' end, mRNA sequence."	Other
101880	4.3	M97925	defensin; alpha 5; Paneth cell-specific	SS
126838	4.2	AA858097	pigment epithelium-derived factor	Other
101684	4.2	M63256	cerebellar degeneration-related protein (62kD)	Other
117634	4.2	N36421	ESTs; Moderately similar to IIII ALU SUBFAMILY SQ WARNING ENTRY IIII [H.sapiens]	Other
132109	4.1	AA599801	ESTs	Other
115054	4.1	AA252883	ESTs	Other
106553	4	AA454967	ESTs	Other
119717	3.9	W69134	ESTs	Other

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FIGURE 11 (CONT)
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PRIMEKEY	Fold Upregulated in Tumors	Exemplar Accession	Complete Title	ORF Structural Info
131945	3.9	M87339	replication factor C (activator 1) 4 (37kD)	Other
128790	3.9	AA281725	secreted frizzled-related protein 4	SS
120562	3.8	AA280036	ESTs; Weakly similar to W01A8.c [C.elegans]	SS
109517	3.7	D60799	ESTs	Other
102618	3.7	U65932	extracellular matrix protein 1	SS
108286	3.7	AA434441	frizzled (Drosophila) homolog 7	Other
133640	3.6	D83004	ubiquitin-conjugating enzyme E2N (homologous to yeast UBC13)	Other
100335	3.6	D63391	platelet-activating factor acetylhydrolase; isoform Ib; gamma subunit (29kD)	Other
104720	3.6	AA018441	ESTs	Other
107348	3.6	U43701	ribosomal protein L23a	Other
134989	3.6	AA236324	ESTs; Weakly similar to IIII ALU CLASS A WARNING ENTRY IIII [H.sapiens]	SS
111345	3.6	N89820	ESTs	Other
107053	3.6	AA600147	ESTs; Weakly similar to Similar to NADH-cytochrome B5 reductase [C.elegans]	Other
107240	3.5	D59368	ESTs	Other
107129	3.5	AA620553	flap structure-specific endonuclease 1	Other
134846	3.5	AA431505	Homo sapiens mRNA for putative Sqv-7-like protein; partial	TM
101897	3.5	S58544	sperm associated antigen 1	Other
107151	3.5	AA821169	ESTs	Other
106012	3.4	AA411621	ESTs	Other
101950	3.4	S79219	propionyl Coenzyme A carboxylase; alpha polypeptide	Other
116844	3.4	H64938	ESTs	Other
128025	3.4	AA937173	ESTs	TM
106785	3.4	AA478587	leukemia associated gene 1; candidate tumor suppressor frequently deleted in B-cell chronic lymphocytic leukemia (B-CLL)	Other
104518	3.4	R09815	proteasome (prosome; macropain) 26S subunit; ATPase; 5	Other
117667	3.4	N39214	ser-Thr protein kinase related to the myotonic dystrophy protein kinase	Other
104954	3.3	AA074514	ESTs; Moderately similar to (define not available 4753768) [H.sapiens]	Other
105372	3.3	AA236481	ESTs	Other
104896	3.3	AA054228	ESTs	Other
113485	3.3	T87863	ESTs	Other
127003	3.3	AA550806	ESTs; Weakly similar to (define not available 3882151) [H.sapiens]	TM
100305	3.3	D50487	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 8 (RNA helicase)	SS
134722	3.2	W47183	ESTs; Weakly similar to IIII ALU SUBFAMILY SB2 WARNING ENTRY IIII [H.sapiens]	Other
126801	3.2	AA512902	ESTs	SS, TM
133503	3.2	M33195	Fc fragment of IgE; high affinity I; receptor for; gamma polypeptide	SS, TM
132183	3.2	L18183	Human MAC30 mRNA; 3' end	TM
105298	3.2	AA233459	ESTs	TM
111046	3.2	N55514	ESTs; Moderately similar to IIII ALU SUBFAMILY SP WARNING ENTRY IIII [H.sapiens]	TM
135309	3.2	D25984	ESTs	SS
102808	3.2	U90426	nuclear RNA helicase; DECD variant of DEAD box family	Other
100552	3.1	HG2167-HT2 237	Protein Kinase H131, Camp-Dependent"	Other
127652	3.1	AA804487	ESTs	Other

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FIGURE 11 (CONT)

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PRIMEKEY	Fold Upregulated in Tumors	Exemplar Accession	Complete Title	ORF Structural Info
118127	3.1	AA459703	ESTs; Moderately similar to coded for by C. elegans cDNA CEESD64F [C.elegans]	TM
131804	3.1	AA143019	ESTs; Highly similar to surface 4 integral membrane protein [H.sapiens]	TM
126547	3.1	U47732	transmembrane 4 superfamily member 3	Other
102823	3.1	U90914	carboxypeptidase D	SS
132298	3.1	N41849	Homo sapiens cytokine receptor related protein 4 (CYTOR4) mRNA; complete cds	Other
127445	3.1	AA906286	ESTs	Other
134395	3.1	L09717	lysosomal-associated membrane protein 2	SS, TM
105743	3.1	AA293300	ESTs; Weakly similar to semaphorin C [M.musculus]	Other
125827	3.1	A1471525	YY1 transcription factor	Other
101229	3.1	L27943	cytidine deaminase	Other
102306	3	U33317	defensin; alpha 6; Paneth cell-specific	SS
107318	3	T74445	"yc82B.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:2242 5', mRNA sequence"	Other
120983	3	AA398209	EST	Other
134700	3	AA481414	golgi SNAP receptor complex member 1	TM
131216	3	D31058	ESTs	SS
127565	3	D79516	"HUM272B04B Human aorta polyA+ (TFujiwara) Homo sapiens cDNA clone GEN-272B04 5', mRNA sequence."	Other
106882	2.9	AA489009	ESTs	Other
130874	2.9	T08287	ESTs	Other
101275	2.9	L37936	Ts translation elongation factor; mitochondrial	Other
111179	2.9	N67239	ESTs	Other
126086	2.9	H70975	"yr73g01.r1 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:210960 5', mRNA sequence."	Other
105365	2.9	AA236275	ESTs	Other
118789	2.9	N75416	ESTs	Other
115117	2.9	AA256482	H.sapiens PAP mRNA	Other
100484	2.9	HG1103-HT1 103	"Guanine Nucleotide-Binding Protein Rai, Ras-Oncogene Related"	Other
101300	2.9	L40391	Homo sapiens (clone s153) mRNA fragment	Other
103075	2.9	X59543	ribonucleotide reductase M1 polypeptide	Other
132184	2.8	U84573	procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase) 2	Other
106718	2.8	AA464962	ESTs	Other
134098	2.8	X06323	Human MRL3 mRNA for ribosomal protein L3 homologue (MRL3	Other
134485	2.8	X82153	cathepsin K (pycnodysostosis)	SS
129634	2.8	AA150726	ESTs	Other
112207	2.8	R49502	ESTs	Other
124904	2.8	R86970	ESTs	Other
125471	2.8	AA477571	UDP-glucose ceramide glucosyltransferase	SS
132180	2.8	AA405569	fibroblast activation protein; alpha	SS
104454	2.8	M84443	galactokinase 2	TM
134282	2.8	T25508	ESTs	Other
101558	2.8	M32011	neutrophil cytosolic factor 2 (85kD; chronic granulomatous disease; autosomal 2)	Other
130529	2.8	AA173238	small inducible cytokine A5 (RANTES)	Other
101804	2.7	M86699	TTK protein kinase	Other

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FIGURE 11 (CONT)

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PRIMEKEY	Fold Upregulated in Tumors	Exemplar Accession	Complete Title	ORF Structural Info
109565	2.7	F01930	ESTs	Other
112427	2.7	R62604	ESTs	Other
116188	2.7	AA261819	ESTs	Other
121831	2.7	AA425374	ESTs	Other
132454	2.7	W78726	ESTs; Highly similar to serine/threonine kinase [H.sapiens]	Other
116399	2.7	AA599729	Homo sapiens homeobox protein A10 (HOXA10) gene; complete cds	Other
100409	2.7	D86957	Human mRNA for KIAA0202 gene; partial cds	Other
130987	2.7	R45698	ESTs	Other
107217	2.7	D51095	ESTs	SS, TM
125698	2.6	AA748483	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene; partial cds; neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes; complete cds	SS
118722	2.6	N73563	ESTs	SS
104521	2.6	R11604	"Y47c1.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:132 5', mRNA sequence"	Other
130800	2.6	AA223386	ESTs; Weakly similar to katanin p80 subunit [H.sapiens]	Other
134415	2.6	AA329274	protein tyrosine phosphatase type IVA; member 2	TM
116461	2.6	AA621557	ESTs; Moderately similar to !!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!! [H.sapiens]	Other
100864	2.6	HG4297-HT4 567	Transcriptional Coactivator Pca4	Other
103818	2.6	AA150614	"z143h5.r1 Soares_pregnant_uterus_NoHPU Homo sapiens cDNA clone IMAGE:54729 5', mRNA sequence"	Other
105713	2.6	AA291321	ESTs	Other
114969	2.6	AA250775	ESTs	Other
130415	2.6	X07290	Human HF 12 gene mRNA	Other
101791	2.6	M83822	Human belge-like protein (BGL) mRNA; partial cds	Other
128131	2.6	A1283162	claudin 3	SS, TM
131564	2.6	AA491465	ESTs	Other
100279	2.6	D42084	Human mRNA for KIAA0094 gene; partial cds	Other
130149	2.6	J04031	methylenetetrahydrofolate dehydrogenase (NADP+ dependent); methylenetetrahydrofolate cyclohydrolase; formyltetrahydrofolate synthetase	Other
119888	2.6	W81710	ESTs	SS
126638	2.6	AA649257	ESTs	Other
131672	2.6	X12901	Human mRNA for villin	Other
134405	2.6	J04177	collagen; type XI; alpha 1	Other
101188	2.5	L20320	cyclin-dependent kinase 7 (homolog of Xenopus MO15 cdk-activating kinase)	TM
104534	2.5	R22303	ESTs; Weakly similar to putative p150 [H.sapiens]	Other
135178	2.5	U43747	Friedreich ataxia	SS
124308	2.5	H93575	ESTs	SS
125621	2.5	A1051602	acetyl-Coenzyme A acetyltransferase 2 (acetoacetyl Coenzyme A thiolase)	TM
101342	2.5	L76191	interleukin-1 receptor-associated kinase 1	Other
129351	2.5	AA167268	ESTs	Other
103774	2.5	AA092898	ESTs; Weakly similar to R07G3.8 [C.elegans]	Other
131289	2.5	AA485697	ESTs	SS, TM
132094	2.5	W01996	ESTs; Highly similar to (define not available 4929683) [H.sapiens]	Other
103223	2.5	X74801	chaperonin containing TCP1; subunit 3 (gamma)	Other

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FIGURE 11 (CONT)
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PRIMEKEY	Fold Upregulated in Tumors	Exemplar Accession	Complete Title	ORF Structural Info
105810	2.5	AA279991	ESTs	Other
115719	2.5	AA416997	ESTs	Other
134888	2.5	AA148094	Tat-Interacting protein (30kD)	Other
105564	2.5	AA262943	ESTs	Other
128689	2.5	AA130158	ESTs	Other
103391	2.5	X94453	pyrroline-5-carboxylate synthetase (glutamate gamma-semialdehyde synthetase)	Other
104182	2.5	AA479990	ESTs; Weakly similar to glioma amplified on chromosome 1 protein [H.sapiens]	SS, TM
123494	2.5	AA599788	ESTs	Other
122905	2.5	AA470070	ESTs	Other
109175	2.5	AA180496	ESTs	Other
129907	2.5	D80170	ESTs	Other
115142	2.4	AA258116	ESTs; Weakly similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]	Other
125474	2.4	AA151216	Homo sapiens 14-3-3 protein mRNA; complete cds	SS
125745	2.4	AI283493	ribophorin II	Other
100103	2.4	AF007875	dolichyl-phosphate mannosyltransferase polypeptide 1; catalytic subunit	Other
102687	2.4	U73379	Human cyclin-selective ubiquitin carrier protein mRNA; complete cds	Other
133170	2.4	U21049	epithelial protein up-regulated in carcinoma	SS, TM
109141	2.4	AA176428	ESTs	Other
132811	2.4	U25435	transcriptional repressor	Other
102862	2.4	X01057	Interleukin 2 receptor, alpha	SS, TM
104300	2.4	D37933	syntaxin 1B	Other
105091	2.4	AA146859	ESTs; Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]	Other
110674	2.4	H89315	"yw25e09.s1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:253288 3', mRNA sequence."	TM
122571	2.4	AA452600	EST	Other
123421	2.4	AA598440	ESTs; Moderately similar to neuronal thread protein AD7c-NTP [H.sapiens]	Other
132181	2.4	AA046939	ESTs; Moderately similar to !!!! ALU SUBFAMILY SX WARNING ENTRY !!!! [H.sapiens]	Other
128445	2.4	AA306121	ESTs	SS
113923	2.4	W80763	ESTs; Moderately similar to FK506-binding protein 65kD [M.musculus]	Other
100598	2.4	HG2463-HT2 559	Guanine Nucleotide-Binding Protein G25k	Other
130869	2.4	AA128100	uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'-decarboxylase)	Other
132393	2.4	W85888	ESTs; Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]	Other
100830	2.4	HG4074-HT4 344	Rad2	Other
133765	2.4	D21255	cadherin 11 (OB-cadherin; osteoblast)	SS, TM
100867	2.4	HG4316-HT4 588	Transketolase-Like Protein	Other
119859	2.4	W80702	ESTs	Other
135269	2.4	M77698	YY1 transcription factor	Other
115140	2.4	AA258030	ESTs; Weakly similar to (define not available 3874821) [C.elegans]	Other
102162	2.4	U18291	CDC16 (cell division cycle 16; S. cerevisiae; homolog)	Other

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FIGURE 11 (CONT)
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PRIMEKEY	Fold Upregulated in Tumors	Exemplar Accession	Complete Title	ORF Structural Info
100372	2.4	D79997	KIAA0175 gene product	TM
106981	2.4	AA521157	ESTs	Other
130114	2.4	AA234717	ESTs	Other
116129	2.3	AA459956	ESTs	Other
122235	2.3	AA436475	ESTs	Other
107315	2.3	T62771	Homo sapiens nucleoplasmin-3 (NPM3) mRNA; complete cds	SS
125905	2.3	T69968	chaperonin containing TCP1; subunit 2 (beta)	Other
133061	2.3	AB000584	prostate differentiation factor	SS
107531	2.3	Y13936	protein phosphatase 1G (formerly 2C); magnesium-dependent; gamma isoform	Other
125820	2.3	AA730136	teratocarcinoma-derived growth factor 1	Other
131725	2.3	AA456264	ESTs; Highly similar to (define not available 4176448) [H.sapiens]	Other
101228	2.3	L27706	chaperonin containing TCP1; subunit 6A (zeta 1)	Other
132571	2.3	R84594	ESTs; Highly similar to (define not available 4809026) [H.sapiens]	SS, TM
100090	2.3	AC002486	"Human BAC clone RG367O17 from 7p15-p21, complete sequence [Homo sapiens]"	Other
103658	2.3	Z74815	collagen; type I; alpha 1	SS, TM
104897	2.3	AA054641	ESTs	Other
106818	2.3	AA480890	ESTs	Other
113077	2.3	T40442	ESTs	SS
128773	2.3	M28879	granzyme B (granzyme 2; cytotoxic T-lymphocyte-associated serine esterase 1)	SS
129506	2.3	AA258286	Homo sapiens mRNA for KIAA0877 protein; partial cds	TM
133746	2.3	U44378	MAD (mothers against decapentaplegic; Drosophila) homolog 4	Other
134272	2.3	X76040	Lon protease-like protein	Other
106267	2.3	AA431873	Homo sapiens clone 24711 mRNA sequence	Other
133493	2.3	AA284143	Homo sapiens chromosome 1 atrophin-1 related protein (DRPLA) mRNA; complete cds	Other
104278	2.3	C02582	ESTs; Highly similar to (define not available 5114045) [H.sapiens]	Other
127211	2.3	AA480935	"aa28c03.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814564 5', mRNA sequence."	Other
110721	2.3	H97678	ESTs	Other
114774	2.3	AA150043	ESTs	TM
132968	2.3	N77151	Homo sapiens mRNA for KIAA0799 protein; partial cds	Other
106916	2.3	AA490814	ESTs	Other
113849	2.3	W60439	ESTs; Moderately similar to cbp146 [M.musculus]	Other
131028	2.3	U20240	CCAAT/enhancer binding protein (C/EBP); gamma	Other
130380	2.3	U55853	Homo sapiens 130 kD Golgi-localized phosphoprotein (GPP130) mRNA; complete cds	SS
125390	2.3	H95094	KIAA0016 gene product	SS, TM
127256	2.3	AA327550	ESTs; Weakly similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]	Other
132116	2.3	AA234767	ESTs	SS, TM
117765	2.3	N47797	ESTs	Other
119126	2.3	R45175	ESTs	Other
129482	2.2	AA435849	ESTs; Moderately similar to unknown protein [H.sapiens]	Other
120493	2.2	AA255933	ESTs	SS
108927	2.2	AA143493	ESTs; Weakly similar to PLECKSTRIN [H.sapiens]	Other

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FIGURE 11 (CONT)

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PRIMEKEY	Fold Upregulated in Tumors	Exemplar Accession	Complete Title	ORF Structural Info
122520	2.2	AA448427	ESTs: Moderately similar to pregnancy-specific beta-1 glycoprotein 2 [H.sapiens]	Other
125982	2.2	R98091	RAE1 (RNA export 1; S.pombe) homolog	Other
132325	2.2	N37065	ESTs: Moderately similar to IIII ALU SUBFAMILY SQ WARNING ENTRY IIII [H.sapiens]	Other
100287	2.2	D43950	Human mRNA for KIAA0098 gene; partial cds	Other
114895	2.2	AA236177	Homo sapiens mRNA for KIAA0887 protein; partial cds	Other
105038	2.2	AA130273	ESTs: Weakly similar to (define not available 4240269) [H.sapiens]	Other
105476	2.2	AA255473	ESTs	SS
108942	2.2	AA496347	ESTs: Highly similar to gene 7442 protein [H.sapiens]	Other
110566	2.2	H59990	ESTs	Other
111068	2.2	N58397	ESTs	Other
127963	2.2	A1299013	"qn13h12.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1898183 3' similar to TR:022813 OZ2813 PUTATIVE NAD(P)-DEPENDENT CHOLESTEROL DEHYDROGENASE. mRNA sequence."	TM
130985	2.2	AA243700	ESTs	Other
132877	2.2	R40685	Homo sapiens mRNA for KIAA0851 protein; complete cds	TM
135242	2.2	M74093	cyclin E1	TM
129468	2.2	J03040	secreted protein; acidic; cysteine-rich (osteonectin)	SS
132616	2.2	AA386264	ESTs	SS, TM
133780	2.2	M14219	decorin	Other
121853	2.2	AA425887	ESTs	Other
114608	2.2	AA079381	ESTs	Other
129017	2.2	H13108	ESTs	SS
132725	2.2	L41887	splicing factor; arginine/serine-rich 7 (35kD)	Other
125606	2.2	R28463	ESTs	SS
105538	2.2	AA258860	ESTs: Highly similar to (define not available 4583654) [H.sapiens]	Other
133221	2.2	AA235289	ESTs: Highly similar to rap2 gene product [H.sapiens]	Other
106389	2.2	AA446949	ESTs	Other
128949	2.2	AA190993	a disintegrin and metalloproteinase domain 12 (meltrin alpha)	Other
120969	2.2	AA398116	ESTs	Other
102495	2.2	U51240	Human mRNA for KIAA0085 gene; partial cds	TM
101124	2.2	L10343	protease inhibitor 3; skin-derived (SKALP)	SS
102778	2.2	U83463	syndecan binding protein (syntenin)	Other
107307	2.2	T52099	creatine kinase; mitochondrial 2 (sarcomeric)	Other
111605	2.2	R11638	ESTs	Other
101959	2.2	S80343	arginyl-tRNA synthetase	Other
101031	2.2	J05070	matrix metalloproteinase 9 (gelatinase B; 92kD gelatinase; 92kD type IV collagenase)	SS
131701	2.2	AA149008	ESTs: Weakly similar to IIII ALU SUBFAMILY SQ WARNING ENTRY IIII [H.sapiens]	Other
105344	2.2	AA235303	ESTs	TM
103166	2.2	X67951	proliferation-associated gene A (natural killer-enhancing factor A)	Other
131463	2.2	X74142	forkhead (Drosophila)-like 1	Other
131412	2.2	U34044	Human selenium donor protein (selD) mRNA; complete cds	Other
134982	2.2	N46086	ESTs	Other
127236	2.1	A1341818	budding uninhibited by benzimidazoles 1 (yeast homolog)	Other
104459	2.1	M91493	EST	Other

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FIGURE 11 (CONT)
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PRIMEKEY	Fold Upregulated in Tumors	Exemplar Accession	Complete Title	ORF Structural Info
124596	2.1	N70088	ESTs	Other
105850	2.1	AA282347	ESTs; Highly similar to (define not available 4454694) [H.sapiens]	Other
134917	2.1	X87241	FAT tumor suppressor (Drosophila) homolog	SS
132478	2.1	H20806	Homo sapiens mRNA for KIAA0746 protein; partial cds	SS, TM
134484	2.1	N79354	ESTs; Weakly similar to Rga [D.melanogaster]	Other
111221	2.1	N68869	ESTs	Other
100892	2.1	HG4557-HT4 962	"Small Nuclear Ribonucleoprotein U1, 1snrp"	Other
117170	2.1	H98153	ESTs	Other
124049	2.1	F10523	primase; polypeptide 2A (58kD)	Other
131692	2.1	D50914	Human mRNA for KIAA0124 gene; partial cds	TM
103003	2.1	X52003	trifoli factor 1 (breast cancer; estrogen-inducible sequence expressed in)	SS
134085	2.1	U20979	chromatin assembly factor I (150 kDa)	Other
126216	2.1	N23870	ESTs	Other
102721	2.1	U79241	Human clone 23759 mRNA; partial cds	Other
128040	2.1	AA918528	ESTs	Other
101038	2.1	J05249	replication protein A2 (32kD)	SS
106060	2.1	AA417287	C-terminal binding protein 2	Other
103622	2.1	Z48042	basic transcription factor 3	Other
127884	2.1	AA768630	ESTs	Other
130911	2.1	W72906	HIRA interacting protein 4 (dnaJ-like)	Other
104260	2.1	AF008192	Homo sapiens putative GR6 protein (GR6) mRNA; complete cds	Other
120714	2.1	AA292689	ESTs	Other
101578	2.1	M34423	galactosidase; beta 1	SS
113443	2.1	T86158	ESTs	SS
101516	2.1	M28249	Accession not listed in Genbank	Other
106480	2.1	AA450373	ESTs; Moderately similar to !!!! ALU SUBFAMILY SB WARNING ENTRY [H.sapiens]	Other
111365	2.1	N92659	ESTs	Other
121121	2.1	AA399371	ESTs; Weakly similar to (define not available 4688925) [H.sapiens]	Other
124768	2.1	R40177	ESTs	Other
102501	2.1	U51586	Human shah binding protein 1 (ShahBP1) mRNA; partial cds	Other
106432	2.1	AA448850	ESTs	Other
132812	2.1	R48108	ESTs	Other
125681	2.1	AA394176	accessory proteins BAP31/BAP28	TM
130511	2.1	L32137	cartilage oligomeric matrix protein	Other
128219	2.1	AA978333	ESTs	Other
130982	2.1	AA102051	transmembrane 4 superfamily member 6	SS, TM
101840	2.1	M93056	protease inhibitor 2 (anti-elastase); monocyte/neutrophil	TM
123928	2.1	AA621363	EST	Other
132073	2.1	N67408	ESTs; Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY [H.sapiens]	Other
101671	2.1	M61832	S-adenosylhomocysteine hydrolase	Other
107059	2.1	AA608545	ESTs	Other
132791	2.1	AA446088	ESTs; Weakly similar to YY1-associated factor 2 [H.sapiens]	Other
103131	2.1	X65614	S100 calcium-binding protein P	Other
104791	2.1	AA029046	ESTs	Other

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FIGURE 11 (CONT)

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PRIMEKEY	Fold Upregulated in Tumors	Exemplar Accession	Complete Title	ORF Structural Info
135181	2.1	AA621349	ESTs; Weakly similar to similar to Yeast hypothetical protein L8167.12 like [C.elegans]	Other
104334	2.1	D82614	ESTs	Other
132103	2.1	AA025086	ESTs	Other
126743	2.1	AA179253	poly(A)-binding protein-like 1	Other
100439	2.1	D87453	Human mRNA for KIAA0264 gene; partial cds	Other
114860	2.1	AA235112	ESTs; Moderately similar to similar to murine RNA-binding protein [H.sapiens]	Other
116732	2.1	F13779	ESTs; Weakly similar to IIII ALU SUBFAMILY J WARNING ENTRY IIII [H.sapiens]	Other
131045	2.1	H30863	ESTs; Weakly similar to The KIAA0132 gene product is related to Drosophila melanogaster ring canal protein. [H.sapiens]	Other
133209	2.1	AA114183	ESTs; Moderately similar to glutamate pyruvate transaminase [H.sapiens]	Other
101758	2.1	M77838	Human pyrroline 5-carboxylate reductase mRNA; complete cds	Other
102214	2.1	U23752	SRY (sex-determining region Y)-box 11	Other
130100	2.1	AA425593	ESTs	Other
109799	2.1	F10770	Homo sapiens clone 669 unknown mRNA; complete sequence	Other
130860	2.1	U66061	T-cell receptor; beta cluster	SS, TM
106685	2.1	AA461551	ESTs; Highly similar to 73 kDa subunit of cleavage and polyadenylation specificity factor [H.sapiens]	TM
125724	2.1	AA083407	stimulated trans-acting factor (50 kDa)	Other
134258	2.1	L28010	heterogeneous nuclear ribonucleoprotein F	Other
129642	2.1	R50008	7-dehydrocholesterol reductase	TM
125336	2.1	T86823	ESTs	Other
125303	2	Z39821	ESTs	Other
100749	2	HG3521-HT3 715	Ras-Related Protein Rap1b	Other
128185	2	AI393989	ESTs	TM
126880	2	AI151406	ESTs	SS, TM
105263	2	AA227926	ESTs	Other
123288	2	AA495836	EST	Other
105807	2	AA393803	ESTs	Other
105040	2	AA131047	KIAA0698 gene product	TM
131977	2	F09788	procollagen-proline; 2-oxoglutarate 4-oxoxygenase (proline 4-hydroxylase); alpha polypeptide II	SS
117992	2	N52000	ESTs	SS, TM
134037	2	X53586	Human mRNA for integrin alpha 6	SS
132744	2	X54326	glutamyl-prolyl-HRNA synthetase	Other
101581	2	M34996	"Human MHC cell surface glycoprotein (HLA-DQA) mRNA, 3'end"	SS, TM
103576	2	Z26317	desmoglein 2	SS
131235	2	AA223284	ESTs; Moderately similar to (define not available 4680395) [H.sapiens]	Other
127910	2	AA781881	ESTs; Weakly similar to sperm fertilization protein sp56 precursor [M.musculus]	SS
101552	2	M31642	hypoxanthine phosphoribosyltransferase 1 (Lesch-Nyhan syndrome)	Other
106318	2	AA436570	Homo sapiens mRNA for pre-mRNA cleavage factor I subunit	Other
101192	2	L20659	Human leukemia virus receptor 1 (GLVR1) mRNA; complete cds	TM
104592	2	R81003	Homo sapiens serine protease mRNA; complete cds	SS
129095	2	L12350	thrombospondin 2	SS

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FIGURE 11 (CONT)
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PRIMEKEY	Fold Upregulated in Tumors	Exemplar Accession	Complete Title	ORF Structural Info
105705	2	AA290767	ESTs	Other
128461	2	M83262	arachidonate 5-lipoxygenase-activating protein	SS, TM

Accession	Gene	Species	Protein
16074	>10	AA001507	ESTs
25047	>10	AA011031	ESTs
25082	>10	AA017257	ESTs
16490	>10	AA026418	ESTs
25179	>10	AA031268	H.sapiens mR
25215	>10	AA035540	APOLIPOPRO
25282	>10	AA044825	ESTs
16810	>10	AA053638	ESTs
16835	>10	AA054438	ESTs
10747	>10	AA055841	ESTs
10748	>10	AA055892	ESTs
16993	>10	AA065300	Human mRNA
17051	>10	AA070801	ESTs
10840	>10	AA084104	ESTs
7296	>10	AA085661	ESTs
7325	>10	AA090842	ESTs Weakly
17419	>10	AA113349	EST
17541	>10	AA127459	ESTs
17559	>10	AA128407	ESTs
25669	>10	AA128978	ESTs
17600	>10	AA130596	ESTs
10992	>10	AA132523	Human sapiens
17654	>10	AA133250	ESTs
17734	>10	AA137246	ESTs
25801	>10	AA148530	EST - RC_AA
25806	>10	AA149007	EST
11121	>10	AA156359	Human TAR D
11160	>10	AA164289	ESTs
25925	>10	AA166494	ESTs Weakly
25934	>10	AA165355	Human clone
17987	>10	AA169379	ESTs
18008	>10	AA171895	Homo sapiens
33953	>10	AA173290	Human HOXA
33980	>10	AA180223	CAMP-DEPEN
34013	>10	AA190888	EST - RC_AA
34014	>10	AA191348	ESTs
34015	>10	AA191353	ESTs
34070	>10	AA196549	ESTs
18260	>10	AA206801	ESTs
34105	>10	AA207123	ESTs
34107	>10	AA209469	ESTs
18330	>10	AA216722	Human mRNA
18362	>10	AA223912	Ribonuclease
18392	>10	AA227751	ESTs
34188	>10	AA228030	ESTs
34197	>10	AA232315	Homo sapiens
25948	>10	AA234365	Homo sapiens
25951	>10	AA234550	EST
11561	>10	AA236533	Evi-1
26059	>10	AA236685	ESTs
26100	>10	AA242835	Human mRNA
11603	>10	AA243052	ESTs Highly
7785	>10	AA243375	EST - AA2433
34372	>10	AA251973	ESTs
26240	>10	AA262282	Human mRNA

FIGURE 12

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34382	>10	AA252512	ESTs	other
34391	>10	AA252703	EST - RC, AA	other
26274	>10	AA253011	ESTs	?
34400	>10	AA253400	ESTs	other
26291	>10	AA253422	ESTs	?
26355	>10	AA256379	ESTs	other
11813	>10	AA258158	ESTs	other
34518	>10	AA278721	ESTs	?
26545	>10	AA278979	ESTs	other
26574	>10	AA279504	ESTs	other
34554	>10	AA280016	DNA polymer	other
34561	>10	AA280298	ESTs	TM
26628	>10	AA280641	ESTs Highly	TM
11969	>10	AA280670	ESTs	SS.
34575	>10	AA280738	ESTs	TM
26677	>10	AA281636	ESTs	?
26700	>10	AA282197	EST	?
34672	>10	AA284372	ESTs	other
34692	>10	AA285079	ESTs	other
12143	>10	AA290991	ESTs	other
8092	>10	AA316272	ESTs	TM
34904	>10	AA321746	EST	other
8111	>10	AA323787	ESTs	other
8125	>10	AA330771	Human protein	TM
26916	>10	AA331393	ESTs	other
26926	>10	AA342402	ESTs	other
26935	>10	AA347193	ESTs Weakly	TM
35038	>10	AA350541	ESTs Moder	TM
35049	>10	AA350857	ESTs	other
35106	>10	AA371561	EST Weakly	?
35197	>10	AA398120	ESTs	other
35277	>10	AA398536	ESTs	other
35309	>10	AA398660	EST	other
35322	>10	AA398710	H. sapiens RM	TM
27037	>10	AA400198	ESTs	TM
35495	>10	AA400527	ESTs	?
27046	>10	AA400670	Homo sapiens	other
35500	>10	AA400715	ESTs	other
12480	>10	AA403116	Homo sapiens	other
35693	>10	AA405485	ESTs Weakly	other
35697	>10	AA405512	ESTs	other
35766	>10	AA406169	Homo sapiens	other
35769	>10	AA406206	ESTs	other
35798	>10	AA410231	ESTs	other
35801	>10	AA410291	ESTs	other
35803	>10	AA410295	ESTs	other
35822	>10	AA411144	ESTs	TM
35874	>10	AA412024	EST	?
35958	>10	AA412550	ESTs	other
36052	>10	AA417027	EST	TM
36258	>10	AA423952	ESTs Weakly	other
36288	>10	AA424502	ESTs	other
36307	>10	AA424803	EST	?
36371	>10	AA426017	ESTs	TM
36395	>10	AA428353	ESTs	other
36405	>10	AA426406	Homo sapiens	other

FIGURE 12
(cont.)

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36506	>10	AA429610	ESTs	other
36571	>10	AA430726	EST - RC_AA	SS,
36695	>10	AA433910	ESTs	other
36739	>10	AA435610	EST - RC_AA	?
36753	>10	AA435688	ESTs	other
36845	>10	AA436198	ESTs	?
13136	>10	AA436560	ESTs	SS, TM
13143	>10	AA436619	ESTs	SS,
36958	>10	AA442060	ESTs	other
36962	>10	AA442082	ESTs	?
36981	>10	AA442845	EST	?
13237	>10	AA443971	ESTs Weakly	?
13242	>10	AA445994	ESTs	other
37057	>10	AA446131	ESTs	other
37068	>10	AA446312	ESTs Weakly	other
37074	>10	AA446344	ESTs	SS,
37084	>10	AA446486	Homo sapiens	?
37135	>10	AA447540	EST	?
37159	>10	AA447714	EST - RC_AA	other
37168	>10	AA447772	ESTs	?
37246	>10	AA449311	Homo sapiens	other
37310	>10	AA451707	ESTs	other
37453	>10	AA454610	ESTs	?
37456	>10	AA454632	ESTs	TM
27787	>10	AA454660	ESTs	?
37492	>10	AA455248	EST - RC_AA	other
37546	>10	AA456641	ESTs	TM
37601	>10	AA458864	ESTs	other
37611	>10	AA458996	Human signal	SS, TM
37615	>10	AA459101	Human serine	other
37653	>10	AA460017	ESTs	other
37677	>10	AA460530	Homo sapiens	other
37777	>10	AA464860	Homo sapiens	other
8848	>10	AA465016	Homo sapiens	?
37816	>10	AA469954	EST	?
37829	>10	AA470084	ESTs	other
28015	>10	AA477421	ESTs	other
37978	>10	AA479294	EST - RC_AA	other
37979	>10	AA479295	ESTs Highly	other
37983	>10	AA479348	H.sapiens mR	other
14054	>10	AA485223	ESTs	TM
38121	>10	AA485724	EST - RC_AA	other
28122	>10	AA485928	ESTs Weakly	other
38167	>10	AA487207	EST - RC_AA	other
38172	>10	AA487424	EST - RC_AA	other
38179	>10	AA487492	Homo sapiens	other
38182	>10	AA487501	ESTs	other
38194	>10	AA487969	ESTs	other
28141	>10	AA488432	ESTs	?
38211	>10	AA488687	ESTs	other
38235	>10	AA489030	ESTs	other
38280	>10	AA489791	EST - RC_AA	other
38316	>10	AA490500	Homo sapiens	other
38330	>10	AA490882	ESTs	other
38456	>10	AA504343	ESTs	SS,
38460	>10	AA504462	ESTs	other

FIGURE 12
(cont.)

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38553	>10	AA521471	ESTs	other
38560	>10	AA598545	ESTs	?
38590	>10	AA598648	Human mRNA	other
38601	>10	AA598738	ESTs	?
28323	>10	AA599639	ESTs	other
38828	>10	AA609177	ESTs	TM
38838	>10	AA609215	EST - RC_AA	?
38867	>10	AA609318	Human cbl-b m	TM
38871	>10	AA609333	EST	?
38970	>10	AA609749	ESTs	other
38984	>10	AA609839	ESTs Modera	?
39045	>10	AA610077	ESTs	other
39062	>10	AA620333	EST	?
39080	>10	AA620552	EST - RC_AA	?
39110	>10	AA620709	ESTs Weakly	other
39176	>10	AA621091	ESTs	other
39218	>10	AA621330	ESTs	other
39221	>10	AA621346	Homo sapiens	other
39232	>10	AA621409	ESTs	other
21	>10	AB000905	H.sapiens hls	?
6963	>10	AFFX-HUMTFAFFX-HUMTF		?
33890	>10	AFFX-HUMTFAFFX-HUMTF		?
39302	>10	C14944	ESTs	other
39329	>10	C20797	EST	?
28644	>10	D12163	ESTs	other
218	>10	D13540	PROTEIN-TYR	other
236	>10	D13645	Human mRNA	other
9127	>10	D30037	PHOSPHATID	other
459	>10	D38293	Human mRNA	TM
39405	>10	D50975	ESTs	other
39433	>10	D52037	Human thymid	other
39438	>10	D52692	Human Ca2+	TM
14708	>10	D59388	EST	?
39488	>10	D60831	ESTs	other
39504	>10	D80632	ESTs	other
765	>10	D86096	Prostaglandin	?
787	>10	D86969	Human mRNA	other
789	>10	D86971	Human mRNA	other
39529	>10	F02202	ESTs	?
39535	>10	F02450	ESTs Modera	TM
18676	>10	F04022	ESTs	other
18718	>10	F04915	ESTs	other
18762	>10	F09458	ESTs	other
18782	>10	F09739	ESTs	other
29080	>10	F13655	ESTs Modera	other
19001	>10	H02890	ESTs	other
19184	>10	H10395	EST	?
39725	>10	H11323	ESTs	other
19203	>10	H11593	ESTs	other
19328	>10	H17808	ESTs	other
19387	>10	H20128	ESTs	?
39787	>10	H20131	ESTs	SS,
19389	>10	H20165	EST	?
39832	>10	H26279	EST - RC_H2	other
19591	>10	H40688	ESTs	other
29229	>10	H48459	Human mRNA	other

FIGURE 12
(cont.)

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19727	>10	H52702	ESTs	?
19787	>10	H56679	ESTs	other
39995	>10	H62474	EST	SS, TM
28331	>10	H68116	ESTs	TM
28344	>10	H68839	EST	?
40064	>10	H72283	Human mRNA	other
40083	>10	H73488	MITOCHOND	other
18949	>10	H78263	ESTs	TM
40204	>10	H88296	EST - RC_HB	other
28523	>10	H88353	ESTs Weakly	?
29551	>10	H90134	ESTs	?
29645	>10	H95840	ESTs	?
20057	>10	H98079	ESTs	other
976	>10	HG2036-HT20EST - HG2036		?
1158	>10	HG3344-HT38EST - HG3344		?
1210	>10	HG37-HT37	EST - HG37-H	?
1346	>10	HG4716-HT5EST - HG4716		?
1349	>10	HG4747-HT5EST - HG4747		?
1445	>10	J03027	MHC class I p	?
1570	>10	K01383	EST - K01383	?
1884	>10	L07541	Replication fa	other
1852	>10	L17328	Human FE22	TM
1856	>10	L18920	MELANOMA-A	?
1863	>10	L19161	TRANSLATIO	other
2070	>10	L37378	Homo sapiens	SS, TM
2123	>10	L40396	Homo sapiens	other
2144	>10	L41349	Phospholipase	SS,
9723	>10	L44542	ESTs	other
2188	>10	L47276	EST - L47276	other
2343	>10	M15353	Eukaryotic tra	other
2627	>10	M29610	Glycophorin E	TM
2857	>10	M58597	Fucosyltransfe	TM
3021	>10	M68941	Protein tyrosin	other
3183	>10	M84424	Cathepsin E	?
3196	>10	M86917	Oxysterol bind	other
20088	>10	N20054	ESTs Weakly	?
28795	>10	N20641	ESTs Highly	other
40427	>10	N21147	ESTs	other
40444	>10	N22140	ESTs Highly	other
28893	>10	N23003	ESTs	TM
40498	>10	N28086	Homo sapiens	SS,
40559	>10	N33024	ESTs	SS,
30190	>10	N33264	EST	?
30207	>10	N33620	H.sapiens mR	other
20304	>10	N34686	Homo sapiens	?
20307	>10	N34830	ESTs	other
30265	>10	N35115	ESTs	other
40594	>10	N35388	ESTs	other
40604	>10	N38893	Homo sapiens	other
40631	>10	N45124	ESTs	other
40660	>10	N49104	NUCLEAR FA	other
30810	>10	N50138	EST	?
30617	>10	N50646	ESTs	other
30831	>10	N50807	EST	?
30790	>10	N52935	EST	?
20584	>10	N55443	ESTs	TM

FIGURE 12
(cont.)

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40760	>10	N57927	ESTs Weakly	other
30938	>10	N58561	Cathepsin B	other
20614	>10	N59230	ESTs	SS,
20657	>10	N62889	ESTs	other
31136	>10	N63512	ESTs Weakly	TM
40827	>10	N64051	Homo sapiens	other
31310	>10	N66831	EST	?
40876	>10	N67607	Human Rho-d	other
20701	>10	N68057	Homo sapiens	?
40905	>10	N68738	ESTs	other
40911	>10	N69114	H.sapiens mR	other
40913	>10	N69218	ESTs	other
31484	>10	N69468	ESTs	other
31619	>10	N73449	ESTs	other
41005	>10	N79516	ESTs	TM
31818	>10	N89774	Homo sapiens	other
31872	>10	N91109	EST	other
41040	>10	N91948	ESTs	other
31944	>10	N93193	ESTs	other
41065	>10	N93618	ESTs	other
32034	>10	N98926	ESTs Modera	other
41107	>10	R01634	ESTs	other
41163	>10	R08176	ESTs	other
21238	>10	R08564	Plasminogen	other
21240	>10	R08613	ESTs	other
21412	>10	R20670	ESTs	other
21519	>10	R27975	EST - RC_R2	other
41381	>10	R42278	H.sapiens mR	?
32189	>10	R43183	ESTs	TM
32195	>10	R43471	ESTs Weakly	other
21902	>10	R43822	EST	?
21946	>10	R44707	ESTs	TM
22072	>10	R49406	ESTs	?
32240	>10	R50976	Ribonuclease	other
32258	>10	R55623	ESTs	other
22258	>10	R56432	ESTs	other
22282	>10	R59197	ESTs	other
32277	>10	R61493	Human mRNA	other
22372	>10	R62831	EST	?
22400	>10	R64109	ESTs	other
41593	>10	R64129	ESTs	other
10233	>10	R71427	ESTs Highly	other
41654	>10	R76437	THROMBOXA	TM
22557	>10	R76722	ESTs	other
22576	>10	R79111	ESTs	other
22593	>10	R79777	EST	?
41678	>10	R80675	EST	?
41719	>10	R89260	EST - RC_R0	other
22793	>10	R96208	ESTs	other
41752	>10	R97063	ESTs	other
3375	>10	S50223	HKR-T1	other
3406	>10	S66896	SQUAMOUS	other
3522	>10	S80267	Spleen tyrosin	other
41793	>10	T03887	ESTs	?
23198	>10	T40530	ESTs Weakly	other
23360	>10	T58531	ESTs	other

FIGURE 12
(cont.)

32635	>10	T61116	ESTs	other
42177	>10	T79786	ESTs	?
23623	>10	T84047	ESTs	?
23662	>10	T86674	ESTs	other
42242	>10	T89579	Homo sapiens	other
23759	>10	T90313	ESTs	other
23832	>10	T92018	ESTs	other
32740	>10	T92950	ESTs	other
42290	>10	T95105	ESTs	?
3598	>10	U01157	Glucagon-like	SS, TM
3659	>10	U04313	Protease inhib	other
3799	>10	U10690	Human MAG	?
3870	>10	U14518	Centromere p	other
3913	>10	U16261	Human MDA-	SS,
4029	>10	U21090	Human DNA p	other
4157	>10	U28811	Human cyste	other
4178	>10	U30246	Human burne	TM
15006	>10	U30246	Human burne	TM
4193	>10	U31116	Human beta-s	TM
4306	>10	U36798	Homo sapiens	TM
4362	>10	U39817	Bloom syndro	other
4386	>10	U40622	DNA repair pr	other
4388	>10	U40714	Human tyrosy	other
4455	>10	U43944	MALATE OXID	other
4477	>10	U45880	Human IAP-lik	other
4680	>10	U55766	Human Rev it	TM
4702	>10	U57341	EST - U57341	other
4713	>10	U57721	Human L-lym	other
4787	>10	U61145	Human enhan	other
4882	>10	U65437	Human homeo	?
4945	>10	U69108	Homo sapiens	other
4975	>10	U71088	Human MEK5	other
4994	>10	U72514	Human C2f m	other
5002	>10	U72761	Human karyop	other
5021	>10	U73524	Human putativ	TM
5149	>10	U79716	Human reel	SS,
5214	>10	U83303	H. sapiens mR	?
5243	>10	U85946	Human brain s	other
32789	>10	W02779	ESTs Modera	other
42354	>10	W19348	ESTs	other
42390	>10	W40150	Homo sapiens	other
33006	>10	W46286	ESTs Weakly	TM
33020	>10	W46891	ESTs Weakly	other
33109	>10	W59961	Human mRNA	other
24197	>10	W67277	ESTs	other
24215	>10	W69425	ESTs	other
33301	>10	W73883	ESTs	other
33343	>10	W79834	ESTs Weakly	other
33377	>10	W81219	ESTs Weakly	other
42602	>10	W86423	ESTs	TM
33556	>10	W90705	Murine leukem	other
33616	>10	W93726	Protease Inhib	other
33666	>10	W95876	ESTs	TM
5510	>10	X05360	Cell division c	?
5558	>10	X07876	Wingless-type	SS,
5603	>10	X14253	Teratocarcino	TM

FIGURE 12
(cont.)

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5619	>10	X14850	HISTONE H2A	SS,
5623	>10	X14875	T-CELL SURF	?
5692	>10	X17644	G1 to S phase	other
5789	>10	X54925	Matrix metallo	other
5799	>10	X55330	Aspartylglucos	SS,
5802	>10	X55544	CYCLIC-AMP	?
5857	>10	X58377	Human mRNA	other
5960	>10	X63575	ATPase Ca++	TM
5963	>10	X63629	Cadherin 3 (R	SS, TM
5988	>10	X64810	Proprotein con	?
6041	>10	X87155	MITOTIC KIN	other
6095	>10	X69962	Fragile X mer	other
6106	>10	X70683	SRY (sex dete	TM
6155	>10	X74331	DNA primase	other
6167	>10	X74987	Ribonuclease	other
6188	>10	X76029	NEUROMEDI	TM
6315	>10	X81889	H.sapiens mR	other
6382	>10	X85133	H.sapiens RE	other
6384	>10	X63137	Human kines	other
6438	>10	X69398	URACIL-DNA	?
6449	>10	X89986	H.sapiens mR	TM
6478	>10	X91648	H.sapiens mR	SS, TM
6479	>10	X91653	EST - X91653	?
6494	>10	X92689	H.sapiens mR	TM
6713	>10	Y08564	EST - Y08564	?
6790	>10	Y12394	Homo sapiens	other
24915	>10	YEL003w	EST - YEL003	?
42773	>10	YEL019c/MM	EST - YEL019	?
24545	>10	Z38462	ESTs	other
33713	>10	Z38427	ESTs	other
33791	>10	Z40883	ESTs	other
42766	>10	Z69394	ESTs Modera	other
21558	>10	R33112	Human AF-6 m	other
26718	>10	AA282576	ESTs	?
40113	.9955090946	H78003	ESTs	?
10801	.9879448276	AA069285	ESTs Weakly	other
37491	.9513600842	AA455239	ESTs Highly	other
23900	.9272347693	T95789	ESTs	other
254	.9198395324	D14657	Human mRNA	other
6885	.8970927914	Z29331	Ubiquitin-con	other
29693	.8850766398	H97819	ESTs	SS,
26482	.8765189024	AA262491	ESTs	other
23123	.8699502035	T25306	EST	?
26525	.8160399123	AA278392	ESTs	other
13110	.7643356605	AA435840	Homo sapiens	other
34863	.7087597628	AA299784	EST	other
39432	.7034550083	D51691	Phosphoribos	?
31312	.6513325388	N68845	ESTs Weakly	?
21112	.6358446349	R01179	ESTs	?
31572	.6254820695	N71294	ESTs	other
17903	.6221229759	AA160259	EST	?
20747	.6094813734	N66842	ESTs	other
4676	.589223908	U55206	Homo sapiens	TM
34363	.5627081023	AA251587	Homo sapiens	other
39094	.540768988	AA620636	ESTs	other
3888	.5372000133	U15128	Human beta-	?

FIGURE 12
(cont.)

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39386	9.506250529	D12184	ESTs	TM
7874	4458059039	AA203742	ESTs	other
4192	4329744134	U31099	Human DP pr	TM
4507	9.422874945	U47050	Human putativ	TM
35606	9.412026255	AA402227	ESTs Modera	other
4970	3649551013	U70862	Human nuclea	?
18829	3432151573	H58813	EST	?
14837	2878584141	T40145	ESTs	TM
17336	2822148675	AA099585	ESTs	other
40541	2532836505	N30160	ESTs	other
29496	2487643833	H85434	EST	?
29943	1797074262	N24786	ESTs Modera	TM
17097	1829681314	AA169633	EST	other
21320	1243463318	R11673	ESTs	other
13883	1178796537	AA476917	ESTs Weakly	other
30539	0886887776	N49072	ESTs	other
32778	0877919549	W02063	EST	?
26380	0809559378	AA257012	EST	?
15888	0595893607	X95632	Human Abl in	other
40812	0012874244	N63419	ESTs	other
903	9640387906	D90070	ATL-derived P	other
22674	9515777733	R87180	ESTs	TM
40807	9510132281	N62995	TRANSCRIP	other
15244	9195644974	W00904	ESTs	TM
32296	8658776567	R67075	Zinc finger pro	other
18289	8575656789	AA209467	ESTs	other
19662	8507626284	H47391	ESTs	other
41607	8.833925517	R67868	CLEAVAGE S	other
2548	8299864699	M25897	Platelet factor	TM
7736	8279341243	AA232121	Human tyrosy	other
34490	7844537273	AA262354	ESTs	other
38658	7669313482	AA599477	ESTs	other
7528	8.765157554	AA149543	ESTs	other
39939	7555031142	H53454	EST - RC_H5	other
25111	7232692309	AA020787	ESTs	other
21655	8.716167279	R38239	EST	?
39663	8.665982852	H04756	ESTs Highly	other
1042	8.652112324	HG2510-HT2	EST - HG2510	?
32330	6361115426	R77776	ESTs	other
25382	6239456487	AA059007	ESTs	other
27074	5900813076	AA401475	ESTs Weakly	SS,
3955	5298909183	U18259	MHC class II	other
4959	8.52646827	U70322	Human transp	other
2315	5259185808	M14123	EST - M14123	?
37253	4896914832	AA449357	ESTs	other
39624	8.471316877	F10836	ESTs	?
23213	4569920887	T40891	ESTs	?
2788	8.455596435	M54995	Connective tis	TM
41154	4413390141	R07499	ESTs	?
32479	4093689549	T16282	WEE1-LIKE P	other
41251	3587565415	R28279	Human clone	other
19081	3583603183	H06701	ESTs Weakly	other
21098	3105927559	R00545	ESTs	other
14723	3061679053	D59894	ESTs	other
37154	2994822341	AA447666	Human CENP	other
8068	2835586361	AA313387	ESTs Highly	other

FIGURE 12
(cont.)

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7485	8.281679348	AA129547	ESTs	other
16501	.2517969834	AA026969	ESTs	other
34527	.2419163754	AA279081	ESTs	other
8700	.1948675663	Y07867	H.sapiens mRNA	other
2852	.1928816537	M58460	Human 75-kD	other
11188	.1862492468	AA172372	ESTs	TM
42293	8.183311084	T95333	ESTs Weakly	TM
5443	.1763317544	X02530	Interferon (gamma)	SS,
40937	.1534810594	N70607	ESTs	TM
23371	.1499496068	T69505	EST - RC, T59	?
26272	.1339974519	AA252981	ESTs Weakly	other
17306	.1332403762	AA086201	ESTs	other
18497	.1192326373	AA233795	ESTs	other
235	.0944363901	D13644	Human mRNA	other
24525	.0860187097	Z38347	ESTs	TM
7826	.0750029554	AA248884	EST - AA2488	TM
32142	.0739258775	R38715	Homo sapiens	other
39067	.0557768803	AA620405	ESTs	other
6235	.0448957236	X78416	Casein alpha	TM
29517	.0017588725	H88261	ESTs	other
28570	.9852455973	C21104	Homo sapiens	other
39344	.9182087762	C21034	ESTs Moderately	other
18951	.9002189759	H00580	ESTs	other
18953	.8709160227	H00615	ESTs	other
18376	.8564099916	AA228925	ESTs	other
19830	7.847878447	H58911	ESTs	other
36023	7.840835828	AA416881	ESTs	other
13347	.8344414518	AA449238	ESTs	other
36614	.8284591351	AA431466	ESTs	other
2192	.8254072032	L48211	Homo Sapien	?
33016	.8006574068	W46577	H.sapiens mRNA	other
17215	.7941954036	AA083044	ESTs	other
34894	.7659738105	AA311881	EST	?
40614	7.695001222	N39257	ESTs	other
36295	.6834749899	AA424534	ESTs	other
19564	.6744302788	H38833	ESTs	TM
16914	.6686405336	AA058665	ESTs	SS,
35967	.6378079107	AA412694	Human splicing	other
21672	.6384823402	R38835	ESTs	other
19918	.6303275831	H69787	ESTs	?
10511	.6297744492	AA024482	ESTs Highly	other
17721	.6057911016	AA136590	ESTs	?
42302	.6031859697	T96130	EST	SS,
26134	.6000619383	AA243763	ESTs	other
18766	.5621789008	F09497	ESTs	other
34492	7.501590494	AA262439	ATL-derived P	other
270	.4512152125	D14822	EST - D14822	other
35975	.4177746986	AA412738	ESTs	other
29842	.4095809971	N21688	ESTs	?
35389	.3913043319	AA395555	ESTs	other
19979	.3868157166	H88477	ESTs	other
5793	.3865664025	X54942	CDC28 protei	other
19978	7.3809697151	H87770	EST - RC, H8	other
1280	.3691089316	HG4126-HT4	EST - HG4126	?
31571	.3676263454	N71250	ESTs	other
23765	.3541191734	T90443	ESTs Weakly	?

FIGURE 12
(cont.)

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35123	.3397833453	AA380927	EST	?
38252	.3341119467	AA489247	ESTs	other
38216	.3282021037	AA488861	ESTs	other
29418	.2489407009	H77915	EST - RC, H7	?
4834	.1980951054	U63541	Human mRNA	other
42504	.1913036522	W69803	ESTs	other
6111	.7.158000198	X71125	H.sapiens mR	TM
41773	.7.154479618	T03024	ESTs Weakly	other
9951	.1363626369	N71513	ESTs	other
28109	.0941968224	AA485212	ESTs	other
988	.0783044659	HG2160-HT2	EST - HG2160	?
29848	.0610688511	N22107	ESTs	other
30628	.0607950168	N50744	ESTs	other
22567	.0225726353	R77771	ESTs	TM
9347	.7.0063230711	H03686	ESTs	TM
11696	.0026773299	AA252894	ESTs	other
40584	.0010096333	N34870	EST	?
193	.9767029188	D10923	PROBABLE G	TM
18305	.9740536051	AA214048	Collagen type	other
6078	.8699682397	X69141	FARNESYL-O	other
26741	.6.902658703	AA283198	ESTs	other
35069	.8992865685	AA358397	EST	?
23504	.8977135983	T71042	ESTs	other
299	.8824513029	D16815	Homo sapiens	other
40583	.8689903023	N34855	ESTs	other
31428	.8623762224	N68594	ESTs	other
6169	.8806959727	X75091	SET PROTEIN	other
39524	.8567355171	F01905	MALATE OXID	other
34578	.8430689439	AA280837	ESTs	other
36678	.6.837527995	AA599920	Small inducib	other
23936	.8251471804	T96930	ESTs	other
9326	.8181321394	D89377	Msh (Drosoph	other
19188	.8067351968	H11255	ESTs Highly	TM
18185	.7882148811	AA194983	Homo sapiens	other
27028	.6.757529124	AA399630	ESTs Weakly	other
41289	.7519531681	R37265	EST	other
34511	.7364448798	AA278298	EST - RC, AA	other
1566	.7056207716	J05614	EST - J05614	?
25675	.6692299748	AA129757	ESTs Highly	other
5814	.6584342828	X56088	CYTOCHROM	SS,
13861	.6236291607	AA470145	ESTs	other
29794	.6026313353	N20598	ESTs	other
39333	.5902382643	C20910	Cyclin B1	other
3770	.5835303599	U09609	Nuclear factor	other
31831	.5829933764	N89894	ESTs	?
33063	.5808125028	W53000	Homo sapiens	other
20326	.5640084836	N35583	ESTs Weakly	?
34384	.5535703492	AA252537	ESTs	other
25599	.5490481991	AA114091	Human (clone	other
39749	.5369363254	H14988	ESTs	other
42596	.5200567072	W85900	ESTs	?
39606	.5119482185	F10243	ESTs Weakly	?
14617	.5105504748	C14983	ESTs	other
27831	.6.45670814	AA456044	ESTs	?
34896	.4496517783	AA312551	EST	?
27360	.4434305006	AA425356	ESTs	other

FIGURE 12
(cont.)

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20128	4326610424	N22015	ESTs	TM
6663	4324809977	Y00291	RETINOIC AC	TM
30692	4196636207	N51563	ESTs	other
36472	4189542265	AA428633	EST	?
9576	3961788753	H87652	Homo sapiens	other
39670	3818496156	H05626	ESTs	other
22697	3652792447	R89218	ESTs	other
37308	3647804993	AA451694	EST	TM
16101	3517262802	AA002147	EST	?
20629	3486854401	N59798	ESTs	other
36100	3364146287	AA417740	ESTs	?
15488	3252590241	W28097	Homo sapiens	other
36667	3131273544	AA432136	ESTs	other
30766	3115037924	N52627	EST - RC, N5	?
32882	2745311453	W37683	ESTs	TM
18072	2675797205	AA180448	EST	?
16231	2652604863	AA199747	Human mRNA	other
38282	2514165678	AA489814	EST	?
28125	6250317021	AA486073	ESTs	other
37484	2484456382	AA454747	ESTs	?
36818	1946328223	AA431478	ESTs	other
5082	1931116815	U78524	Human Gu b1	other
1441	1777287039	J02963	Integrin alpha	other
42105	6.14875944	T67710	ESTs	?
6061	1394863141	X68314	Glutathione pe	SS,
32570	1156028796	T30222	ESTs Weakly	TM
32504	1019612076	T17063	EST	?
23335	0977927504	T56804	EST	?
10867	0970991075	AA088458	ESTs Weakly	other
30883	0911993489	N56923	EST	?
14528	0859008453	AA620295	ESTs	TM
29454	0685955036	H81308	EST	?
6798	0539173276	Y13153	Homo sapiens	TM
21248	0525426545	R08871	ESTs	?
21940	0499964138	R44538	ESTs	?
29066	0455247653	F10927	Homo sapiens	other
18774	0446826953	F09609	ESTs	?
36722	0172343991	AA435512	ESTs	SS,
18062	0034342988	AA179845	ESTs Modera	other
22989	9992817406	T16305	ESTs	other
41745	9905623898	R95895	ESTs	?
8787	9894877658	AA504307	X-LINKED HE	other
20550	5.984881795	N55013	ESTs	other
26470	9417764101	AA262179	ESTs	other
16574	9356497569	AA031926	EST	other
693	9169537389	D80007	Human mRNA	other
4093	5.914830973	U25182	Human antiox	TM
1192	9086284407	HG3548-HT3	EST - HG3548	?
22956	8954735623	T10248	ESTs	other
36723	5.891606409	AA435524	EST	?
2114	8844986595	L40384	EST - L40384	other
26872	5.868236789	AA291137	ESTs	other
6602	8663883018	X98266	EST - X98266	other
42701	8594493433	Z38612	ESTs	other
28573	5.84591116	C21118	ESTs	other
18290	8189427595	AA211901	ESTs	other

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732	.804391794	D83781	Human mRNA	other
5330	.801414561	U91327	EST - U91327	?
33503	.798071518	W88720	EST	?
2553	.779750586	M26167	Human platelet	?
34705	.785880625	AA286907	ESTs Weakly	other
42665	.759409104	W93659	ESTs	other
38180	.753931079	AA487495	EST - RC_AA	other
4244	.747673880	U33286	Human chrom	other
32822	.741895745	W16834	ESTs	TM
3977	.724588555	U18991	Retinal pigme	?
24673	.720238815	Z39301	ESTs	TM
6928	.712026112	Z46629	SRY (sex-dete	other
38726	.703079625	AA608733	ESTs	?
39290	.689237205	C14573	Human mRNA	other
11405	.681887379	AA232231	ESTs	other
22538	.679200659	R73567	Homo sapiens	TM
40747	.660539320	N56872	Homo sapiens	TM
31596	.655402460	N72094	ESTs	other
6329	.641565251	X82279	EST - X82279	?
31578	.627332366	N71361	ESTs	other
33207	.627181848	W70051	H.sapiens mR	other
2545	.610586014	M25753	Cyclin B1	other
22580	.598840264	R79156	ESTs	other
33592	.593531451	W93127	ESTs	other
28843	.573469875	D60252	ESTs	other
6160	.568905061	X74794	CDC21 HOMO	other
37987	.561345667	AA479666	ESTs	other
42515	.521786881	W72118	Homo sapiens	other
4732	.513066852	U58522	Human huntin	other
3299	.509985067	M95623	Hydroxymethyl	?
28320	.547340698	AA509574	ESTs	?
746	.547126089	D84454	Human mRNA	TM
39373	.463580495	C21517	ESTs	other
3117	.439841353	M81182	Peroxisomal m	other
21257	.434361244	R09196	ESTs Moderat	other
31487	.431884885	N69507	ESTs	other
28954	.413713051	F03153	ESTs	other
38828	.538978272	AA609595	ESTs	other
29903	.372232062	N23366	EST	?
30925	.343743231	N58295	ESTs Weakly	?
19091	.334461566	H07864	ESTs	TM
28209	.313895191	AA491250	ESTs	other
9470	.311889798	H46617	EST - H46617	other
9435	.307005665	H30201	EST - H30201	?
28552	.295443257	C20914	ESTs	other
27411	.294016426	AA428137	ESTs	other
30815	.292412526	N50556	ESTs	other
28313	.265797716	AA599309	ESTs	TM
39321	.264903538	C20632	ESTs	?
28934	.253104739	N24194	ESTs	other
1094	.249670312	HG2846-HT2	EST - HG2846	?
39578	.248112638	F08925	ESTs	TM
11232	.246679842	AA186804	ESTs Weakly	other
2466	.242634932	M21539	Human small	other
26843	.238775856	AA287450	ESTs	?
40331	.235338558	H97582	ESTs Weakly	other

FIGURE 12
(cont.)

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8035	.5205798365	AA305116	EST - AA3051	other
28793	.1955426722	N20593	ESTs Weakly	other
34109	.1481590107	AA210722	EST	?
28408	.1432577257	AA258177	ESTs Weakly	other
19263	.1427029807	H15054	ESTs	TM
24596	.1416089352	Z38810	ESTs	other
28589	.1365059753	C21245	H.sapiens mR	other
5684	.1121931412	X17098	Pregnancy-sp	other
30710	.1079347344	N51761	EST	?
35765	.0973514948	AA406167	EST	?
26360	.0863127861	AA256460	ESTs	?
2351	.0849612092	M15798	Proliferating c	?
30282	.0836877534	N35065	Homo sapiens	other
41792	.0737512463	T03866	ESTs	?
36710	.0703839884	AA434411	ESTs	other
39090	.0546885407	AA620628	ESTs	TM
42185	.0539926381	T79951	ESTs	?
18745	.0460321557	F09134	ESTs	other
35746	.0396841996	AA406063	ESTs	other
35356	.0354809581	AA399053	EST	?
38769	.0312706876	AA435750	EST	?
36900	.0279911548	AA436866	H.sapiens mR	other
27595	.0244757301	AA443326	ESTs	TM
16290	.0056611904	AA016145	ESTs	?
27117	.0016146593	AA405098	ESTs Weakly	other
4304	.9951954397	U36764	Eukaryotic tra	other
33458	.9907402027	W86835	Homo sapiens	other
26693	.980090679	AA282120	EST	?
12669	.9758138651	AA417030	Homo sapiens	other
29701	.9708526387	H97970	EST	?
20480	.9557253636	N52168	ESTs	TM
8720	.9439110602	AA481218	EST - AA4812	other
34828	.9431269475	AA292436	Homo sapiens	SS, TM
14985	.9416210321	U15128	Human beta-	?
16115	.9377553522	AA004420	ESTs	?
42506	.9348587118	W70074	EST	other
34761	.9316637443	AA267833	ESTs	other
11870	.9281056201	AA262587	ESTs	TM
23211	.9258391854	T40889	ESTs	other
40611	.9160502275	N39138	Homo sapiens	other
42611	.9128605354	W87006	Homo sapiens	other
39652	.9045174605	H03099	ESTs	other
17581	.8896747511	AA129395	EST	?
37239	.8704375386	AA449121	ESTs	?
18712	.8703618781	F04677	ESTs	other
30709	.8611171953	N51752	ESTs Weakly	other
34179	.8503613948	AA227903	ESTs Highly	other
21433	.825670988	R22183	EST	?
39731	.8186142741	H11760	ESTs	other
31295	.8116614607	N66653	ESTs	other
24647	.804163055	Z39108	EST	?
31292	.8008671817	N66615	ESTs	other
1285	.7997542393	HG4157-HT4	EST - HG4157	?
1106	.7932425858	HG2981-HT3	EST - HG2981	?
18212	.7912262565	AA196506	ESTs	other
34367	.782207045	AA251758	Homo sapiens	other

FIGURE 12
(cont.)

34802	.7797760205	AA291468	ESTs	TM
34762	.7775301546	AA287834	ESTs	other
11595	.7696612848	AA242819	ESTs	other
8285	.7639839111	AA405082	ESTs	?
17622	4.758635576	AA131584	ESTs Weakly	other
35781	.7572463523	AA406335	ESTs	other
34754	.7483874972	AA287642	Human mRNA	other
23237	.7444854356	T47291	EST	?
37667	.7280445357	AA460318	ESTs Highly	other
11568	.7257189975	AA236786	ESTs	other
38622	.7190695733	AA598967	ESTs	?
5137	.7057359474	U79296	Dihydrolipoam	other
25038	.7002244728	AA010065	CDC28 prote	other
19288	.7000147312	H16587	ESTs	other
32503	.6979488292	T17045	Collagen type	other
3278	.6953739298	M94055	SODIUM CHA	TM
8696	.6942061018	L38961	Integral trans	TM
35400	.6901390898	AA399591	Homo sapiens	other
35246	.6862691303	AA398367	EST Weakly s	?
36387	.6822499271	AA426270	ESTs	other
21509	.6730072542	R27314	ESTs	other
31381	.6729672124	N87889	ESTs	other
26723	.6727894925	AA282781	ESTs Highly	other
36326	.6703621086	AA425151	Human GAP S	other
17409	.6688418667	AA113136	EST - RC_AA	other
4908	.6552339935	U67156	Human mitoge	other
30594	.6496238328	N49967	ESTs	other
38286	4.64639735	AA489847	ESTs Weakly	?
13073	.6426509458	AA433950	ESTs	other
40435	.6240181066	N21814	Homo sapiens	other
14474	.6228694379	AA609427	ESTs Moderat	other
38213	4.6153099071	AA488847	ESTs Weakly	?
5312	4.606644198	U90716	Human cell su	SS, TM
24225	.6041550359	W70328	ESTs	?
35588	.5868982366	AA401750	EST	?
29739	.5863199051	H99626	EST	?
7203	.5792992577	AA053096	EST - AA0530	other
2157	.5772055868	L41939	Homo sapiens	SS, TM
32086	.5661024279	R11510	ESTs	?
8085	.5648114738	AA314779	ESTs Weakly	SS,
224	.5622018888	D13633	Human mRNA	other
34006	.5609980241	AA188781	DNA polymera	other
33656	.5557384389	W95477	ESTs	other
34065	.5537335124	AA195517	ESTs Weakly	TM
6028	.5357922097	X66503	Adenylosuccin	other
4166	.5032930671	U29463	Cytochrome B	?
40262	.5024727522	H93562	ESTs	TM
22687	.5018672549	R88209	ESTs	TM
41069	.4977510482	N93969	H.sapiens mR	SS,
8264	.4793100575	AA401334	ESTs	other
27588	4.472017297	AA443187	ESTs	other
35882	.4717597552	AA412047	ESTs	?
34479	4.465519191	AA262080	Human bumet	TM
15921	.4548516438	Y12065	Homo sapiens	?
11279	.4380038671	AA195399	ESTs	other
39222	.4367650786	AA621348	ESTs Highly	other

FIGURE 12
(cont.)

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34428	.4364736766	AA256526	ESTs	other
8771	4.432067373	AA491188	ESTs	other
22193	.4189810024	R53891	Homo sapiens	other
7898	.4066170674	AA263032	ESTs	other
19902	.3886145805	H86736	ESTs	other
9276	.3888095205	D82374	ESTs	other
10716	.3794529068	AA053319	ESTs	TM
13183	.3751913512	AA442763	ESTs Highly	other
5690	.3723059412	X17620	NUCLEOSIDE	other
35102	4.37147138	AA371509	EST - RC_AA	TM
17983	.3612985467	AA169226	ESTs	other
24982	.3497206825	AFFX-HUMT	AFFX-HUMT	?
31680	.3416539668	N74438	ESTs	other
27168	4.3303068894	AA410258	ESTs	other
28731	.3231846659	D20981	EST	?
28348	.3212284906	AA608752	ESTs	other
18335	.3019961487	AA018587	ESTs Weakly	?
33036	.2915644973	W48580	ESTs Weakly	other
30180	.2897721925	N33144	ESTs	SS.
35691	.2895541242	AA401758	ESTs Weakly	?
25340	.2721717135	AA054554	EST	?
28108	.2659103745	AA485084	ESTs	other
38690	.2649184307	AA600121	ESTs	other
20203	.2626499431	N26855	ESTs Modera	other
10251	.2608780694	R76185	ESTs Weakly	SS.
12684	.2604192389	AA417558	ESTs	SS.
31636	.2509463427	N73680	Natural resista	TM
20769	.2479765348	N67277	ESTs	other
1572	.2353281083	K01884	EST - K01884	?
10923	.2292322072	AA116036	ESTs	other
34380	.2283792392	AA252414	ESTs	other
10132	.2222816115	R35733	EST - R35733	other
16629	.2161752119	AA036811	ESTs	?
25146	.1969883794	AA026356	ESTs	?
28730	.1865943098	D20959	ESTs Modera	other
10200	.1874912391	R64521	ESTs	other
38695	.1545794663	AA600176	ESTs	other
31365	4.150549979	N67550	ESTs	other
42379	.1486120688	W37699	ESTs	other
28050	.1428703354	AA479139	Acid phosphat	other
2620	.1386565707	M29474	Human recom	?
8927	.1340593744	AF008442	Homo sapiens	other
13379	.1269549188	AA449741	ESTs Weakly	other
5134	.1218251808	U79293	Human clone	other
2626	4.1213948	M29581	Zinc finger pro	other
38005	.1160483666	AA479969	ESTs	other
36575	.1127196584	AA431085	EST	?
18296	.1121837207	AA213820	ESTs Weakly	?
28531	.1111458313	H88953	EST - RC_H8	TM
143	.1095880506	AFFX-HUMT	AFFX-HUMT	?
10970	.0967613396	AA129390	ESTs	other
25836	.0952825397	AA152305	Interferon (gam	SS.
19735	.0937927853	H53038	EST	?
40711	.0909709431	N53564	ESTs	other
4149	.0901471427	U28386	RAG (recomb	TM
5767	.0862784557	X53793	MULTIFUNCT	other

FIGURE 12
(cont.)

5503	.0861035825	X05232	Sirometysin	SS,
20310	.0841711856	N34893	ESTs Highly	other
456	.0599824566	D38145	Prostaglandin	SS,
7814	.0559685576	AA248406	ESTs	other
40230	.0447282719	H90161	ESTs	SS,
33651	4.039204804	W95409	ESTs	other
16777	.0231657929	AA046968	EST	?
19110	.0094905222	H08778	ESTs	other
34442	.0077010365	AA258093	HKR-T1	other
5099	4.004992433	U79247	Human clone	TM
6209	.9990473163	AA384220	ESTs	other
24408	.9976586074	W90146	ESTs	other
26596	.9974919787	AA279943	ESTs	other
18485	.9811264008	AA026269	Spleen focus	other
32969	.9804901745	W42451	ESTs	TM
27006	.9799768093	AA398695	ESTs Weakly	other
29809	.9526765967	N21043	EST	?
8596	.9440163451	H91564	ESTs	TM
29024	.9377933938	F09315	Homo sapiens	other
21694	.9356365584	R39317	Homo sapiens	other
13207	3.929998104	AA443321	ESTs	other
37865	.9143752629	AA476623	ESTs Highly	other
35201	.9129828172	AA421164	ESTs	?
8961	.8981160269	AFFX-HUMT	AFFX-HUMT	?
17444	.8927133917	AA115933	ESTs	other
25869	.8919834527	AA157267	ESTs Highly	TM
24862	3.89042252	Z41415	ESTs Highly	other
26685	3.889303206	AA281950	ESTs	?
42300	.8850230366	T95850	ESTs	?
6495	.8830844863	X92715	Zinc finger pro	other
38604	.8828045942	AA598803	ESTs	TM
38358	.8828713718	AA425756	ESTs	other
30560	3.873276445	N49284	MYB PROTO	other
14413	.8724466158	AA600150	ESTs	other
23823	.8574824967	T91805	Homo sapiens	other
38158	3.853096838	AA487021	EST	?
2572	.8518747554	M27281	Vascular endo	other
40100	.8464168967	H75933	Laminin recep	other
40258	.8462992993	H93340	ESTs	TM
20944	.8461821525	N74443	ESTs	other
20411	.8459400966	N48963	Homo sapiens	other
10345	.8457714481	AA001663	ESTs	other
31261	.8451974374	N66248	EST	other
8513	.8378410994	AA446990	ESTs	other
13877	.8363409835	AA476604	ESTs	other
40748	.8253562321	N56879	EST	?
14509	.8152852193	AA609943	ESTs	other
10281	.8065567331	R60333	ESTs	other
25284	.8044158642	AA045074	ESTs Weakly	other
6730	.7900025129	Y09305	H.sapiens mR	other
16033	.7884592402	AFFX-HUMIS	AFFX-HUMIS	?
39242	.7827164808	AA621523	ESTs	other
27354	.7794760439	AA425221	ESTs	?
4552	3.777263605	U49188	Human placen	SS, TM
18385	.7756199108	AA227219	Homo sapiens	other
16754	.7677416053	AA046067	EST - RC AA	other

FIGURE 12
(cont.)

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12752	.7871137403	AA421250	ESTs	other
42463	.7601033106	W60180	ESTs	other
10614	.7581669016	AA037357	ESTs	?
867	.7459337969	D87716	Human mRNA	other
7608	.7336047135	AA180907	ESTs	other
31785	.732738742	N80703	ESTs	other
35377	.7273784603	AA399453	EST - RC_AA	?
22828	.7243928524	R98192	ESTs	other
25240	.7243198336	AA039713	ESTs	other
11008	.7197361356	AA134289	ESTs Weakly	?
4341	.7162349944	U38545	Human ARF-a	other
28833	.7147818393	D59787	EST - RC_D9	?
3750	.7121007154	U09279	Collagen type	SS,
17483	.6943413512	AA122147	ESTs	TM
16854	.691520847	AA055552	ESTs Weakly	TM
3709	.689165677	U07550	Heat shock 10	other
1608	.6852978422	L00205	KERATIN TYP	?
24577	.6617721053	Z38727	Homo sapiens	TM
31032	.6570916386	N62508	ESTs	other
4851	.6536195433	U69546	Human RNA b	other
37680	.6523275307	AA460225	ESTs	other
20418	.649535709	N49209	ESTs	other
27695	.6485167436	AA470155	Homo sapiens	?
7871	.6434397185	AA287423	ESTs	other
27606	.643030453	AA443793	ESTs	other
24677	.6427250633	Z39338	ESTs Highly	other
11070	.6406198277	AA148521	ESTs Weakly	TM
9328	.6356048599	D89518	Homo sapiens	other
36826	.634699802	AA435996	ESTs	other
17678	.6300045795	AA134275	Human HIV1	other
36209	.6274694477	AA421266	ESTs Weakly	other
34120	.6258090412	AA211615	EST	?
38152	.6248442011	AA486737	H.sapiens mR	TM
38463	.6184693268	AA504491	ESTs Weakly	TM
20064	.6183699978	H98653	ESTs	TM
31256	.5992620732	N88152	EST	?
9713	.5985228843	L44338	Homo sapiens	other
28622	.5768056147	D11837	ESTs	?
38057	.5736105703	AA481549	EST - RC_AA	other
28763	.5688723791	D45568	EST	?
16996	.5680705709	AA069038	EST - RC_AA	TM
28628	.5604144817	D11888	ESTs Modera	?
25804	.5442954572	AA148885	ESTs	?
2492	.5423964239	M22898	Tumor protein	?
14904	.5411970737	T83389	ESTs Highly	other
25265	.5347588502	AA043785	H.sapiens RY	other
13606	.5327912417	AA458437	ESTs Weakly	other
42307	.5318436465	T96595	EST - RC_T96	TM
1544	.3.526232414	J05068	TRANSCORBA	SS,

FIGURE 12
(cont.)

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FIGURE 13A

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118085	3.0	N71781	ESTs
100552	3.4	HG2167-HT22Protein Kinase H31, Camp-Dependent	
120471	2.5	AA251829	ESTs; Moderately similar to (define not available 4880597) [H.sapiens]
126547	4.2	U47737	transmembrane 4 superfamily member 3
106057	3.3	AA417007	ESTs
126103	4.0	T95333	ESTs; Weakly similar to Strabismus [D.melanogaster]
135243	3.4	AA215333	ESTs
121457	2.5	AA411448	ESTs; Moderately similar to alternatively spliced product using exon 13A [H.sapiens]
131218	2.7	C31058	ESTs
112971	2.4	T17185	ESTs
111179	2.1	N67239	ESTs
123533	2.3	AA608751	ESTs; Moderately similar to [H] ALU SUBFAMILY SC WARNING ENTRY [H] [H.sapiens]
105175	2.4	AA186004	ESTs; Weakly similar to unknown [S.cerevisiae]
105156	2.7	AA172372	ESTs; Moderately similar to [H] ALU SUBFAMILY SQ WARNING ENTRY [H] [H.sapiens]
111223	2.5	N68921	ESTs; Weakly similar to neogenin [H.sapiens]
132180	2.7	AA405569	fibroblast activation protein; alpha
106400	2.1	AA447621	ESTs
126260	3.1	AA093834	ESTs; Highly similar to (define not available 4679014) [H.sapiens]
115291	3.9	AA279943	ESTs
128828	2.1	C14037	ESTs; Weakly similar to Yel007c-ap [S.cerevisiae]
116399	2.7	AA599720	Homo sapiens homeobox protein A10 (HOXA10) gene, complete cds
130987	3.5	R45698	ESTs
105082	2.6	AA143763	ESTs; Weakly similar to Similarity to S. Pombe BEM1/BUD5 suppressor [C.elegans]
103453	3.2	X09585	H.sapiens mRNA for SMT3B protein
115947	2.6	AA443793	ESTs
105012	2.8	AA118036	ESTs; Highly similar to (define not available 4589929) [H.sapiens]
105507	3.2	AA256878	ESTs; Moderately similar to (define not available 4108091) [H.sapiens]
130800	2.6	AA223385	ESTs; Weakly similar to katanin p80 subunit [H.sapiens]
116461	3.4	AA621557	ESTs; Moderately similar to [H] ALU SUBFAMILY SQ WARNING ENTRY [H] [H.sapiens]
129945	2.5	AA232104	ESTs; Highly similar to (define not available 4929575) [H.sapiens]
100864	2.1	HQ4297-HT45Transcriptional Coactivator Pca	
128131	2.3	A1283182	claudin 3
131564	2.8	AA481465	ESTs
100278	3.1	D42084	Human mRNA for KIAA0094 gene; partial cds
134425	1.8	J04177	collagen; type XI; alpha 1
130287	2.6	AA113149	tumor suppressing subtransferable candidate 3
108828	2.1	AA131584	ESTs; Weakly similar to coded for by C. elegans cDNA cm16f6 [C.elegans]
131289	2.2	AA485697	ESTs
109141	4.2	AA176428	ESTs
119307	2.5	T32108	ESTs
134319	2.1	AA129547	ESTs; Moderately similar to [H] ALU SUBFAMILY J WARNING ENTRY [H] [H.sapiens]
133458	5.0	M18728	non-specific cross reacting antigen
116732	2.3	F13779	ESTs; Weakly similar to [H] ALU SUBFAMILY J WARNING ENTRY [H] [H.sapiens]
CGAB 115239	3.0	AA278650	ESTs

FIGURE 13B

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Code	PRIMEKEY	Accession	Complete Title
CZA8	111929	3.7	R40057 prominin (mouse)-like 1
BCX2	128790	4.0	AA291725 secreted frizzled-related protein 4
CBC2	101800	5.7	M86849 Homo sapiens connexin 26 (GJB2) mRNA, complete cds
CBC1	100365	4.6	D78611 mesoderm specific transcript (mouse) homolog
CBC3	102618	2.5	U65932 extracellular matrix protein 1
CJA8	115697	8.1	AA411502 ESTs: Weakly similar to airway trypsin-like protease [H.sapiens]
CJA9	116176	5.7	AA463725 ESTs: Weakly similar to KIAA0226 [H.sapiens]
CGA7	115522	8.1	AA331303 ESTs
BCN5	112244	3.1	R51309 ESTs (now Sulfatase by in-house sequencing)
CQA1	132592	5.6	AA126390 ESTs
BCN7	117280	5.4	N22107 ESTs: Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]
CQA2	104050	6.0	AA007160 ESTs

FIGURE 14

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[illegible]

FIGURE 15

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ATGACCATGATTACGCCAAGCTTGGCAGCAGGAGACAGCCACTTGGCCATGTCACCAAAACAAGGAGAAGGTGCAAGAC
TGTCCGTGTGGACCCCTGACTCAGCAGAGATTCAGAGATAAAATAAGTAATCCCCTGAATCCAGAAATCATGAAA
AGCAGGAAAGCCAGGATCTCAGAGCTACTGCAAAAGTTCCCTCTCCACUAGACGAGCACCAGAAAGCTGAGAATGCTGTT
TCCTCAGGTAACAGAGATTCAAGGTACCTTCAGAAGGAAAGAAATCTCTACACAGATGAGTCATCCAAACCTGGAAA
AATAAAGAACTGCAATCACTACTCCAAACTTTAAGAAGCTTCATGAAGTCAATTTAAGGAAATGGAGTCCATTGATC
AATATATTGAGAGAAAAAGAAACATTTTGAAGAACACAATTCATGAATGAAGCAGCAGCCCATCAATAAGGGA
GGGCTCAGGACTCCAGTACCTCCAAGAGGAAGACTCTCTGTGGCTTCTACTCCCATCAGCCAACGACGCTCGCAAGGCG
GTCTTGTGGCCCTGCAAGTCAGAGTACCTTGGGTCTGAAGGGTCACTCAAGCGCTCTGCTATCTCTGAGCTAAAACGG
GTGTCAAGTTTTTCAGCTGCTACTAAAGATAATGAGCATAAGCGTTCACTGACCAAGACTCCAGCCAGAAAGTCTGCACAT
GTGACCGTGTCTGGGGCACCCAAAAGGGCAGGGCTGTGCTTGGGACACACAAATTAAAGACCATCACGGGGAATCTGC
TGCTGTTATTACCCCATTCAGTTGACAACTGAGGCAACGCAGACTCCAGTCTCCAATAAGAAACCACTGTTTGTATCTTA
AAGCAAGTTTGTCTCGTCCCTCAACTATGAACCAACAAAGGAAAGCTAAAACCATGGGGGCAATCTAAAGAAATAAT
TATCTAAATCAACATGTCAACAGAAATTAATTTCTACAAGAAACTTACAACAACCCCATCTCCAGCAAGGAAGAGCA
ACGGAAGAAACGCGAGCAAGAACGAAAGGAGAAAGCAAGGTTTTGGGAATGCGAAGGGGCTCATTTTGGCTGAAG
ATTA

FIGURE 16

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MTMITPSLARGROPLGHVTKTRRRCKTVRVDPDSQCNHSEIKISNFTFONIEKQESQDLRATAKVSPPPDEHQEAENAV
SSGNRDSKVPSEGGKSLYTDSSKPGKNKRTAITTPNFKKLHÉAHFKEMESIDQYIERKKKHFEHNSMNELKQQPINKG
GVRTPVFPRGRLSVASTPISQRRSQGRSCGPASQSTLGLKGLKRSASAAKTGVRFSAAKDNHKKRSLTKTPARKSAH
VTVSGGTQKGEAVLGTHLKTITGNSAAVITPFKLTTEATQTPVSNKKPVFOLKASLSRPLNYEPHKGKLPWGQSKENN
YLNQHVNRINFYKKTYKQPHLQTKKEQKKREQERKEKKAKVLGMRRGLILAED

FIGURE 17

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Amino-CKVLG MRRGL ILAED-COOH

FIGURE 18

Acetyl-KQPHL QTKEE QRKKC-Amide

FIGURE 19

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```
human_CAA2 -----KKHFEFHNSMNELKQIPINKGGVRTPVPPFGRLSVASTFISQRRS
mouse_CAA2 AREKKMESIDENIRKKKKHLKEHSSLNEIKLUKK--GI VTPVPFGRLSVPTPARQQCP
          .....*..... : * : .....*..... :
human_CAA2 QGRSCGPASQSTLGLKGSILKRSASAAKTGVRFSAATKDNEHKSLTKTPARKSAHVTVS
mouse_CAA2 QG-----H--S-ATKMNVRFSAATKDNEHKSLTKTPARKSPHVTAP
          ** : * : .....*..... :
human_CAA2 GGTQKGEAVLGTHKLKTI TGN SAAVITPFKLTTEATQTFVSNKKPVFDLKASLSRPLNYE
mouse_CAA2 GSASKGOAVERTPKSKATERTSIAVITPFKLMTEATQTPSSSKKPVFDLKASLSRPLNYK
          * : * : .....*..... :
human_CAA2 PHKGKILKPWGQSKENNYLNQHVNRI NFYK KTYKOPHLQTKEEQRKKREQERKEKKAKVLG
mouse_CAA2 PHKGKILKPWGQAKENNSLNERVSRVTFHRKTYKOPHLQTRERWKRQEQERKEKKKELLE
          ***** : * : * : * : * : * : * : * : * : * : * : * : * :
human_CAA2 MRRGLILAED-
mouse_CAA2 ARRN LGVTKAQ
          **.* : : :
```

FIGURE 20

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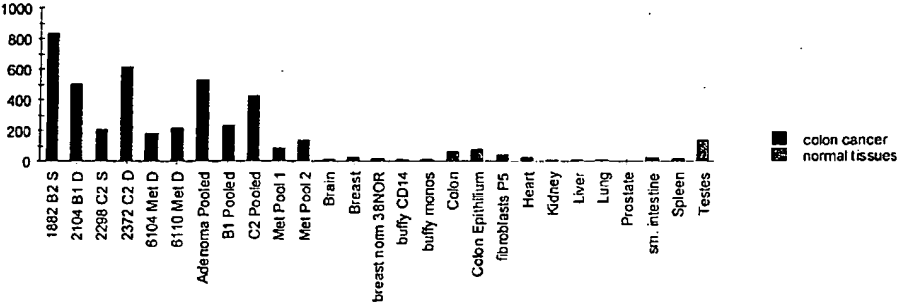


FIGURE 21

[illegible]

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FIGURE 23

ATGGAGCCGCGGCCACGCGCCCTCCTCCGGCGCCCGGGACTGGCCGGGGTCGGGGAGACGCCGTGAGCCGTGCGCT
GGCCGAGCCAGG3TGGAACTGCCCGGCACGGCTGTGCCCTCGGTGCCGGAGGATGCTGCCCGCCGAGCCGGGACGGCG
GCGGGGTCCGCGATGAGGGCCCCCGGGCGGCCGGGACGGGCTGGGCAGACCTTGGGGCCACCCGAGCCAGAGCCGT
TTCCAGGTGGACCTGGTTTCCGAGAACGCCGGGCGGGCCGCTGCTGCCGGCGCGCGCGCGCGCGCGCGCGCGCGCG
TGGTGCTGGGCGCGGGCCAAAGCAGACCCCCCGGACGGGGAAGCCAGCGGCGAGAGCCAGCCAGCTAAAGGCAGCGAGS
AAGCCAAAGGGCGCTTCCGCGTGAACCTTCGTGGACCCAGCTGCCCTCCTCGTGGCTGAAGACAGCCTGTGATGCTGCC
GGGGTCCGAGTCGACCGGCCCAACGTGAGCTTCCAGAACGGCGGGGACACGGTGCTGAGCGAGGGCAGCAGCCTGCACTC
CGGCGCGCGCGCGCGCAGTGGGCACCCAGCAGCTACTATTATGATACCCACACCAACACCTACTACTGCGCACCTTCG
GCCACAACACCATGGAGCCTGTGCCAGGATCGATCACTACCGGCACACAGCCGCGCAGCTGGGCGAGAAGCTGCTCCGG
CCTAGCCTGGCGGAGCTCCACGACGAGCTGGAAAAGGAACCTTTTGGAGTGGCTTTGCAAAATGGGGAAGAACTACTCC
AACCAGAGATGCTGTGGTCAGTATATGACAGAAAGTAAAGGAGTGTGAAAGTTGGCTGGATCAAGGGTGTATTAGTAC
GTTGTATGTTAAACATTTGGGGTGTGATGCTTTTCATTAGATTGTGATGATTGGGTCAAGCTGGAATAGGTCTATCA
GTCTTGTATAATGATGCCACTGTTGTGACAACTATCACAGGATTGTCTACTTCAGCAATAGCACTAATGGATTGT
AAGAGGAGGAGGAGCATATTATTAAATATCTAGAAGTCTAGGGCCAGAATTTGGTGGTGCAATTTGGTCTAATCTTCCGCT
TTGCCAACGCTGTTGCAGTTGCTATGTATGTTGGATTGTCAGAAACCGTGGTGGAGTTGCTTAAGGAACATTTCCATA
CTTATGATAGATGAAATCAATGATATCCGAATTTATGGAGCCATTACAGTCCGTGATTCTTTTAGGTATCTCAGTAGCTGG
AATGGAGTGGGAAGCAAGCTCAGATTGTTCTTTTGGTGTATCTACTCTTGGTATTTGGTGTATTTGGTGTATTTGGTGTAT
TTATCCCACTGGAGAGCAAGAAGCCAAAGGGTTTTGGTTATAAATCTGAAATATTAAATGAGAAGCTTTGGGCCCGAT
TTTCGAGAGGAAGAGACTTTCCTTTCTGATTTTGGCATCTTTTCTGCTGCAACTGGTATTCTGGCTGGAGCAAAATAT
CTCAGGTGATCTTGCAGATCTCAGTCAGCCATACCCAAAGGAACACTCCTAGCCATTTAAATTAATACATTTGGTTACG
TAGGAATTCAGATATCTGTAGGTTCTGTGTGTTGTCGAGATGCCACTGGAAACGTTAATGACACTATCGTAACAGAGCTA
ACAAACTGTACTTCTGCAGCCTGCAAAATTAACCTTTGATTCTTATCTGTAAGCAGTCCCTGTTCTTATGCGCTAAT
GAACAACCTTCCAGGTAATGAGTATGGTGTGAGGATTACACCACTAATTTCTGCAGGTATATTTTACGCCACTCTTCTT
CAGCATTAGCATCCCTAGTGTGCTCCCAAAATATTTCAGGCTCTATGTAAAGCAACATCTACCCAGCTTTCCAGATG
TTTGCTAAAGGTTATGGGAAAAATTAATGAACCTCTTGGTGGCTACATCTTAACATTCTTAATGCACTTGGATTTCATCTT
AATTGCTGAACGTAATGTTATGACCAATTTATCTCAAACTCTTCTCTGTCATCATATGCATTGATCAATTTTTCAGTAT
TCCATGCATCACTTGCAAAATCTCCAGGATGGCGTCTGCAATTAACATATGATAGTCTTGGGCTGTATAT
TTATGTTACCTACAAAAACAGATGTGAATTTGGGGATCTCTACACAAGCCCTGACTTACCTGAATGCACTGCAGCAAT
CAATTCGTCTTCTGGAGTGAAGACCGTGAAGAACTTTAGGCCACAGTGTCTTGTATGACAGGTGCTCCAAACTCA
CGTCCAGCTTTACTTCATCTTGTTCATGATTTTCAAAAAATGTTGGTTTGATGATCTGTGGCCATGTACATATGGGTCC
TCGAAGACCAAGCCATGAAGAGATGTCCATCGATCAAGCCAAATATCAGCGATGGCTTATTAAGAAACAAATGAAGCAT
TTTATGCTCCAGTACATGCAGATGACTTGAGAGAAGGTGCACAGTATTTGATGCAGGCTGCTGGTCTTGGTCTGTATGAG
CCAAACACACTTGTCTTGGATTTAAGAAAGATTGGTTGCAAGCAGATATGAGGGATGTGATATGTATATAAACTTATT
TCATGATGCTTTTGACATACAAATATGAGTAGTGGTTATTCGCCCTAAAGAGGCTTGGATATATCTCATCTTCAAGGAC
AAGAAGAATTATTGTCATCACAAGAGAAATCTCCTGGCACCAGGATGTGGTAGTAAGTGTGGAATATAGTAAAAAGTCC
GATTTAGATACTTCCAACCACTCAGTGAAAAACCAATTACACACAAAGTTGAGGAAGAGGATGGCAAGACTGCAACTCA
ACCACTGTTGAAAAAAGAAATCCAAAGGCCCTATTGTGCCTTTAAATGTAGCTGACCAAAAGCTTCTTGAAGCTAGTACAC
AGTTTCAGAAAAACAAGGAAGATACTATTGATGTCTGGTGGCTTTTGTATGATGGAGGTTTGACCTTATTGATACCT
TACCTTCTGACGCAAGAAAAATGGAAGACTGTAAGATCAGAGTATTCAATGGTGGAAAGATAAACAGAAATAGACCA
TGACCGGAGAGCGATGGCTACTTTCCTTAGCAAGTTCCGGATAGACTTTTCTGATATCATGGTTCTAGGAGATATCAATA
CCAAACCAAGAAAGAAATATTATAGCTTTTGAAGAAATCATTGAGCCATACAGACTTCATGAAGATGATAAGAGCAA
GATATTGCAGATAAAATGAAAGAGATGAACCATGGCGAATAACAGATAATGAGCTTGAACCTTATAAGACCAAGACATA
CCGGCAGATCAGGTTAAATGAGTTATTAAAGGAACATTCAAGCACAGCTAATATTATTGTATGATGCTCCAGTTGCAC
GAAAAGGTGCTGTGCTAGTGTCTCTACATGGCATGGTTAGAAGCTCTATCTAAGGACCTACCACCAATCTCTCTAGTT
CGTGGGAATCATCAGAGTGTCTTACCTCTATTCTA

MEPRPTAPSSGAPGLAGVGETPSAAALAAARVELPGTAVPSVPEDAAPASRDGGGVRDEGPAAAGDGLGRPLGPTPSOSR
FQVDLVSENAGRAAAAAAAAAAAGAGAGAKOTPADGEASGESEPAKGSEEAAGRFRVNFVDPAASSSAEDSLSDAA
GVGVDPNVSPONGGDTVLSESSSLHSCGGGGSGHHOHYYDDTHTNTYLRFTGHNTMDAVPRIDHYRHTAAQLGEKLLR
PSLAELHDELEKEPFEDGFANGEESTPTRDAVVITYAESKGVVKFGWIKGVLVRCMLNINWVMLFIRLSHIVGOAGIGLS
VLVIMMATVVTITGLSTSAIATNGFVRGGGAYYLSRSLGPEFGGAIGLIFAFANAVAVAMYVVGFAETVVVELLKEHSI
LMIDEINDIRIIGAITVVILLQISVAGMEWEAKAOIVLLVILLLAIGDFVIGTFIPLSKKPKGFFGYKSEIFNENFGPD
FREEETFFSVFAIFPPAATGILAGANISGDLADPQSAIPKGTLLAILITTLVYVGIASVSGSCVVRDATGNVNDTIVTEL
TNCTGAACKLNFDPFSSCESSPCSYGLMNNFQVMSMVSGFTPLISAGIFSATLSSALASLVSAPIFOALCKDNIYPAFQM
FAKGYGKNNELRGYILTFILALGFIILIAELNVIAPILISNFFLASVALINFSVFHASLAKSPGWRPAFKYYNMWISLIGA
ILCCIVMEVINWMAALLTYIVLGLYIYVYKKPDVNWGSSTQALTYLNALQHSIRLSGVEDHVKNFRPQCLVMTGAPNS
RPALLHLVHDFTKNVGLMICGHVHMGPRROAMKEMSIDQAKYQRWLIKNNKMAFYAPVHADDLREGAQYLMQAAGLGRMK
PNTLVLGFKKDWLQADMRDVMYINLFHDAFDIQYGVVIRLKEGLDISHLOQGEELLSSQEKSPGTDVVVSVEYSKKS
DLDTSKPLSEKPIHKVEEEDGKTATQPLLKESKGPVPLNVADQKLEASTQPKKQGGNTIDVWWLFDDGGTLTLLIP
YLLTTKKKWKDCKIRVFIGGKINRIDHRRAMATLLSKFRIDFSDIMVLGDINTKPKKENTIAFEEIIEPYRLHEDDKEQ
DIADKMKEDPWIRITDNELELYKTKTYRQIRLNELLKEHSSTANIIVMSLPVARKGAVSSALYMAWLEALSKDLPPILLV
RGNHQSVLTFYS

FIGURE 24

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FIGURE 25

Peptide names	Solubility	
CAA9p1	1mg/1ml H2O	H-CDPAASSSAEDSLSD-NH2
CAA9p2	1mg/1ml H2O	Ac-KKSDLDTSKPLSEKC-NH2
CAA9p3	1mg/1ml H2O	Ac-PLKKESKGPVPLC-NH2
CAA9p4	min.amt.DMSO/H2O	Ac-EHSILMIDEIC-NH2
CAA9p4MAPS	1mg/ml buffer pH7.5	Ac-EHSILMIDEIC-on 8-Branch Maps
CAA9p5	1mg/1ml H2O	Ac-DFREEETC-NH2
CAA9p5MAPS	1mg/1ml H2O	Ac-DFREEETC-on 8-Branch Maps

GUCACGAGGAGGAACCTTAAAGAAATTCAGATATGTGAAGTGTGATTTCCGAAACCTCGTCA
 TCCTCTGATGACAGTTGTGACAGCTTTGCTTCTGATAATTTTGGCAACACGAGGCTGCGCATCA
 GTTCGGGAAAGGCTGTAGGACGCCGACCGCATGCAAGGCATCTGGACGCTCTCAGGCTGGCGAT
 GAAGTTTCCAGCGCGGAGTACCAGGCGGACCAACAAAAAGACGATGCTCCGCCAGCCCT
 CAGAGAAATCTCTGACTGATTCCAACCTCCGATTACGAAGAATGAAAGTGGAAATGAAATTTTGTG
 AGAAAAGGGCTTTAAATATAAAGCAAAAGCAATGCTTGCAAACTCATGTCTGAATTA
 GAAAGCTTCCCTGGTCTGTTCCGTGGAAGACATCCCTCCGAGCTCCGACTCACAATCAAGG
 AGACCGCGAAGGCGTACATTCCCGGGTGTGTCTCCAGGAGAAACCCCTGGAACGGAGAGCTCG
 TCCTCTCTACAGGCTCAAGGTCGCCGATCTCTCGGTCCTTGACGCTCTACCCATGGAGAGGA
 GGAGGAAGAGGATAAGTACATAGTTGGTGGAAGAGGAAGACCGTGGATGGCTACATGAAT
 GAAGATGACCTGCCCAAGCAACCGCTGCTNCAGATCATCCGTGACCTTCGCCATATAATTCGC
 CCAGTGGAAAGAAATACAGAAGGAGGAGTGGAGAACGCTCGAGCAATTTCCGAAGAGA
 AGATTATAACGGTTACTCTGGGTTCTACTTGTCAATGCCGTGAGAAGACTATTGATACCAA
 AACAACTGAGGAACCCAGACTGTGGGCGTTCGAGGCAAGCTTGTGGCCCTGCCTTCG
 AAACCGTTATGGTGAAGAGGTCAGGATGCTCTGTGTCGAGTCCGAATGCAATTCGCCCGCTTG
 TCGAGGAATTCGAACCTGCAAGTTCTGCGCGCAGCGAGATGGACGGTGTGCGACTGGGGTCTT
 TGTGTATTGACCAAAATCATATGGCTTTGGGAATGTGCATGCCTATGTAAAGCTCGAACA
 GGAAATTTGAAATGCAAGCATATAATCTGGAATAATTTGCTGCTGCCTCTTCACTTCTAAATCTT
 TCTTGTAAGAAAGTTTCCAAATTTTTCCTGAAACCTGAGTTAAAAATCTTGATGATACCGCTGT
 TTCATAAGAAACTCCAATCAAGTTAATCTTGACAGACATGTGTTTCTGGAGCATCAGAGAAG
 TATATTGTCTAGTACACTTGTGCCCTGCGAGTTTCTCTCTGCCACCCCATCTCATAGC
 ATTCCCGCTCTAATTTTCCAATGCTCCCTCTCCCAACCCCGTATGTTTCTGAATTTTCTTTTA
 AAWTTACAGTTTAAAGGAAAAGCCATATTTTAACTGGGTGTGGAAATAGCCCGCTCAT
 AAAACCTTAAGCATCTGGAACACCAATAATAGTATAACCTAAGTAGATTCTTATGAATTTCA
 GAGAAGAGCCTTCTAAGTTGTTACACAAACCAAGAGTAGTATTAGCTATCTAAGTATTGAA
 ATTITTTATAAGATAAGCAAGGCAAAAGCTTAAACCATGTGGAAAATATAGGTAATTTAKG
 ARATTGAAGKGTTCYCYCAATCCCAAGWTAKGSGTITAGKTACMARKKGKGTGTCMCAAGTTTAG
 ACYTAATTTTCYCCTAATTTCTTCYGSCCGAAGGKWAAGKGKGGCTCCRGCTACMCGATCAT
 AATTGMAAGGKTTGGKGGCAATGTAAYMCTTAATTAATAATKRWGGAAGAGCYATTCTGG
 AGATTAWGAGTAGAGCTGATTGAAATTTGATTTTCAATTAATAAAGCTTGTAGTAAATTTGATG
 GKTTATTTGAGTTTCAATGTAAGGKATTTGCAATAAATTTCTTGACCAATTTTGKATGGAAAC
 TGTATTTAAAAAAGCTAGTCTGTGGKTCCTTGTGAGTTTCTGTGATTTATAAACCAAGGCAAG
 GTTCAAGTTTGTAGTTTAAAGCATTTTATAACAATGATAAGTGCCCTTTTGGAGATGTAACCTT
 TAGCAGTTTGTAAACCTGACATCTCGGCAAGTGTAGTTTGTGGAGGCTTCTGTGTGAGTAT
 TCCCGCTCTCTTTGATATAATCAAGGTAATTTGTTAGTGGTGGAAATCAAGTTTGTGATGTC
 CAATTTACTTGCATATGTAAACCATTTGCTGTGCCATTCATGTTTGTAGTCAATTTGGAC
 CTGTAATTCGATAAGTGTAAATACAGCTTTTGTCTGTAATGCTTTTATACAAAAGTTTATT
 TTAATAATAAAGTTTGTCTTAAAAAATAAATAAATAAATAAATGCGGCGCAAGCTTATT
 CCCWTTAGTGAGKSWTAATTTAGCTTGGCACTGCGCGTCTTTACAAGCTCGTGACCTGGGA
 AAACCCGTCGGCTTACCCCAATTAATGCGCTTGACAGCATATCCCTTTTGCAGCTGCGGTA
 TAGCGAAGAGGCCCGCAGCATGCGCTTCCCAACAGTTCGCAGAGCTGAATGGCGAATGGG
 ACGCGCCTGTGAGGCGCATTAAGACGCGCGGGTGTGGTGGTTACCGCAACGCTGACCCGTA
 CACTTTCGACGCGCCTAGCGCCGCTCTTTCGCTTCTTCTTCTCTCTCGCMGCTTTCGCGG
 CTTTTCGCCCAAGCTNTAAATCGGGG

One position equals 20 bases
■ if more than 2 bases disagree with consensus sequences
■ if more than 10 positions are unknown
■ if more than 10 positions are gap characters

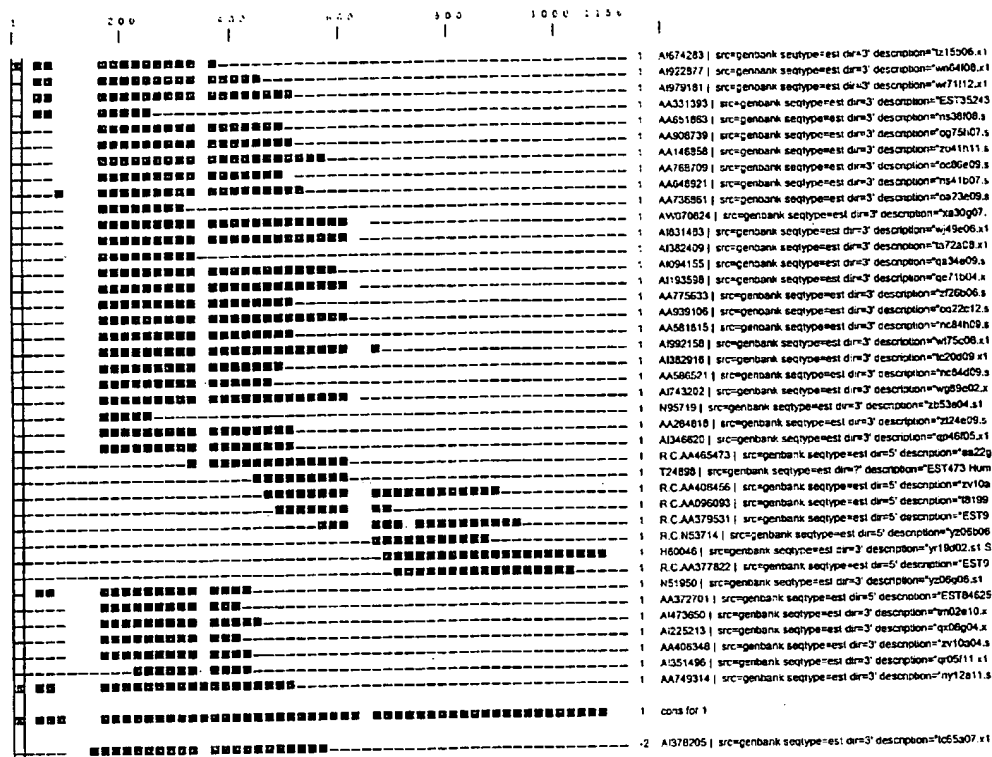


FIGURE 28A

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	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
1	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
2	2	4	6	8	10	12	14	16	18	20	22	24	26	28	30	32	34	36	38	40	42	44	46	48	50	52	54	56	58	60	62	64	66	68	70	72	74	76	78	80	82	84	86	88	90	92	94	96	98	100	102	104	106	108	110	112	114	116	118	120	122	124	126	128	130	132	134	136	138	140	142	144	146	148	150	152	154	156	158	160	162	164	166	168	170	172	174	176	178	180	182	184	186	188	190	192	194	196	198	200
3	3	6	9	12	15	18	21	24	27	30	33	36	39	42	45	48	51	54	57	60	63	66	69	72	75	78	81	84	87	90	93	96	99	102	105	108	111	114	117	120	123	126	129	132	135	138	141	144	147	150	153	156	159	162	165	168	171	174	177	180	183	186	189	192	195	198	201	204	207	210	213	216	219	222	225	228	231	234	237	240	243	246	249	252	255	258	261	264	267	270	273	276	279	282	285	288	291	294	297	300
4	4	8	12	16	20	24	28	32	36	40	44	48	52	56	60	64	68	72	76	80	84	88	92	96	100	104	108	112	116	120	124	128	132	136	140	144	148	152	156	160	164	168	172	176	180	184	188	192	196	200	204	208	212	216	220	224	228	232	236	240	244	248	252	256	260	264	268	272	276	280	284	288	292	296	300	304	308	312	316	320	324	328	332	336	340	344	348	352	356	360	364	368	372	376	380	384	388	392	396	400
5	5	10	15	20	25	30	35	40	45	50	55	60	65	70	75	80	85	90	95	100	105	110	115	120	125	130	135	140	145	150	155	160	165	170	175	180	185	190	195	200	205	210	215	220	225	230																																																						

7 7 7 7 7 7 7

1	2	3	4	5	6	7
1	2	3	4	5	6	7

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METSSSSDDG QDSFASDNFA NTRLQSVREG CRTSQCEHS GFLRVAMKFF
ARSTRGATNK KAESRQPSFN SVTDNSDSE DESGMNFEK RALNINQNK
MLAKLMSELE SFPQSFRGRH PLPGSDSQSR RFRRTFPGV ASRRNPERRA
RPLTRSRRI LGSIDLALPME EEEEEKYML VRKRTVDGY MNEDDLPRTR
RYRSSVTLPH IIRPVVEIQK ERSWRTSAI LEEKIITVHW ALLVINAVRR
LLIPKQTAET QTAGAFEASS VAPAFETVMV KRSGMLCWIR TGIARLVEES
ATAVSAGSEM GGVRLGSLCI

FIGURE 29

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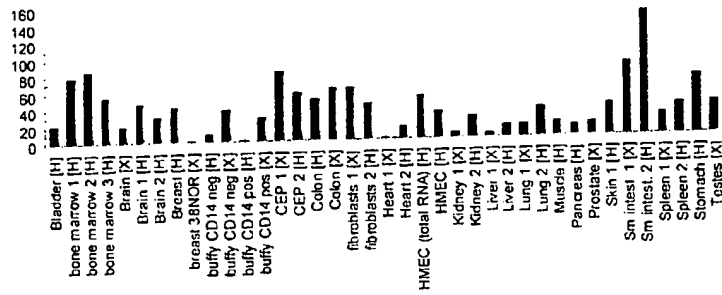


FIGURE 30A

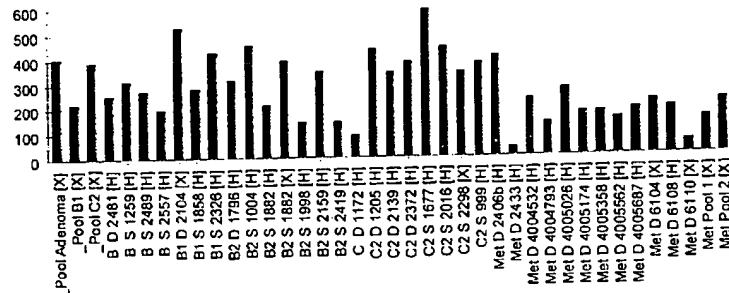


FIGURE 30B

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ACTCACTATNGGGCGAATGGGCCCTCTNNATGCATGCTCGAGCGCCCGCCAGTGTGATGGATA
TCTGCAGAATTCCGCCCTTAAGCAGTGGTAACAACGCAGAGTACGCGGGGGGAGACCGGAGGG
CAGAAGGCAGAGTCCAGGCTTAGACTGCAGTTCCTCGCTTACCTGTGCAGTCTAATTTTGAGC
TGCCCTCTTTGTAGTCTTAAAAGGCAGGAGCTTCGTGTTGTGGGTCTGCTAACCCGTACGTTTC
GTGGGCAAGTCGTGTGTACTCCTCGCCCTGCTCAGCTCCAAACACGCTTCTACACTGATAAC
AAGAAATATGCCGTAGATGATGTTCCCTTCTCAATCCCTGCTGCCCTCTGAAATTGCCGACCTTA
GTAACATCATCAATAAACTACTAAAGGACAAAAATGAGTTCCACAAACATGTGGAGTTTGATT
TCCTTATTAAGGGCCAGTTTCTGCGAATGCCCTTGGACAAACACATGGAAATGGAGAACATCT
CATCAGAAGAAGTTGTGGAAATAGAATACGTGGAGAAATATACTGCACCCAGCCAGAGCAA
TGCATGTTCCATGATGACTGGATCAGTTCAATTAAAGGGGCAGAGGAATGGATCTTGACTGGT
TCTTATGATAAGACTTCTCGGATCTGGTCTTGAAGGAAAGTCAATAATGACAATTGTGGGA
CATACGGATGTTGTAAGGATGTGGCCTGGGTGAAAAAGATAGTTTGTCTGCTTATTATTG
AGTGCTTCTATGGATCAGACTATTCTTATGGGAGTGGAAATGTAGAGAGAAACAAAGTGAA
AGCCCTACACTGCTGTAGAGGTGATGCTGGAAGTGTAGATTCTATAGCTGTTGATGGCTCAGG
AACTAAATTTTGCAGTGGCTCCTGGGATAAGATGCTAAAGATCTGGTCTACAGTCCCTACAGA
TGAAGAAGATGAAATGGAGGAGTCCACAAATCGACCAAGAAAGAAACAGAAGACAGAACAG
TTGGGACTAACAAAGGACTCCCATAGTGACGCTCTCTGGGCACATGGAGGCAGTTTCTCAGTT
CTGTGGTCAGATGCTGAAGAAATCTGCAGTGCATCTTGGGACCATACAATTAGAGTGTGGGT
GTTGAGTCTGGCAGTCTTAAAGTCAACTTTGACAGGAAATAAAGTGTTAATTGTATTTCTATT
CTCCACTTTGTAAACGTTTAGCATCTGGAAGCAGATAGGCATATCAGACTGTGGGATCCCC
GAACTAAAGATGGTTCCTTTGGTGTGCTGTCCTTAACGTCACATACTGGTTGGGTGACATCAG
TAAAAATGGTCTCCTACCCATGAACAGCAGCTGATTTCAGGATCTTTAGATAACATTGTTAAGC
TGTGGGATACAAAGAGTTGTAAGGCTCCTCTCTATGATCTGGCTGCTCATGAAGACAAAGTTC
TGAGTGTAGACTGGACAGACACAGGGCTACTTCTGAGTGGAGGAGCAGACAATAAATTGTAT
TCCTACAGATATTACCTACCACTTCCCATGTTGGGGCACTAAGTGAACAATAATTGACTA
TAGAGATTATTTCTGTAATGAAATTTGGTAGAGAACCATGAAATTACATAGATGCAGATGCA
GAAAGCAGCCTTTTGAAGTTTATATAATGTTTTCACCTTTCATAACAGCTAACGTATCACTTT
TTCTTATTTTGTATTTATAATAAGATAGGTTGTGTTTATAAAATACAACTGTGGCATACA
TTCTCTATACAACTTGAAATTAACCTGAGTTTACATTTCTTTAAARGTAAAAA
AAAAA

FIGURE 31

One position equals 17 bases.
■ if more than 1 bases disagree with consensus sequences.
* if more than 6 positions are unknown.
- if more than 6 positions are gap characters.

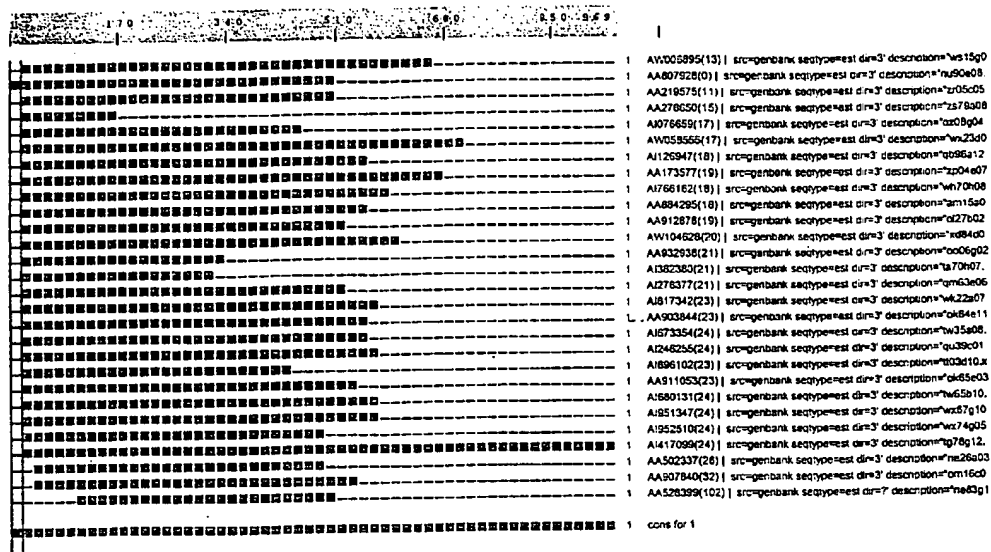


FIGURE 32A

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AW060953(13) | srgenbank|scplseq|est|dm3|description="w51g01.xl NCI_CGAP_Kel1 Homo sapiens cDNA clone IMAGE:2487296 3' siml" srgenbank|37735306
AA807828(20) | srgenbank|scplseq|est|dm3|description="w06083.xl NCI_CGAP_P72 Homo sapiens cDNA clone IMAGE:217990 3' mRNA" srgenbank|675988
A011875(11) | srgenbank|scplseq|est|dm3|description="w05003.xl Stragmate N2 neural precursor B2730 Homo sapiens cDNA of srgenbank|1172843
A027650(15) | srgenbank|scplseq|est|dm3|description="w57800.xl NCI_CGAP_GG6 Homo sapiens cDNA clone IMAGE:703070 3' mRNA" srgenbank|214143
A073650(17) | srgenbank|scplseq|est|dm3|description="w0230g01.xl Soares_t12119g_k18en_INFLS_1 Homo sapiens cDNA clone IMAGE:3823490
AW06555(17) | srgenbank|scplseq|est|dm3|description="w23607.xl NCI_CGAP_KC4 Homo sapiens cDNA clone IMAGE:2544493 3' mRNA" srgenbank|951329
A112594(18) | srgenbank|scplseq|est|dm3|description="w09612.xl Soares_t12119g_k18en_INFLS_1 Homo sapiens cDNA clone IMAGE:1707" srgenbank|2503275
AA17357(12) | srgenbank|scplseq|est|dm3|description="w204967.xl" | Soares_t12119g_k18en_INFLS_1 Homo sapiens cDNA clone IMAGE:2381843 3' siml" srgenbank|327826
A176861(20) | srgenbank|scplseq|est|dm3|description="w17005.xl NCI_CGAP_Kel1 Homo sapiens cDNA clone IMAGE:2368143 3' siml" srgenbank|327826
AA084295(18) | srgenbank|scplseq|est|dm3|description="w156061.xl Soares_NFL_2_GBC_51 Homo sapiens cDNA clone IMAGE:1254651 3' srgenbank|125252
AS11287(19) | srgenbank|scplseq|est|dm3|description="w07102.xl NCI_CGAP_Kel1 Homo sapiens cDNA clone IMAGE:2643003 3' srgenbank|676072
AA04628(20) | srgenbank|scplseq|est|dm3|description="w06083.xl NCI_CGAP_P72 Homo sapiens cDNA clone IMAGE:165426 3' srgenbank|278801
AS23533(21) | srgenbank|scplseq|est|dm3|description="w12067.xl Soares_t12119g_k18en_INFLS_1 Homo sapiens cDNA clone IMAGE:202307" srgenbank|256831
AS23380(21) | srgenbank|scplseq|est|dm3|description="w12067.xl Soares_t12119g_k18en_INFLS_1 Homo sapiens cDNA clone IMAGE:165426 3' srgenbank|278801
A027387(21) | srgenbank|scplseq|est|dm3|description="w052003.xl Soares_plasma_2NHLFBL5C90 Homo sapiens cDNA clone" srgenbank|253348
AB17344(23) | srgenbank|scplseq|est|dm3|description="w142207.xl NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2143044 3' siml" srgenbank|3517498
AS13344(23) | srgenbank|scplseq|est|dm3|description="w046111.xl NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1518784 3' siml" srgenbank|127601
AB73354(24) | srgenbank|scplseq|est|dm3|description="w035080.xl NCI_CGAP_Kel1 Homo sapiens cDNA clone IMAGE:2201054 3' siml" srgenbank|317661
A246255(24) | srgenbank|scplseq|est|dm3|description="w039301.xl NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:1587136 3' siml" srgenbank|256231
AB56110(25) | srgenbank|scplseq|est|dm3|description="w030101.xl NCI_CGAP_G06 Homo sapiens cDNA clone IMAGE:223869 3' mRNA" srgenbank|1305255
AA00134(25) | srgenbank|scplseq|est|dm3|description="w056101.xl NCI_CGAP_G06 Homo sapiens cDNA clone IMAGE:151884 3' siml" srgenbank|17457
AA00134(25) | srgenbank|scplseq|est|dm3|description="w056101.xl NCI_CGAP_G06 Homo sapiens cDNA clone IMAGE:224539 3' siml" srgenbank|14484
AA551347(24) | srgenbank|scplseq|est|dm3|description="w071010.xl NCI_CGAP_U03 Homo sapiens cDNA clone IMAGE:2548770 3' siml" srgenbank|3720164
AA551347(24) | srgenbank|scplseq|est|dm3|description="w071010.xl NCI_CGAP_U03 Homo sapiens cDNA clone IMAGE:2548770 3' siml" srgenbank|3720164
A017009(24) | srgenbank|scplseq|est|dm3|description="w071010.xl NCI_CGAP_U03 Homo sapiens cDNA clone IMAGE:2114950 3' siml" srgenbank|737375
AA02337(28) | srgenbank|scplseq|est|dm3|description="w026031.xl NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:289444 3' mRNA" srgenbank|1548330
AB07940(32) | srgenbank|scplseq|est|dm3|description="w018008.xl Soares_NFL_2_GBC_51 Homo sapiens cDNA clone IMAGE:1541188 3' siml" srgenbank|214257
AA23099(102) | srgenbank|scplseq|est|dm3|description="w061012.xl NCI_CGAP_Kel1 Homo sapiens cDNA clone IMAGE:9101918 mRNA sequ" srgenbank|1574499

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FIGURE 32B

MAQLQTRFYTDNKKYAVDDVPFSIPAASELADLSNIINKLLKDKNEFHKHVEFDF
 LIKGQFLRMPLDKHMEMENISSEEVVEIEYVEKYTAPQPEQCMFHDDWISSIKGA
 EEWILTGSYDKTSRIWSLEGKSIMTIVGHTDVVKDVAWVKKDSLSCLLLSASMD
 QTILLWEWNVERNKV KALHCCRGHAGSVDSIAVDGSGTKFCSGSWDKMLKIWS
 TVPTDEEDEMEESTNRPRKKQKTEQLGLTRTPIVTL SGHMEAVSSVLWSDAEEIC
 SASWDHTIRVWVVEGSLKSTLTGNKVFNCISYSPLCKRLASGSTDRIHRLWDPR
 TKDGSLSVLSLTSHTGWVTSVKWSPTHEQQLISGSLDNIVKLWDTRSCAPLYDL
 AAHEDKVLSDWDTDTGLLLSGGADNKLYSYRYSPTTSHVGA.

FIGURE 33

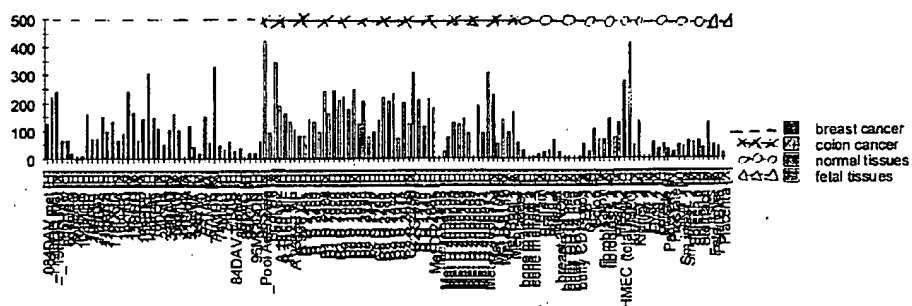


FIGURE 34

FIGURE 35

FIGURE 36

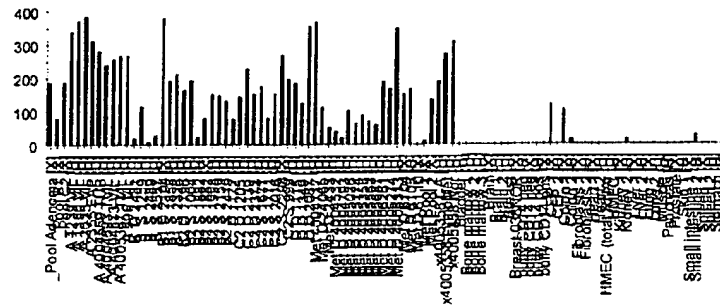


Figure 37

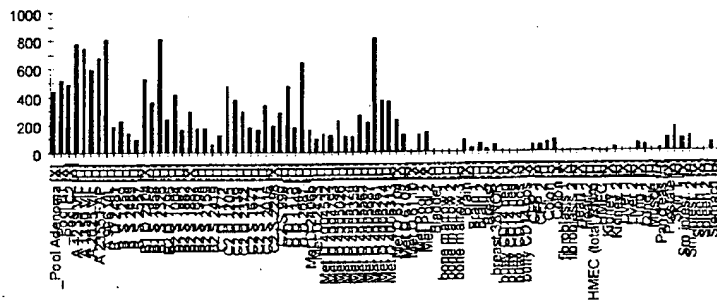


Figure 38

AGAATCGCTTCGGCTCCITTCGCCGCCGGTATCTCTGTATATGATCCCACTCTCACTCTCATAGGAGAC
GATCTCGAAGTAGATCATATACACCAAGATACCGGCCGCGAAGGAGCCGAAGCTCAAGGGTAAAGACAGTA
GAAATATTATTCAGTAACAATAATGTGTGAACCTTTAAGATGGATAATAGGGCATGGACTGAGTGCTGCT
ATCTTGAAATGTGCACAGGTACACTTACCTTTTTTTTTTTTTTTTTTTTAAAGCTTTCCCATTCAGGATAACA
ACATIGTGATCTGTACTACAGGAACCAATGTCAATCCGTATACATGTGGCTATAAAGTACAT/AAAAATA
TCTAATCTATTCAT/ATGTGGGGTGGGTAATACTGTCTGTGAATAATGTAAAGAGCTTTCACTTAAAAAA
AATGCAATTAATTTCACTTAACACTAGACACCGGTGGA/AAATTTCAAGGTTATAGTACTTATTCAACAA
TTCTTAGAGATGCTAGCTAGTGTTGAAGCTAAAAATAGCTTTATTTATGCTGAATTGTGATTTTTTATGC
CAAAATTTTTTAGTTCTAATCATTTGATGATASCTTGG/ATAAATAATTATGCCATGGCATTGACAGTT
CATTTATTCCTATAA/AAATAAATTGAGTTTAAAGAGAAATGGTCGTGTGAGCTGATTATTAACAGTTACTG
AATTCAAATATTTATTTGTTACATTATTCATTTGTATTTTAAAGCTTTCCCTTTACATTTCTTTATATGCA
TTCTGACATTACATTTTTTTAAGACTATGGA/AAATAATTTAAAGATTTAAGCTCTGGTGGATGATTATCTG
CTAAGTAAGTCTGAAAAATGTAATTTTGA/AAATACCTGTAATATACCTGTACACAAATGCTTTTCTAATG
TTTTAACCTTGAGTATTCCAGTTGCTGCTTTGTAAGAGGTTACTGCAATAAAGGAAGTGGATTCAATTAA
CCTAAAAA

FIGURE 39

CCAAGTTCTACCTCATGTTTGGAGGATCTTGCTAGCTATGGCCCTCGTACTCGSCTCCCTGTTGCTGCTGG
GGCTGTGCGGGMACTCCITTTTCAAGAGGGGAGCCCTTCATCCACAGATGCTCCTAAGGCTTGGAAATTATGAA
TTGCCCTGCAACAAATATGAGACCCAGACTCCCATAAAGCTGGACCCATTGGCATTCTCTTTGAAGTAGT
GCATATCTCTTCTCTATGTGGTACAGCCGCGTGATTTCCAGAAAGTACTTTGAGAAAATTCTTACAGAAAG
CATATGAAATCCAAAATTSATTATGACAAAGCAGAACTGTAACTCTTAGGTCTAAAGATTGTCTACTATGAA
GCAGGGATTATTCTATCTGTGCTCGTGGGCTGCTGTTTATTCTGATGCCCTCTGGTGGGGTATTTCCTT
TTGTATGTGCTGCTGTGTAACAAATGTGGTGGAGAAATGCACAGCAGAGAGGAAAATGGGCCCTTCC
TGAGGAAATGCTTTGCAATCTCCCTGTTGGTGATTGTATATAATAAGCATTGGCATCTTCTATGTTTTT
GTGGCAATCACCAGGTAAAGAACCCGGATCAAAAGGAGTCGGAAACTGGCAGATAGCAATTTCAAGGACTT
GGCAATCTCTTGAATGAACTCCAGAGCAATCAATATATATTTGGCCCACTACACACTACCAAGGACT
AGCGCTTCACAGATCTGAACAGTATCAATTCAGTGCTAGGAGGCGGAATTTCTGACCCAGTACAGACCAAC
ATCATCCCTGTTCTTGTATGAGATTAAAGTCCATGGCAACAGCGATCAAGGAGACCAAGAGGCGTTGGAGAA
CATGAACAGCACCTTGAAGAGCTTGACCAACAAAGTACACAGCTTAGCAGCAGTCTGACCAGCGTGAANA
CTAGCCCTCGGTCATCTCTCAATGACCCCTCTGTGCTTGGTGATCCATCAAGTGAACCTGCAACAGCATC
AGATTGTCTTAAGCCAGCTGAATAGCAACCCCTGAATCTGAGGCGAGCTTCCACCCCTGGATGCAGAACTTGA
CAACGTTAATTAAGTTCTTAGGACAGATTGGATGGCCTGGTCCACAGGGCTATCAATCCCTTAATGATA
TACCTGACAGAGTACAAACCCAAACACAGACTGTGCTAGCAGGTATCAAAAGGGCTTGAATTCCTTGGT
TGAGATATCGACAATGTAACCTCAGCGCTTCTCTATTGAGATATCTCTCAGCATCTCTCTGTTTATGTTAA
TAACTCTGAAAGTTTACATCCACAGAAATTTACCTACATTTGGAAGAGTATGATTCTACTGTTGGCTGGGTG
GGCTGGTCATCTGCTCTCTGCTGACCCCTCATCGTGATTTTACTACCTGGGCTTACTGTGTGGCGTGGC
GGCTATGACAGGCATGCCACCCCGACCCCGAGGCTGTGTCTCCAAACACCGGAGGCGTCTCTCTCATGTT
TGGAGTTGGATTAAAGTTTCTCTTTTGGTGATATTGATGATCAATTGTGGTCTTACCTTTGCTTTGGTG
CAATGTGGAAAACCTGATCTGTGAACCTTACACAGCAAGGAATTTATCCCGGTTTGGATACACCCCTAC
TTACTTAATGAAAGCTGGGAATACTATCTCTCTGGGAAGCTATTTAATAAATCAAAATGAAGCTCACTTT
TGAAACAGTTTACAGTGACTGCAAAAAAATAGAGGCACTTACGGCACTCTTCACTGCAGAACAGCTTCA
ATATCACTGATCTCAACATTAAAGCATACCTGGAAGCATAAGCAGTGAATGGAAAGCTGAAGGTA
AACTTAATATCTTCTGTTGGGTGACAGCAGGAAGAAACCTTCAAGATTCTGCTGCTTGTGGAAATAGA
CAAGATGAATTAATGACAGCTACTTGGCTCAGACTGGTAAATCCCCCGAGGAGTGAATCTTTTATCATTTG
CATATGATCTAGAGCAAAAGCAACAGTTTGGCCCGAGGAAATTTGAGGAATCCCTGAAAAGAGATGCA
CAAACTATTAAACAAATTCACAGCAACGAGTCTCTCTATAGAACAATCACTGAGCACTCTATACCAAG
CGTCAAGATACTTCAACGCACAGGGAATGGATTGTTGGAGAGGTAATAGGATTCTAGCTTCTCTGGATT
TTGCTCAGAACTTCAACCAAACTACTTCTCTGTTATTATTAGGAAACTAAGAGATATGGGAGAAC
ATAATAGGATATTTTGAACATTATCTGCACTGGATCGAGTTCTCTATCAGTGAGAAAGTGGCATCGTGCA
ACCTGTGGCCACCGCTCTAGATACTGCTGTTGATGCTTTCTGTGTAGCTACATTATGACCCCTTGAATT
TGTTTTGGTTTGGCATAGGAAAGCTACTGATTTTACTTCCGGCTCTAATTTTGGCGTAAACTGGCT
AAGTACTATCGTCGAATGGATTGCGAGGACGTTGACGATGATGTTGAACTATACCCATGAAAATATGGGA
AAATGGTAAATAGGTTATCAATAAGATCATGTATATGGTATTCACAATCCCTGTTATGACAGCCCATC
AACATGATAGCTGATGTTGAAACTGCTTGAACATCAGGATACCTCAAGTGGAAAGGATCACAGATTTTGG
GTAGTTTCTGGGTCTACAAGGACTTCCAAATCCAGGAGCAACGCGAGTGGCAACGTAGTGACTCAGGCGG
GCACCAAGGCAACGGCACCATTGGTCTCTGGGTAGTGCTTAAAGATGAACCAATCACGTTATAGTCCAT
GGTCCATCACTATTCAAGGATGACTCCCTCCCTTCTGCTATTTTGTGTTTACTTTTACACTGAGT
TTCTATTAGACACTACACATATGGGGTGTGTTGCCATGGATGCAATTTCTATCAAACTCTATCAAA
TGTGATGGCTGATTTCAACATATTGCCATGTGTGGAGTGTGCTGAACACACACAGGTTTACAGGAAGAT
GCATTTTGTGTACAGTAACGGTGTATATACCTTTTGTACCACAGAGTTTTTAAACAAATGAGTATTAT
AGGACTTTCTTAAATGAGCTAAATAAGTCAACATTGACTTCTTGGTGCTGTTGAAAATTAATCCATTTT
ACTAAAGTGTGAAACCTACAGCATATTTCTTACGCAGAGATTTTCTATCTATTATCTTTATCAAGAT
TGGCCATCTTCACTTGGAAATGGCATGCAAAAGCCATCATAGAGAACTGCGTAACCTCATCTGACAAA
TTCAAAAGAGAGAGAGATCTTGAAGAGAAATGCTGTTTCAAAAGTGGAGTTGTTTTAACAGATGC
CAATTACGGTGTACAGTTTACAGAGTTTCTGTTGCTTAGGATTAACATTAATTGGAGTGCAGCTAACA
TGAGTATCATCAGACTAGTATCAAGTGTCTAAATGAAATATGAGAAGATCCTGTCACAATCTTAGATC
TGGTGTCCAGCATGGATGAAACCTTTGAGTTTGGTCCCTAAATTTGCATGAAAGCACAGGTAATATTCA
TTTGTCTCAGGAGTTTCAATGTTGGATCTGTCATTATCAAAAGTATCAGCAATGAAGAACTGGTGGACAA
AATTTAAGCTGTATGTAATGAAATCCAGATGTAGGCATTTCCCCAGGCTCTTTTATGTGAGATTCAG
TTCTGATTCATTGAAATAAAAGGAATCTCG

FIGURE 40

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CAGCGGCGCTGAATTCATGGGCGGGTTCGGCGCCCGAAGGCTGAGAGCTGGCGCTGCTCGTGGCCCTGTG
TGGCAGACGGCGGAGCTCCGCGGCGGACCCCGCGGCGCGCTTGTGCTCCGACATGGAGTTTGGGGGAAG
AAACTCTCTCTCGCCCCAGAGATTTCTTCCTCGGCGAAGGACAGCGAAAGATGAGGGTGGCAGGAAGA
GAAGGCGCTTTCTGTCTGCCGGGTCGACGCGGAGAGGGCAGTGCCATGTTCTCTCCATCCTAGTGGC
GCTGTGCTGTGGCTGCACCTGGCGCTGGCGGTGCGCGGCGCGCCCTGGGAGGCGGTGGCATCCCTATG
TGGCGGCACATGCCCTGGAACATCAGCGGATGCCCAACCACTGCACACAGCAGCGAGGGAACGCCA
TCTGTGGCCATCGAGCAGTACGAGGAGCTGGTGGACGTGAACCTGCAGCGCGTGTCTGGCTTCTTCTGTG
TGCCATGTACGCGCCATTGGCAGCTGGAGTTCTGACGACCCCTATCAGCCGTGCAAGTGGTGGTGG
CAACGCGCGCGGACGACTGCGAGCCCTCATGAAGATGTACAACCACTGAGCTGGCCCGAAAGCCTGGCCT
GCGACGAGCTGCTGTCTATGACCGTGGCGTGTGCATTTGGCTGAAGCCATGCTCAGGACCTCCCGGA
GGATGTTAAGTGGATGACATCAGCCAGACATGATGGTACAGGAAGGCTCTTGATGTTGACTGTAA
CGCCTAAGCGCGGATCGGTGCAAGTGTAAAAAGGTGAAGCCACTTTGCCAAGTATCTCAGCAAAACT
ACAGCTATGTTATTATGCCAATATAAAGCTGTGACAGGAGTGGTGCATGAGGTGACACGCTGGT
GGATGTAAAGAGATCTTCAAGTCTCATCAGCCCTCCCTCGAAGTCAAGTCCGCTCATACAAATCT
TCTTGGCAGTGTCCACACATCTGCCCATCAAGATGTTCTCATCATGTTTACGAGTGGCGTTCAGGA
TGATGCTTCTGMAATGTCTTAGTTGAAAAATGGAGAGATCAGCTTAGTAAAGATCCATACAGTGGGA
AGAGAGGCTGCAGGAACAGCGGAGAACAGTTTCCAGGACAGGAAGAACAGCGCGGCGCAGCAGTGGTGT
AATCCCCCAAAACCAAGGGAAAGCCTCTGCTCCCAACAGCAGCTCCCAAGAGAACATTAATACTA
GGAGTGGCCAGAGAGAACAAACCCGAAAGAGTGTGAGCTAACTAGTTTCCAAAGCGGAGACTTCCGAC
TTCCTTACAGGATGAGGCTGGGCTTGGCTTGGTACAGAGGTGAGTTAAAGCTGAGTTAAAGCTGGTGA
ACTCACTGCAGTGTCTTCATAGACACATCTTGACGATTTTTCTTAAGGCTATGCTTCACTTTTTCTTT
CTAAGCCATCACAAGCCATAGTGGTAGTTTGGCTTGGTACAGAGGTGAGTTAAAGCTGGTGA
GGCTTATTCATTTGATTGAGATACCTGTGTGATCTCTAGAGAGTGGGAAATATGCTTGTGA
CAATTCGACCTAATATGTGATTTGAAATTAATGCCATATTTCAAAACAAACAGTAAATTTTTTACAG
TATGTTTTATTACCTTTTGATATCTGTTGTTGCAATGTTAGTGTGTTTTAAATGTGATGAATATAA
TGTTTTTAAGAGGAACAGTAGTGGATGATGTTAAAGATCTTATGTTTATGGTCTGCAGAGGA
TTTTTTGTGATGAAGGGGTTTTTTTGAATAATTAGAGAGTAGCATATGAAATTAATATGTTTTTT
TACCAATGACTTCAGTTTCTGTTTTTAGCTAGAACTTAAAAACAAATATATTAAGAAAAATTAAT
AAAGAGGAGGAGACATGCTGATTCCTGTTTTTGGTTACCTGATTTCCATGATCATGATGCTTC
TTGTCACACCCCTTTAAGCAGCACCAGAACAGTGAATTTGCTGTACCATAGGAGTGGTACTAAT
TAGTTGGCTAATGCTCAAGTATTTATACCCACAGAGAGGTATGTCTCATCTTACTTCCAGGACAT
CCACCTGAGATAATTTGACAGCTTAATAAGGCTTCAATGTGAGTGGCAATTTGTTTTTCTTCAT
TTAAATATTTCTTTGCTAAATACATGTGAGGAGTTAAATATAATGTACAGAGGAAAGTTGAGT
TCCACCTCTGAATGAGAATTACTTGACAGTTGGGATACTTTAATCAGAAAAAAGAACTTATTTGCGC
ATTTTATCAAAATTTTATATTTGTGGACAAATGGAGGCAATTTTAAAAAACAAATTTTATTGGCCT
TTTGCTAACACAGTAAGCATGTTTTATAAGGCATTCATAAATGCACACGCCCAAGGAATAAAT
CCTATCTAATCTACTCTCACTACACAGAGGTATCACTATTAGTATTTGGCATATPATTCTCCAGGT
GTTTGCATTATGCATTATAAATGATTTGAACAAATAAACTAGGAACCTGTATACATGTGTTTCATAAC
CTGCTCTCTTTGCTTGGCCTTTATTGAGATAAGTTTCTGTGCAAGAGCAGAAACCTCTCATTTCT
AACAGCTGTGTTATATTCATAGTATGCAATTAACCAACTGTTGTGCTATTGGATACTTAGTGGT
TCTTCACTGACAATACTGAATAAACAATCTCACCGAATTC

FIGURE 41

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GA'TTAAATCCTATGACAACTAAGTGGTTCCTCTCACCTGTTTGGTGAGGTTGTGTAAGAGTTGGT
GTTTGGCTCAGGAAGAGATTAAGCATGCTTGCTTACCCAGACTCAGAGAAGTCTCCCTGTTCTGTCTAG
CTATGTTCTGTGTTGTGTGCTTCGTCTTTCCAGAGCAACCGCCAGAGTAGAAGTGGATTGGGGC
ACGCTGCAGACGATCCTGGGGGGTGTGAACAAACATCCACCAGCATTGGAAAGATCTGGCTCACCGTCC
TCTTCATTTTTCGCTATATGATCCTCGTGTGTGGCTGCAAGGAGGTGTGGGAGATGAGCAGGCGGACTT
TGTCTGCAACACCCCTGCAGCCAGGCTGCCAAGACGTGTGCTACGATCACTACTTCCCATCTCCACATC
CGGCTATGGGCGCTGCAGCTGATCTTGTGTCCAGCCAGCGCTCCTAGTGCCCATGCACTGGGCTTACC
GGAGACATGAGAAGAAGAGGAAGTTCATCAAGGGGGAGATAAAGAGTGAATTAAGGACATCGAGGAGAT
CAAAACCCAGAACGTCGCTCGAAGGCTCCCTGTGGTGGACCTACACAAGCAGCATCTTCTCCGGGTG
ATCTTCGAAGCCGCTTCATGTACGCTCTCTATGTCTACGACGGCTTCTCCATGCAGCGGCTGGTGA
AGTGCACGCTGGGCTTGTCCCAACACTGTGGACTGCTTGTGTCCGGGCCACGGAGAAGACTGTCTT
CACAGTGTTCATGATTGCAGTGTCTGGAATTTGCATCCGTGCTGAATGTCACTGAATTTGTATTATTGCTA
ATTAGATATTGTTCTGGGAAGTCMAAAAGCCAGTTTAAAGCATTGCCAGTTGTAGATTAAAGAAATAG
ACAGCATGAGAGGGGATGAGGCAACCCGCTGCTCAGCTGTCAAGGCTCAGTCGCCAGCATTTCCCAACACAA
AGATTCTGACCTTAAATGCAACCATTTGAAACCCCTGTAGGCTCAGGTGAAGTCCAGATGCCACATG
AGCTCTGCTCCCTAAAGCCTCAAAACAAAGGCCATAATCTATGCTGTCTTAATTTCTTTCACTTAAG
TTAGTTCCTGAGACCCAGGCTGTAGGGGTTATTGGTGTAAAGTACTTTCATATTTAAACAGAGGA
TATCGGCTTTGTTCTTCTCTGAGGACAAGAGAAAGCCAGGTTCCACAGAGGACACAGAGAAGGT
TTGGGTGTCTCTGGGGTTCTTTTGCCAACTTCCCCACGTTAAAGGTGAACATTGGTCTTTCTATT
GCTTTGGAGTTTAAATCTCTAACAGTGGACAAAGTTACAGTGGCTTAAACTCTGTACACTTTTGGGA
AGTGAAGACTTGTAGTATGATAGGTTATTTGTATGTAAAGATGTTCTGGATACCATTATATGTTCCCCC
TGTTTCAGAGGCTCAGATTGTAAATGTAAATGTATGTCTCGCTACTATGATTAAATTTGAATATG
GTCTTTTGGTATGAATACTTTGCGACACAGCTGAGAGAGGCTGTCTGTTGTATTCATTGTGGTCAATAGC
ACCTAACACATTGTAGCCTCAATCGAGTGAGACAGACTAGAAGTTCCTAGTTGGCTTATGATAGCAAT
GGCCTCATGTCAAAATATTAGATGTAAATTTGTGTAAAGAAATACAGACTGGATGTACCACCAACTACTACC
TGTAATGACAGGCTGTCCAACACATCTCCCTTTCCATGCTGTGGTAGCCAGCATCGGAAGAAGCGTG
ATTTAAAGAGGTGAGCTTGGGAATTTTATTGACACAGTACCATTTAATGGGGAGACAAATGGGGCCA
GGGGAGGGAGAAGTTCTGTCTGTAAACAGAGTTTGGAAAGACTGGACTCTAAATTCGTTGATTAAAG
ATGACCTTTGTCTACCTTCAAAAGTTTGTGTGGCTTACCCCTCAGGCTCCAATTTTAAAGTGAAT
ATAACTAATAACATGTGAAGAATAGAGCTAAGGTTTAGATAAATATTGAGCAGATCTATAGGAAGAT
TGAACCTGAATATTGCCATTATGCTTACATGGTTTCCAAAAATGGTACTCCACATCTTCACTGAGGG
TAGATATTTCCTGTTGTCAAGAATAGCATTTGTAAGCATTTTGTAAATAAAGAAATAGCTTTAATGA
TAGCTGTAACTAAATTAATTTGTAAATGTATCAATACATTTAAACATTAAATATAATCTCTATAA
T

FIGURE 42

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CGGCGACAGCACCCCGGCACCTCCTCTCGGGCAGCTGCGCCTCGCAAGCGCAGTGGCCGACGGCAGCGCC
GAGTGGCTGTAGCTGCCCTGGSCGCGCTGCCGCCCTGCGCGGGCTGTGGGCTGTGGGCTCGGCCCGCCCT
GCTGGCCAGCTCTGCACGCGCTCGGGGCTCTCGGGCGCGGCTGCTCTCGACACGCTGTGGCGGGCGGCAT
GCAATACGGCGCGCATGTGTGGCCGAGATCGCTCCGACAGCTGAGGAGTGGTGGGTCCAGGTGGGGCTG
CTGGCGCTGGCCCTGCTTGTCTGCTGATCTGCACATCCCAACCCCTCAGCTCTCCCTGCCCTCACTCAT
CGGAATCTTCAGGCAAGTTTTCACTTACAAAGGACACTGGGTATCTTCTACCAAGACTCTGGGGTGTGGT
TGAAGTCTCAGAGATGATGTGTGTTTACACGGTTTCCACACATCCAGCTACGACTGGTACMAATTTGCG
AAGGCTCTGACCTTGTAGGTTTTCATCGGTGATTGCCCTTGATTTCTTAGGCTTTGGCTTCAGTGACAAAC
CGAGACCACTCACTATTTCATATTATAGCAAGCCAGCATCTGGAGAGCGCTTTTGGCGCATCTGGGGCT
CCGAGACCGCAGAAATCAACCTCTTCTCTCATGACTATGGAGATATTGTCTGCTCMATGGAGGTATCTTCCGT
TACAGCAGAAATGATCTGTGGCGGATACCATTAAGAGTCTCTGTCTGCMATGGAGGTATCTTCCGT
AGACTCACCGTCCACTGCTCTCTCCMAAGCTCATMAAGATGGAGGTGTGCTGTCAACCCATCTCACAGG
ACTGATGAACCTCTTTGTATTCTCTCGAGGTCTCACCCGATCTTTGGCGCTGTATCTCGGCCCTCTGAG
AGTGAAGCTGTGGGACGTGTGGCGAGGATCCGCAACATGACGGGMAATAGTCACTGACAGTCTCTTAC
AGTCATCAATCAGCAGGAGGAAGTTTCAGAAAGCGCTGGGTGGGAGCTCTTGCTCTGTAACTATCCCCAT
TCATTTATCTATGGGCCATTGGATCTCTGAATCCCTATCCAGAGTTTGGAGCTCTACAGGAAACG
CTGCGCGCGCTCCACAGTGTGCAATCTGGAATGCCACTTAGCCATCTACCAAGCTAGAGGATCCCTGG
GCTTCTGAATGCTATATGGGCTTCATCAACTCTCTCTGAGCTGGAAGAGTAGCTCTCCCTGTATTACC
TCCCTCACTCCCTTATGTGTTGTGATTCCACTTAGGAAGATGCCCAAGAGGCTCTGGCCATCAAA
CAATATCTCTCAAAAGTCCACTTTACTCMATTTGGTGAACAGTGTATAGGAAGACCCAGCAGAGCT
CTGACTAAGGTTGACATAATAGTCCACTCCCATCTTTGATATCTGATCAAATGTATAGACTTGCTGCT
TGTTTTGTGCTATTAGGAATCTGATGAGCACTACTACTGACTGACAGAGAGGCTCTTTTGGCA
TAAAGAGCTTTTTTAAACCTTTGGACTTCTCTGAAATATTTAGAAGTGCTAATTTCTGGCCCAACCCC
AACAGGAATCTATAGTAAAGGAGGAGAGAGGGGGCTCTCTCCCTCTCCATGACGTATGGGCA
CATGGCTTTTAAAGTCTTTTAAAGCAACAGAGCTGAGTCCCTTTGTATACCTTTGGATTTAGTGTT
TCATCAGCTGTTTTTAGTTATMAACATTTTGTATAATAGATATTTGTTTAAATGATACAGATTATAGG
TATGATTTTAAAGATGATTTACCTATACCTATATATATTTTAAAGACTCAACACAGATACCTCTT
ACCTCTGGCAGGTAGTAGCAATATAACAGGTTTGGTTCTGAATAAATGMACTAAATCCAACATTT
TTCTTAAATCAGAGCAATTAAAGCAACATGACTCTGCGCAGAGGCTCTGTTATTAGCTGGGAAG
NCCAATCTTACAGCAAAATAACGCTCTGAGACTCTCATACCTAGTGGTGAAGCAATGCTCTCTTGA
GCTACAGTAGAGGAGAGGAGATGTGTGTAGTCAAGTCACCATCTGATGTGATGATGATGCTCTTATG
ATGACTGCTTTAACTCCCACTGCTCTTGAAGAGAGGCTTCCCAATGATGACTAGTATGCTCTTATG
TACAGACAGGAAGTTTCAGAAATTTAGCAACAAACTTCCAAAGCACTATGACAAATGGTCTGAATA
CTTTTTTTTTAAAGCCACATTTCATGTCTAGTCAAGCAGGATTTAAGTGATTATTTAAATTCGT
TTTTTAAATAGCAACTTCAAGATTAAACAACTTTGAACCTGGAATAGTGTTTATTTCTATTATAAA
AATGAATGTGACAAAAAAGGCGG

FIGURE 43

CTCTGAGTGTCCAGTGGTCAGTTGCCAGGATGGGGACCACAGCCAGAGCAECCTTGGTCTTGACCTAT
TTGGCTGTGTGCTTCTGCTGCCTCTGAGGGAGGCTTCACGGCTACAGGACAGAGGCAGCTGAGGCCAGAGC
ACTTTCAGAAAGTTGGCTACGCAGCTCCCCCTCCCCACCCCTATCCCGAAGCCTCCCATGGATCACCC
TGACTCTCTCAGCATGGCCCTCCCTTTGAGGGACAGAGTCAAGTGCAGCCCTCCCTCTCAGSAGGCC
ACCCCTCTCCAAACAGGAAAGCTGCTACCTGCCAACTCCCTGCTGAAAGGAAGTGGGTCCCCCTCTCC
CTCAGGAAGCTGTCCCCCTCCAAAAGAGCTGCCCTCTCTCCAGCACCCCAATGAACAGAAGGAAGGAAC
GCCAGCTCCATTTGGGGACACAGCCATCCAGAACCTGAGTCC1GGAATGCAGGCCCAAGCACTGCCAACAG
SACCGGTCCCAAGGGGGCTGGGGCCACCGGCTGGATGGCTTCCCCCTGGGCGGCCCTTCTCCAGACAATC
TGAACCAATCTGCCTTCTTAACCGTCAGCATGTGTATATGGTCCCTGGAACCTACCCAGTCCAGCTA
CTCCACCTCACTCGCCAGGGTGAACCCCTCAATTTCTGGAGATTGATATTCCTGCTGTGCCACTGC
CGCACCCACACAAACCGCTAGAGTGTGCCAACTTGTGTGGGAGGAAGCAATGAGCCGATTCTGTGAGG
CCGAGTTCTCGGTCAAGACCCGACCCCACTGGTGTCCACGCGGGGAGGGCTCGGTTCTCTGCTT
CCAGGAGGAAGCTCCCCAGCCACACTACCAGCTCGGGGCTGCCCGAGCCATCAGCCTGATATTTCTCTG
GGTCTTGAGCTCCCTTCTCTCTGGGGTGCACATTGGACAATATCAAGAACATCTGCCACCTGAGGC
CTTCCGCTCTGTGCCACCGAACCTGCCAGCTACTGACCCCTACAAAGGGAGCTGCTGGCACTGATCCA
GCTGGAGAGGGACTTCCAGCGCTGCTGCCGCCAGGGGAACAATCACACCTGTACATGGAAGGCCCTGGGAG
GATACCTTGACAAATAGTGTGACCGGGAGTATGCTGTGAAGACCCACCACTTGATGTGCGGCCACC
CTCCAGCCCTACTCGGGATGAGTGCTTGGCGGTGGGGCTCTTACCCCAACTATGACCGGGACATCTT
GACCATGACATCAGTCCAGTCAACCCCAACCTCATGGGCCCTCTGTGGAAACCAAGAGTTCTCACC
AAGCATAAACATATCTGGGCTGATCCACAACATGACTGCCCGCTGCTGTGACCTGCCATTTCCAGAAC
AGCCCTGCTGTGCAGAGGAGGAGAAATTAACCTTCATCAATGATCTGTGTGGTCCCGACGTAACTCTG
GCGAGACCCCTGCCCTCTGCTGTACCTGAGTCTGGGATGAACAGGTCACTGCTTCAACATCAATTAT
CTGAGGAACGTGGCTCTAGTGTCTGGAGACACTGAGAACGCCAAGGGCCAGGGGAGCAGCGCTCAACTG
GAGGAACAAATATCAGCTCCACCTCTGAGCCCAAGGAAGAAATGATCACCCACAGCCCTAGAGGGTCAAG
ATG

FIGURE 44

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ACTACATATATAGSGCTCGAGCGGCCGCCCGGGCAGGTGGCCACCACCATCATCTAAAGAAGATAAACTTGG
CAUATGACATSGAGGTTCTTCAGGCAAGAAATATCGACAGAACTCTTCAAAGAGCCCTATCTTCAGATGTTT
CTGGAATACCTTTCAGAAATAGAAATGATTAATTCACAGAGATACCTAATCAAGAAATCCAGAAATCAGGA
CAGGAAGACATTTTGTGAGTTTTEGACCAATTGGACCAAAATACAAATGAAGTATTTCTGCTGTGTCTCTGGTTT
TGGCTGTCTCTGGGACAGAAATTTGGTGGGAAGCCCTCTCTCGACGTCTCAGATCCCCCGAGTTTCAGAGAGCGG
ATACAGCAGAGACGMAAAGAAATCGACGCCAACATATTTCTGTGCTTACGATGATCAAGATGTGGAGGCT
GGGCTCCCTGCAAGTCATGAACAAACGAGAAAGTATGSAACATGGGGGGGCCACCTATCATATGCTAT
TTGTCGATACCAACCAATTTGCTGCCCGTCAGGGTCTTCATGCTCACCGGAGTATGTGCACAATGCAT
GTCTACACACACAGAGAACTGCTCTCTCCCCCTGTGGCAGGCAATGATAGAGCTTCGACATTTTGTGT
ATATCTTAAACMACATTTGGCTACAGAACGCTCTTTTGTGAAATATCACTCAATGAATATAATGGCAGCTG
TCCGCTCTGGTGGCGAGATGGCTGGATTAACAGAAATCTGCTGTTCTATTAATTAACCTTTTGTGCG
AATGGCATACAAAGAAGCATGGTTTGAATATGCAAAGGACTACTTCACAGACTTAATCACTAACGAGAG
CATTAATTACTCAAAATGTCTAGAGAAATATTCCTCAATAGGCCGTTATGATGGTGTACGCCACGCTG
CGCCCAACGGCCCGAGGAGCTCAGCCGCAAGTTTCTAAAGTATACCCCAATGCTTCCCAACACATAACT
CCTAGTTATACATATGCACCAAAATATGGATAAACATGTGATATGCAATACAGCAAGTATGCTGCCCAT
CCACATGGAAATTTACAAATCTCTACAGCGCAAAAGGCTCCAGACTTTGATGTACAGTGGATGATTTCTGG
AGGGCTGTATTAATCTGCTGTGGAGACGGGGAGCTGGAGAACTACTTACTATTTTACACGGCGACCAT
GGTTACCATATTTGGGCAGTTTGGCATGTGTCAGGGGAAATPCATGCCATATGACTTTGATATTCGTGTGCC
TTTTTTTATTCGTCCCAAGTGTAGAACCAAGATCAATAGTCCCAAGATGCTTCTACACATTGACTTGG
CTCCACAGATCTGTGATATTTGCTGGGCTGCACACACCTCTCTGATGTGGAGCGCAAGTCTGTCTCAAACT
CTGACCCGACAGAGCGGATCAACAGGTTTCGAACAAACAGAAAGGCGCAAAATTTGGCTGTGATACATTTCT
AGTGGAAGAGGCAAAATTTCTACGTAAGAAGAGAAATCCAGCAGAAATATCCACAGCTCAAACTCACTTGC
CCAAATATAGAACGGGTCAAGAAACTATGCCAGACGCCAGGTTCAAGCAAGGTGTGAACACACCGGGGAC
AAGTGGCAATTCATTGAGGATACATCTGGCAAGCTTCGAATTCACAGATGTAAAGGACCCAGTGCAGCT
CAGACTCCGGCAGAGACCGGGAACCTCTACGCTCTCGCGCTTCCATGACAAAGACAAAGAGTGCAGTTGTA
GGAGATCTGTGTACCGTGCACAGCAAGGCCAAAGAAAGTCAACGGCAATCTTGAGAACACAGGAGGAT
CCAAATGACAAAGCCAGATTTGTCCATATCGGCAGACAGCTTCTTCTGCTCGAATTTGAGGTGAAAT
ATTATGACATACTTGGAAAGTGAAGAAGAAATTGCAGTCTTGCACCAAGAAATCTGTCTAAGCGCATG
ATGAAGGCCCAAGGAGGCAAGAGATCTCCAGGCTTCCAGTGGTGGCAGAGCGGCGAGGATGCTGGGCAT
AGCAGAACCGGCTGGGCCCACTACCACTTCGAGTGTGCAGTAGACAGATGTTTATTTCTCCCAATGACAT
TATCCATTGTGAGAGAGAACTGTACCAATCGGCCAGAGCTGGAGGNCATTAAGGCATATCAATTGACAAAG
AGATTGAAGAGCTCTGCAAGATAAAATTAAGAATTTAAGAGAGTGAAGACCATCTGAAGAGAGAGAGCT
GAGGAATGTAGCTAGTACAAACAAAGCTATTAACAATAAGAGCAAGGTTGATAAAAGCAAGAGAAATTAAG
GGGCATCTTCCACCAATCAAGAGGAGCTGTCTGAGGAATAGATACCAATGCACTTTCTGAGGAGAAACA
ACCTGAGGAGGAAG
CTCATTTGCTTACGCGATGACAAACCAACTGGCAGACAGCCCGCTTGTGAACCTGGGATCTTTCTGTGTC
TTGCAAGAGATCTTCAAAATACCACTCTCTGTTTGGCTAGAGCTTAATGAGACGATTAATTTCTTTCTGT
GTGAGTTTGTCTAGCTGCTTTTGGAGATTTTGTATATGAATACAGATCCCTATAGCCTCAACAAATCAGT
CACACGGTAGAACGAGGATTTTGAATCAGCTACAGCTACAACTATAGGAGCTCAGAGCTGTCAAGGATA
TAAGCAGCTGCAACCCAGAGACCTTGAAGATCTTGTATTTGAAATTAAGATGAGAGAGAGCTATGACATACCA
GAGGACAGTTATGAGATGATGGGAAGGTTTATCAGCCCCGTCTCACTGCAGACATCAACTGGCAAGGCT
AGAGGAGCTACACAGTGTGAATGAAGACATCTATGATGACAGCAAACTACAGACTTGTCTTGGTGGACT
GGATTAATTTGATGAGGATTTAGATAGAGTATTTGACGTCTGAGAGAGCTCATATGAGCAAAATAAACCA
ATAAGACCTCAATCTGCTCAAAGTACCGGTTCTTGGTTCTCTGCTGTAGCAGCGTGTCTATAGGAAAT
GGCCTCTGCTGACTCAGTGAAGACCCAGGCAATAAGTTGGGAAACACCTCATTTGACCTTGGCAGCTG
ACCTTCAAAGCCCTGATTTGACGCCAGCAAACTTAAGTCCAGAGATTAACCTGAATGGAATAACGACATT
CCAGAGGTTAATCAATTTGAATCTGAAACATGAGAAAGAACCAAAATGAGCAGGGGCTAGAGAGACTTAA
TCTATCGGAACCGATTTCAAGTGGCGATGGCATGGAGAGAGCTASAGCTCGGGCCGACCCCGACCTGCAGC
CCATTCGACAGGCACCCGAAAGAAATCTCCCAAGTATGGTGTGCTTGAAGAGCATTTTGAATACACTATA
TATCTCTCTGTGATCTCCGATGGAAATTCAGTTCTCAGATTTCCACATGGCCACCGCAGACCAAGAG
TAATTCAGCATAGCGGGAAGATGTGCACAGGTGGAGAAGATACAGAAAGAGAGATCAGAGCACC
TAGAAGAGAGCGGCTCTCTCTCACTCTCTCTCTGATAGATGAATCTACCTTACCTTACCTTAAACAGTATAT
TCTTTTAACTTTTATTTTGAAGCAATTAAGGTAATCAGGCCACCACTATCAAGGCTACCCCTGGGT
ACCTTTGTGCAGTAGAAGCTAGTGAGCATGTGACAGCAAGGGTGTGCACAGGAGACCTATCGTTTATCTAT
ACTATCTGCCAGAGATGAGAAAGGAGCTGGGAGATATTTGGTTGGCTTGGTTTGTATTTTGTGTGT
CTGTGTTTGTGATCAAAACGATTAATCTTTGAATATCGTAGGACATAGATATATACATGTTATCCAAAT

FIGURE 45A

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GAAGATGGCTAGAAATGGTGCCTTCTGAGTGTCTAAACTTGACACCCCTGGTAAATCTTCAACACACTT
CCACTGCCCTGCGTAATGAAGTTTGGATTCATTTTAACCACTGGAAATTTTCATGCCGTCATTTTCAGTT
AGATGATTTTGCACTTTTGAGATTAAATGCCATGCTATTTGATTAGTCTTATTTTTTATTTTACAGGC
TTATCAGTCTCAGCTGTTGGCTGTCTATTGTGACAAAGTCMAATAAACCCCCAAGGACGACACACAGTATGGA
TCACATATTGTTTGACATTAAAGCTTTTGCCAGAAATGTTGCATGTGTTTTACCTCGACTTGCTAAATCG
ATTAGCAGAAAGGCATGCCTAATAATGTTGTTGGTGAATAAATAAATAAGTAAACAAWRAARAWHGC
CTGCTCTCTCTGTGCCCTAGCCCTCAAAGCGTTCATCATACATCATACCTTTAAGATTGCTATATTTGGGTT
ATTTCTTGCACAGGAGAAAGATCTAAAGATCTTTATTTTCATCTTTTTGGTTTTCTTGGCATGACTA
AGAAGCTTAAATGTTGATAAAATATGACTAGTTTGAATTTACACCAAGAACTTCTCAATAAAGAAATC
ATGAATCCTCCCAATTTCAACATACCACAGAGAGTAAATTTCTTAACATTGTTCTATGATTATTTG
TAAGACCTTCACCAAGTTCTGATATCTTTAAAGACATAGTTCAAAATTCCTTTTGAATCTGATTTCTT
GAAATATCCTTGTGTGTATAGGTTTTAAATACCAGCTAAAGGATTACCTCACTGAGTCATCAGTACC
CTCCTATTAGCTCCCCAAGATGATGTTTTTGCCTACCCTAAGAGAGGTTTTCTTCTATTTTAGATA
ATTCAAGTGTCTAGATAAATTATGTTTTCTTAAGTGTATGTTAACTCTTTAAAGAAAATTTAATAT
GTTATAGCTGAATCTTTTSGTAACTTTAAATCTTATCATAGACTCTGTACATATGTTCAAAATAGCTGC
TTGCCCTGATGTGTATCATCGGTGGGATGACAGAACAAACATATTATGATCATGAATAATGTGCTTTGT
AAAAAGATTCAAGTTATTAGGAAGCATACTCTGTTTTTAATCATGTATAATATCCATGATACITTTAT
AGAACAATTTCTGGCTTCAGGAAGTCTAGAAGCAATATTTCTTCAATAAAGGTGTTTAACTTTAAAAA
AAAAAAAAAAAAAAAAAAAA

FIGURE 45B

CAAGAAATTCGGCAGCAGGGCGTGTCCAGAAGTCTGGATACTGTCAAGTAGTTAATTCTCAGCTGGCAGG"
TCCCCTGAGTGCAGCTGGCTCGATAGTCGTAATAAGAGAGTGTCGCGAAAGAGTTTGAATCCAGTATGAA
TGTATGACAGCGAAATTAATTTAACTCTAGGATCAGAGGAGTCCAGGAGCTGGCTCTCTGATATTCAA
TCATATTAAATATCTTACCCACCACTCAGAGGAGACCTTGTGGTGGCAGCCAGAATTTTTCTGTCCGGCG
TGTGGAACTCCAGTAGAGGCTAAGTTTGTAAAGCGGCTCCGGTACTCTGGCAATACCTGAGGGAATTTCTT
TGACTGCTGCCACTATATGCAAGAGCTGTGCATCTGCTGCCGAATCTGTATGTGGGAGTCAAGAAG
ACTAGCTGCAGCAATTTCTCCAAACAGCTGCTGCAGACGATATGGCACCAGCCCAATTTCAATTTGCTGAGC
ATCGGCCAAAGCTCTATCGGAAGCCGCAAGGAGCTGGACAGAGTGAAGGAATTCAGSAGCTTCTTCCA
TATCAAGAAGAGCTGTGAAGACCTGTAGGTTTCTCACTAGTGCATTAAAGAGAGTTCGAGCAGGTGCCGGCA
CACTTGACTGATGACTCCACCTGTCTCCCTTAGGACCTGGTCAGGATCAAGAAGGGCTCTGGCAGCTT
TACCTCAAGGACATTCTGAAGAGTTCCCTTGCACTATGTTCTGGCTGTAGCTGTCAAGGAAGAGGCTTT
ATTGTGGAATTTCCAGAAATGCGACTGTCTCTCCCAATTCAGACAGCAACATGTGCGAGGATCTCAGC
GTGCAAGGCTTCTGTTTCAACAAGACTGCTCCGAGCTCCGAGTGCGCCCGGTGTGCGAGGATCAGCGGA
GGCAGAAACCTTTGGAAGATGTGGCCCTTCGACGACATATGSCCCTGAGACTGTGAAAGAGCTGTT
AACATGCGCTTATGATAACACCGGATTGTGTCTATTATGTGTGATCTGTTTATGATATGGGATTTGATATA
TTAAGGAAAAGAGTGGTCTATATTCTCTTTATGCAATACTATAATGTTTCAAGAGATGCAGACTCTGTG
TTTAAGCAGAGGCTGAGTATGTGGTTTCTTTACAAATGTTCTGTTTTGGCTGCTATTGGTTTTTAA
GAGGTTTTTATACATTGTGATTGGAATAGTTATGTTTCACTAGCTGTCGAGCGGATTTGTATGTGTGCA
TATATGTGAAGCTGTAACTGACAGTGAATGAAATCTACGTTTCTCTTCTAAAGGTTGTTTATGTAAGCT
GTGGTGCTTTCAAGTGMMAAAWATATGACCCCAAAAAAAGCAATGCGAGGTTG
CTAATCTCTGAGGCTCGTGTGGCGGCTCGGGCTCTGCTCTCGGAGCAGCAATGGSCGACAAAGGAGAA
CGAGGCGCTGCGCCCAAGCTTGTCTGACGCGCAACCCGG

FIGURE 46

GGAAATTATAGATCTTCATATTGAATCCATCAGTGATTCAAGAGATACACCTATTTCGCCATAAACACACCTA
ACATGTATATGGTTATGGAATCATGTCTGTGGATAGGTTCTTAGAGACCTGTTCCTCAAACTCTGCACACGTT
TTCACAGGTGGGCTTATGTACTTGCACCGTTGGGCAGATATCCAGATTACCTAAGATTGGGTAAAAAAGT
CATCTGTGCATTTGCTGGCAGGGCATTTGCTAAGTGGAGTACAGGATCAAAAGAGGTTTCTTAGAAGGG
CAATATTGTCCAATGGAATTAAGCACAAGGAATCTGGGTAGAGGCATCTGCACAAAACTGGTGAGACCTA
CTCTCCACTCTCTGCAGCTGGATGGCTGATGGCAGGCTGAGGCAGTGGGGAGCGAGSTTTAAGCNCAGGG
ATGTCCTCCAGGTCATGATATTAGTAGAGAAACATAAAACATAGTCTCTTACATCTCCGAGGTACGCCCTT
CTCTCTTCTTTATAATATGAATATGCAATGCGAGCTTTGTGAAAGCGAGGTCATCATGTACCAATGGCTTTA
TACCCATCATCATGATGATTTTTAGCATGGTCAGAACTTGTGAATATGTCCTTAGATGATTTTGG
GGAGATGTGATTTATTTTCATATTTTCAAAATGCATTTTCATTCATATGTCATTTATTTGAGCACCC
GAAATAAAAAAATAAAAAA

FIGURE 47

AATTTTGGCCCCCTCCGAGGCCCAAGAAATTTCCGGCCACCGANGGAATTTTGGTACCCACCCAGGGGG
 GGAATGGAAATGCTGCTTTTCAAAACTTAGTTTCCTTCCATTTTCTCCTAGTCTGGCCCTTGACACAAAT
 CTGGTAGAAAGAGCCTATAAATTGAGGGCAGTTGTACCCCTCCCTGTGCCCCAGAGGTTCTTGGAGAG
 AAGTGCAAGAAATTTGTAACACGGCCGTGAGGGCCGCTGATGGCCATGGGCTGGCCCTCCGTATCAGGC
 CTGCTCACCTTGCTGGGAGCTTTATTCGTATCTCATTTCGAATGTCCAGAGGGAGCATCAAGAGGCCA
 CAGCTCCGATTTCCAAAGAGTGATATTGACATTTATGGAGATTGGTGTGTAACATATTTTGATAAACTACT
 AACTTATTTTGGTGGGCTTTGGTTGTCTCTGTCTTAGGACCTGGTAGTTATTTGCTTGATTTTTTTTTC
 CGTTATTTTCTACATAGGCCAAAGAGAATTCGAGGGATAGACAGTCTCCAAAGAAAAGTGAAGTGGTGGGAGA
 GAAATGCTTTTCTTTTCTTTTCTCTAGTTTCTTTCTGGCTGAGATTTCCTGGCAAGACAGCAC
 CCAATAGACTATTAGAGTTGACATTTGACATTTAATGGGCGCCATGGCTCATTTTGTAGATTGAGAAGG
 TGGCTCTCCCTGCTCCAGTCTCATCATGACAGCGTGTGACAGCTGGGAGTCTGTGGCCTTCCTCACGC
 AGAGGCTTAAAGCTGGACACAAAGCACGCCCTAGGCTGGGAGGGATGGGACCCATGCCCTCTCTTAGA
 GAGCGGGCTTCTGGTTAGGAAAGGACAGCGTGGGGTGCTTGCAATAAGTTCACTGGTCACCGTGGCTT
 TATGAGTAGTGTITTTGTGCACTTGCCAGGGTTTCTCTCTGTGTGGGAGGGAGTGATTAAGCAATGG
 TGTCTGGAGTAGGCTTACAATTTAATAGACTTTTCTTATCATATCCCTCATTCTTCTCCCTGAATAA
 AATATACACACAGCAAAAGAAATATGATAGTTTACATCTCTTAGTTCCTTGGCCAAACAGAAATATCT
 TAGTTCACCTGGCCAGGATTTTCTACATAGTCAGAACTTACACATTACTAGAGGACACCCACCCAGGAG
 TATTGTGCTACTTTTATCTGTGACCCAGCCACAAATACCCACATTGGAAAGACCCATTGTGATGGGTAA
 ACATCTCTCTGCTGCCACACACCCCTGTGACTGCCCTGCTGTGTGTGATGACCTCCGAGGGCCCTAAT
 CATGAAGCAGCAAAACCCAGCAGATCTCCACCCCTGCTCAGGACCTCTGCTGAAGAGGGGATGAAGTG
 GGTCTCCAGGGAGGCAUTGGGGGCTTGTGGCAGCTGGCTCGGGAGCCGGCTTACAGGAGGGCAGCTCTG
 CAGTTGGGAGGGGACCCGTCCGGAGGAGACAGGCCCTTACACACCCCTCTACTTATCATCCCTGCT
 CACACACCCCTTGTCCAGGCTTTATGCAATCGGATTTATTTTCCAAATCGAGAGGACAGTGATAGATGCA
 TTTCCCCAGGCTGTCTCAGAAAGGTCCTAAATGTATAGTGTGTGAGAAATGCTGAGATCTCCCCCACT
 TTTGGTTTTTGCAGCAGTAAAACTCTTTCCACTGTGACTTATTTTCTCTCTCAGGACCCAGCCACTGG
 TCCCTTGTGCTGACTCTAGCACAGTGGCCAGGATCCAATACGAGTCCAGGGGTGACCCGAGGATGGTGGG
 GCAGCGGGCTTCTCAGCTACCCAGCCACCAAGGCCCTGACGCACTGCTCCTGCACTTACAGCAGATCC
 CTGTGCAAGCTGGAGGGGTGATGGCCCGCTCAGCTTTGTTCAGATGGGTGGAAACGCTGATGATACAG
 CTCTCTCCCTGCCGTGCCCTGCCACGGAGCAGGCATTGTGAACCTGGCTGGTGTTCAGTCCACGTTGGCA
 TGGCTCCAGCCCAACCCACAGTGGAGACTGGAGACAGGCAATGAGTCTGGTGGGGGACGTTGGACATG
 CCCCATAGGGGCCCCACCCAGACTTAACAGGCAAGGTCTGGGCATTGCCGACGAGGACTCAATGCTAA
 ACCAAGCCTGCTGCTCTGTGCCAGGGCCCTCTCTGATTTACACATCCATTTTACACAGACCCCTTC
 CTCTTAATAAAGGCTGACAGTCTGTGTGGCAGCCAGAACCCACACCATGAAGACAGGGAGTGGGGGCC
 TTTGTGCCCAACTCCAGCACAGCTGCGTCTGGGGTGTGTGAGAGGCAATGTCGTCTGTGGCTGGTGG
 TCTCTGTGAGACAGTTCCGAGGACGGGAAATTCAGGGGTGGTGGGGGCGTGAGGCTTATATGTGGAAGTGA
 TGCAGAGTTCCGCTGCAAGCGGATCTGGATATACACTATGTATAATTGTTACGTTGTAATTTAAATATATC
 TGTTCGCCATCGTCATGAGAAGATTATATGAAGGCTCTGAAGGGAGAGGAGATGTACATTTCTGCCAGGC
 TCCTGGGCACTTAICGAGTCAATGAATGTGACTGTTGATCCAGTGGTGAAGAGCTACACTCCATG
 TGTCACTACGCTTATGACTCTAATGTATTTTAAGGCAAAATGTACCCGACTCCATCTTCAACCCCTC
 GATTCTCGAGTCCAGCCTTTCTGTGCCAGTGTCTACTGAGCCACACGCTCTCGCCATCGGGACCCGGC
 TGGGCTCGAGTCTCGGGGCACAGTTGCCATGGAGCCCTCCTGGGTCTTCAAAATGTGCTGAGTGCCA
 GCTGAATAACCCACAGGAGATGAGTACCTTGGCCAGCTTAAGAGAAAGATTTTCTCAGGGTATTTATTA
 GTGTGTCCAGCAGGGTCAGGAAGCAGGATGGAAGATGCATTACAGCTGTTAATTTATTAACAGGCAAA
 GATTTTGTGTTTCTGTGATGACAGACTATTAAGTTTGGGACTTATTTCCCATTTGAGAAGTTATAATATAT
 ATTTAAGATGATAAGTTTCTGCTTAAGTTTGTGCTTTTCAAGCTTCAATGAGTTTAAGGAGCACTAAGGGTA
 ATGATACCAATGAGGGTTGGTTTATATCAACCTGAATAGCTGTGGTTTCTCCAGTAAATATTTTCTCT
 ACTGAACATGGAGCCATTAATGAAGTGTGTGTTTTTATATGTACATTTGTATATTTTGTGCTTGT
 TGAATGTTCTATTTTCTAATAGTTTCTTTTGTGTTTAAAGTTGTGATAGTATAGATTAGATTCTGATGC
 TAACTGCAAAATCAGGTTGCTCTGCTGGGTCTCTCTGCTTTTATTTTACTTAAAGGACAGTGTAGTTG
 TGGTCCACCACTTTCAAAATGTGAAGTGGCTGCCCTCCCTTTTGTGCTGACACACTGTGTATCTG
 ACCACTTCTTACCATCTTTATGTGTAAATCAAACTCTTTGTGGTACATTTATCTCATGCTTCTGCAAA
 TTCGANTAAATCTATGGCTTCCAAAAAAGAAAAAAGAAAAA

FIGURE 48

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